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(54) Title: METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MOD-**ULATORS OF LUNG CANCER**

(57) Abstract: Described herein are methods and compositions that can be used for diagnosis and treatment of lung cancer and similar pathologies. Also described herein are methods that can be used to identify modulators of lung cancer and similar pathologies.

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METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF LUNG CANCER

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CROSS-REFERENCES TO RELATED APPLICATIONS

This application is related to USSN 60/284,770, filed April 18, 2001; USSN 60/290,492, filed May 10, 2001; USSN 60/334,370, filed November 29, 2001; USSN 60/339,245, filed November 9, 2001; USSN 60/350,666, filed November 13, 2001; and USSN 60/xxx,xxx, filed April 12, 2002 (Docket OMNI-002P); each of which is incorporated herein by reference in its entirety.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in lung cancer; and to the use of such expression profiles and compositions in diagnosis and therapy of lung cancer. The invention further relates to methods for identifying and using agents and/or targets that inhibit lung cancer or related conditions.

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BACKGROUND OF THE INVENTION

Lung cancer is the second most commonly occurring cancer in the United States and is the leading cause of cancer-related death. It is estimated that there are over 160,000 new cases of lung cancer in the United States every year. Of those who are diagnosed with lung cancer, 86 percent will die within five years. Lung cancer is the most common visceral cancer in men and accounts for nearly one third of all cancer deaths in both men and women. In fact, lung cancer accounts for 7% of all deaths, due to any cause, in both men and women.

Smoking is the primary cause of lung cancer, with more than 80% of lung cancers resulting from smoking. About 400 to 500 separate gaseous substances are present in the smoke of a non-filter cigarette. The most noteworthy substances include nitrogen oxides, hydrogen cyanide, formaldehyde, benzene, and toluene. The particles present in cigarette smoke contain at least 3,500 individual compounds such as nicotine, tobacco alkaloids (nomicotine, anatabine, anabasine), polycyclic aromatic hydrocarbons (e.g., benzo(a)pyrene, B(a)P), naphthalenes, aromatic amines, phenols, and tobacco-specific nitrosamines.

Tobacco-specific nitrosamines are formed during tobacco curing and processing, and are suspected of causing lung cancer in humans. In rodent studies, regardless of the where or how it is applied, the tobacco-specific nitrosamine known as NNK produces lung adenomas and lung adenocarcinomas. The tobacco-specific nitrosamine known as NNAL also produces lung adenocarcinomas in rodents.

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Many of the chemicals found in cigarette smoke also affect the nonsmoker inhaling "secondhand" or sidestream smoke. Indeed, the smoke inhaled by non-smokers has a chemical composition similar to the smoke inhaled by smokers, but, importantly, the concentrations of the carcinogenic tobacco-specific nitrosamines are present in higher concentrations in second hand smoke. For this and other reasons, "passive smoking" is an important cause of lung cancer, causing as many as 3,000 lung cancer deaths in nonsmokers each year.

In addition to smoking, other factors thought to be causes of lung cancer include onthe-job exposure to carcinogens such as asbestos and uranium, exposure to chemical hazards such as radon, polycyclic aromatic hydrocarbons, chromium, nickel, and inorganic arsenic, genetic factors, and diet.

Histological classification of various lung cancers define the types of cancer that begin in the lung. See, e.g., Travis, et al. (1999) Histological Typing of Lung and Pleural Tumours (International Histological Classification of Tumours, No 1. Four major cell types make up more than 88% of all primary lung neoplasms. These are: squamous or epidermoid carcinoma, small cell (also called oat cell) carcinoma, adenocarcinoma, and large cell (also called large cell anaplastic) carcinoma. The remainder include undifferentiated carcinomas, carcinoids, bronchial gland tumors, and other rarer types. The various cell types have different natural histories and responses to therapy, and, thus, a correct histologic diagnosis is the first step of effective treatment.

Small cell lung cancer (SCLC) accounts for 18-25% of all lung cancers, and occurs less frequently than non-small cell lung cancers, and generally spread to distant organs more rapidly than non-small cell lung cancer. In general, at the time of presentation small cell lung cancers have already spread beyond the beyond the bounds where surgery and curative intent can be undertaken. Hoever, if identified early enough, these cancers are often responsive to chemotherapy and thoracic radiation treatment.

Non-small cell lung cancers (NSCLC) are the more frequently occurring form of lung cancer. They comprise squamous cell carcinoma, adenocarcinoma, and large cell carcinoma

WO 02/086443 PCT/US02/12476 and account for more than 75% of all lung cancers. Non-small cell tumors that are localized

and account for more than 75% of all lung cancers. Non-small cell tumors that are localized at the time of presentation can sometimes be cured with surgery and/or radiotherapy, but usually are not identified until significant metastasis has occurred, which are typically not very responsive to surgical, chemotherapy, or radiation treatment..

The screening of asymptomatic persons at high risk for lung cancer has often proven ineffective. In general, only 5 to 15 percent of lung cancer patients have their disease detected while they are asymptomatic. Of course, early detection and treatment are critical factors in the fight against lung cancer. The average survival rate is 49% for those whose cancer is detected early, before the cancer has spread from the lung. Lung cancer often spreads outside of the lung, and it may have spread to the bones or brain by the time it is diagnosed. While the prognosis may be better for lung cancers that are detected early, because of the lack of effective curative treatments, early detection does not necessarily alter the total death rate from lung cancer.

Thus, methods for diagnosis and prognosis of lung cancer and effective treatment of lung cancer would be desirable. Accordingly, provided herein are methods that can be used in diagnosis and prognosis of lung cancer. Further provided are methods that can be used to screen candidate therapeutic agents for the ability to modulate, e.g., treat, lung cancer. Additionally, provided herein are molecular targets and compositions for therapeutic intervention in lung disease and other metastatic cancers.

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SUMMARY OF THE INVENTION

The present invention provides nucleotide sequences of genes that are up- and down-regulated in lung cancer cells. Such genes are useful for diagnostic purposes, and also as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. The methods of detecting nucleic acids of the invention or their encoded proteins can be used for a number of purposes. Examples include early detection of lung cancers, monitoring and early detection of relapse following treatment of lung cancers, monitoring response to therapy of lung cancers, determining prognosis of lung cancers, directing therapy of lung cancers, selecting patients for postoperative chemotherapy or radiation therapy, selecting therapy, determining tumor prognosis, treatment, or response to treatment, and early detection of precancerous lesions of the lung. Examples of benign or precancerous lesions include: atelectasis, emphysema, brochitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis (HP), interstitial pulmonary fibrosis (IPF), asthma, and

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bronchiectasis. Other aspects of the invention will become apparent to the skilled artisan by

bronchiectasis. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

In one aspect, the present invention provides a method of detecting a lung cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16. Alternatively, the sample may be contacted with a specific binding reagent, e.g., antibody.

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In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-16. In another embodiment, the polynucleotide comprises a sequence as shown in Tables 1A-16.

In one embodiment, the biological sample is a tissue sample, or a body fluid. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label. In one embodiment, the polynucleotide is immobilized on a solid surface. In one embodiment, the patient is undergoing a therapeutic regimen to treat lung cancer. In another embodiment, the patient is suspected of having lung cancer. In one embodiment, the patient is a primate, e.g., a human.

In one embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy. Or the sample may be evaluated for protein, e.g., contacting the sample with an antibody.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated transcript to a level of the lung cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. Or the sample may be evaluated for comparison of protein.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a

biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated antibody in the biological sample by contacting the biological sample with a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, wherein the polypeptide specifically binds to the lung cancer-associated antibody, thereby monitoring the efficacy of the therapy.

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In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated antibody to a level of the lung cancer-associated antibody in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated polypeptide in the biological sample by contacting the biological sample with an antibody, wherein the antibody specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated polypeptide to a level of the lung cancer-associated polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1A-16. In one embodiment, an expression vector or cell comprises the isolated nucleic acid. In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16. In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical. In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting lung cancer in a a patient, the method comprising contacting a biological sample from the patient with an antibody or protein as described herein.

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In another aspect, the present invention provides a method of detecting antibodies specific to a lung cancer gene in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprises a sequence from Tables 1A-16.

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In another aspect, the present invention provides a method for identifying a compound that modulates a lung cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a lung cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16; and (ii) determining the functional effect of the compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect. In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant. In one embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation or another critical process of a lung cancer-associated cell to treat lung cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein. In one embodiment, the compound is an antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having lung cancer or a cell isolated therefrom; (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of lung cancer.

In one embodiment, the control is a mammal with lung cancer or a cell therefrom that has not been treated with the test compound. In another embodiment, the control is a normal cell or mammal, or a non-malignant lung disease.

In another aspect, the present invention provides a method for treating a mammal having lung cancer comprising administering a compound identified by the assay described herein.

In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having lung cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

DETAILED DESCRIPTION OF THE INVENTION

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In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and treatment of lung disease or cancer, as well as methods for screening for compositions which modulate lung cancer. "Treatment, monitoring, detection or modulation of lung disease or cancer" includes treatment, monitoring, detection, or modulation of lung disease in those patients who have lung disease (whether malignant or non-malignant, e.g., emphysema, bronchitis, or fibrosis) as well as patients with lung cancers in which gene expression from a gene in Tables 1A-16 is increased or decreased, indicating that the subject is more likely to have disease. In particular, while these targets are identified primarily from lung cancer samples, these same targets are likely to be similarly found in analyses of other medical conditions. These other conditions may result from similar pathological processes which affect similar tissues, e.g., lung cancer, small cell lung carcinoma (oat cell carcinoma), non-small cell carcinomas (e.g., squamous cell carcinoma, adenocarcinoma, large cell lung carcinoma, carcinoid, granulomatous), fibrosis (idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), interstitial pneumonitis, nonspecific idiopathic pneumonitis (NSIP)), chronic obstructive pulmonary disease (COPD, e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, and esophageal cancer. See, e.g., the NCI webpage and USSN 60/347,349 and USSN 60/xxx,xxx (docket LFBR-001-1P, filed March 29, 2002), each of which is incorporated herein by reference. The treatment may be of lung cancer or related condition itself, or treatment of metastasis.

In particular, identification of markers selectively expressed on these cancers allows for use of that expression in diagnostic, prognostic, or therapeutic methods. As such, the invention defines various compositions, e.g., nucleic acids, polypeptides, antibodies, and small molecule agonists/antagonists, which will be useful to selectively identify those markers. For example, therapeutic methods may take the form of protein therapeutics which use the marker expression for selective localization or modulation of function (for those markers which have a causative disease effect), for vaccines, identification of binding partners, or antagonism, e.g., using antisense or RNAi. The markers may be useful for molecular characterization of subsets of lung diseases, which subsets may actually require

very different treatments. Moreover, the markers may also be important in related diseases to the specific cancers, e.g., which affect similar tissues in non-malignant diseases, or have similar mechanisms of induction/maintenance. Metastatic processes or characteristics may also be targeted. Diagnostic and prognostic uses are made available, e.g., to subset related but distinct diseases, or to determine treatment strategy. The detection methods may be based upon nucleic acid, e.g., PCR or hybridization techniques, or protein, e.g., ELISA, imaging, IHC, etc. The diagnosis may be qualitative or quantitative, and may detect increases or decreases in expression levels.

Tables 1A-16 provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in lung cancer samples. The tables also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster. In Table 1A, genes marked as "target 1" or "target 2" are particularly useful as therapeutic targets. Genes marked as "target 3" are particularly useful as diagnostic markers. Genes marked as "chron" are upregulated in chronically diseased lung (e.g., emphysema, bronchitis, fibrosis) relative to lung tumors and normal tissue. In certain analyses, the ratio for the "chron" category was determined using the 70th percentile of chronically diseases lung samples divided by the 90th percentile of lung tumor samples divided by the 90th percentile of lung tumor samples divided by the 90th percentile of normal lung samples.

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Definitions

The term "lung cancer protein" or "lung cancer polynucleotide" or "lung cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologs that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1A-16 and conservatively modified variants thereof; or (4)

have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "lung cancer polypeptide" and a "lung cancer polynucleotide," include both naturally occurring or recombinant forms.

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A "full length" lung cancer protein or nucleic acid refers to a lung cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains the elements normally contained in one or more naturally occurring, wild type lung cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translational processing or splicing, including alternative splicing.

"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a lung cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, archival materials, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or other mammal; or a bird; reptile; fish. Livestock and domestic animals are of interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues or materials, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the

same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using, e.g., a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site http://www.ncbi.nlm.nih.gov/BLAST/ or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions and/or insertions, substitutions, and naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer

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Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) <u>Current Protocols in Molecular Biology</u>.

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Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) <u>Proc. Nat'l. Acad. Sci. USA</u> 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between

two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be negative large numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

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An indication that two nucleic acid sequences are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells *in vivo*, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least about 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant or component from the composition to be purified.

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In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymer.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refer to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain some basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refer to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that function similarly to another amino acid.

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Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU each encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of

conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally similar molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions include for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton, Proteins (1984)).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts, et al. (1994) Molecular Biology of the Cell (3rd ed.) and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50 or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, 5 etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have at least one different linkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or Omethylphophoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford University Press); and peptide nucleic acid backbones and 10 linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, in Sanghui and Cook, eds. Carbohydrate Modifications in Antisense Research, ASC Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. 15 Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made. 20

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

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The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary

strand; thus the sequences described herein also provide the complement of the sequence.

The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, physiological, chemical, or other physical means. For example, useful labels include ³²P, fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The labels may be incorporated into the cancer nucleic acids, proteins, and antibodies. Many methods known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter, et al. (1962) Nature 144:945; David, et al. (1974) Biochemistry 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth., 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope tags, a toxin; activatable moieties, a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting "hard" e.g., beta radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method

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using high affinity interactions may achieve the same results where one of a pair of binding
partners binds to the other, e.g., biotin, streptavidin.

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As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, e.g., through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, preferably one that does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled, e.g., with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e., using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered

WO 02/086443 PCT/US02/12476 recombinant for the purposes of the invention. Similarly, a "recombinant protein" is a protein made using recombinant techniques, i.e., through the expression of a recombinant nucleic acid as depicted above.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

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A "promoter" is typically an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed in operable linkage to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule selectively to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to essentially no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in ٠5 "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Techniques in Biochemistry and Molecular Biology-Hybridization with Nucleic Probes (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) 10 at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m, 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., 15 10 to 50 nucleotides) and at least about 60° C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions are often: 50% formamide, 5x SSC, and 1% 20 SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32° C and 48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50° C 25 to about 65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90° C - 95° C for 0.5 - 2 min., an annealing phase lasting 0.5 - 2 min., and an extension phase of about 72° C for 1 - 2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis, et al.(1990) PCR Protocols, A Guide to Methods and 30 Applications.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This

WO 02/086443 PCT/US02/12476 occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy

occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous reference, e.g., Ausubel, et al. (ed.) Current Protocols in Molecular Biology Lippincott.

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a lung cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the lung cancer protein or nucleic acid, e.g., a physiological, enzymatic, functional, physical, or chemical effect, such as the ability to decrease lung cancer. It includes ligand binding activity; cell viability, cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein expression in cells undergoing metastasis, and other characteristics of lung cancer cells. "Functional effects" include *in vitro*, *in vivo*, and *ex vivo* activities.

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By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a lung cancer protein sequence, e.g., physiological, functional, enzymatic, physical, or chemical effects. Such functional effects can be measured by many means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the lung cancer protein; measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation. Determination of the functional effect of a compound on lung cancer can also be performed using lung cancer assays known to those of skill in the art such as an *in vitro* assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein

expression in cells undergoing metastasis, and other characteristics of lung cancer cells. The functional effects can be evaluated by many means known to those skilled in the art, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for lung cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β-gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

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"Inhibitors", "activators", and "modulators" of lung cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of lung cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of lung cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may seem to inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate lung cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of lung cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules and the like. Such assays for inhibitors and activators include, e.g., expressing the lung cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of lung cancer can also be identified by incubating lung cancer cells with the test compound and determining increases or decreases in the expression of 1 or more lung cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50 or more lung cancer proteins, such as lung cancer proteins encoded by the sequences set out in Tables 1A-16.

Samples or assays comprising lung cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a lung cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more

WO 02/086443 PCT/US02/12476 preferably 200-500% (i.e., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics *in vitro* or *in vivo*, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., Freshney (1994) <u>Culture of Animal Cells a Manual of Basic Technique pp. 231-241</u> (3rd ed.).

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

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"Cancer cells," "transformed" cells, or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy (see, Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (3rd ed.)).

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul, Fundamental Immunology.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible

WO 02/086443 PCT/US02/12476 for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce F(ab)'2, a dimer of Fab which itself is a light chain joined to V_H-C_H1 by a disulfide bond. The F(ab)'2 may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the F(ab)'2 dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see Paul (ed. 1999) Fundamental Immunology (4th ed.). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized *de novo* either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized *de novo* using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty, et al. (1990) Nature 348:552-554).

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many technique known in the art can be used (see, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. (1985), pp. 77-96 in Monoclonal Antibodies and Cancer Therapy; Coligan (1991 and supplements) Current Protocols in Immunology; Harlow and Lane (1988) Antibodies, A Laboratory Manual; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.)). Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens (see, e.g., McCafferty, et al. (1990) Nature 348:552-554; Marks, et al. (1992) Biotechnology 10:779-783).

A "chimeric antibody" is an antibody molecule in which, e.g, (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the

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variable region, or a portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

Identification of lung cancer-associated sequences

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In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different lung cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of lung cancer (chronic disease, adenocarcinoma, etc.)

The identification of sequences that are differentially expressed in lung cancer versus non-lung cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to downregulate lung cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, a treatment step may induce other markers which may be used as targets to destroy tumor cells. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Malignant diseasemay be compared to non-malignant conditions. Metastatic tissue can also be analyzed to determine the stage of lung cancer in the tissue, or origin of primary tumor, e.g., metastasis from a remote primary site. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the lung cancer expression profile. This may be done by making biochips comprising sets of the important lung cancer genes, which can then be used in these screens. PCR methods may be applied with selected primer pairs, and analysis may be of RNA or of genomic sequences. These methods can also be done on the protein basis; that is, protein expression levels of the lung cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the lung cancer

nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the lung cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs or as protein or DNA vaccines.

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Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in lung cancer relative to normal tissues and/or non-malignant lung disease, or in different types of lung disease, herein termed "lung cancer sequences." As outlined below, lung cancer sequences include those that are up-regulated (i.e., expressed at a higher level) in lung cancer, as well as those that are down-regulated (i.e., expressed at a lower level). In a preferred embodiment, the lung cancer sequences are from humans; however, as will be appreciated by those in the art, lung cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other lung cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (dogs, cats, etc.). Lung cancer sequences from other organisms may be obtained using the techniques outlined below.

Lung cancer sequences can include both nucleic acid and amino acid sequences. As will be appreciated by those in the art and is more fully outlined below, lung cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the lung cancer sequences can be generated.

A lung cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the lung cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, e.g., using homology programs or hybridization conditions.

For identifying lung cancer-associated sequences, the lung cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, cancer and non-malignant conditions, non-malignant conditions and normal tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing lung cancer samples with metastatic cancer samples from other cancers, such as, breast, other gastrointestinal cancers, prostate, ovarian,

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etc. Samples of, non metastatic disease tissue and tissue undergoing metastasis are applied to

biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix, Santa Clara, CA. Gene expression profiles as described herein are generated and the data analyzed.

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In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal lung, but also including, and not limited to colon, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the lung cancer screen that are expressed in significant amounts in other tissues (e.g., essential organs) are removed from the profile, although in some embodiments, this is not necessary (e.g., where organs may be dispensible at a later stage of life). That is, when screening for drugs, it is usually preferable that the target expression be disease specific, to minimize possible side effects on other organs.

In a preferred embodiment, lung cancer sequences are those that are up-regulated in lung cancer; that is, the expression of these genes is higher in cancerous tissue than in normal lung or other tissue. "Up-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater. Another embodiment is directed to sequences up-regulated in nonmalignant conditions relative to normal. Unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, DA, et al (1998) Nucleic Acids Research 26:1-7 and http://www.ncbi.nlm.nih.gov/. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, such as FGENESH (Salamov and Solovyev (2000) Genome Res. 10:516-522). In other situations, sequences have been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, lung cancer sequences are those that are downregulated in the lung cancer, that is, the expression of these genes is lower in cancerous tissue

or normal lung or other tissue. "Down-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater, or, when the ratio is presented as a number less than one, that the ratio is less than one, preferably 0.5 or less, more preferably 0.25 or less.

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Informatics

The ability to identify genes that are over or under expressed in lung cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with lung cancer. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (1998) Pharmaceutical Proteomics: Targets,

Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA (June 11-12, 1998)). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

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Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for assay data acquired using an assay of the invention.

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The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample representing lung cancer, i.e., the identification of lung cancer-associated sequences described herein, provide an abundance of information, which can be correlated with

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pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, genedisease causal linkages, identification of correlates of immunity and physiological status,
among others. Although the data generated from the assays of the invention is suited for
manual review and analysis, in a preferred embodiment, data processing using high-speed
computers is utilized.

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An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing 10 information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity 15 between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multidimensional database comprising a functionality for multi-dimensional data analysis 20 described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as 25 the merger of two or more such tree structures.

See also Mount, et al. (2001) Bioinformatics; Durbin, et al. (eds., 1999) Biological

Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids (; Baxevanis and

Oeullette (eds., 1998) Bioinformatics: A Practical Guide to the Analysis of Genes and

Proteins); Rashidi and Buehler (1999) Bioinformatics: Basic Applications in Biological

Science and Medicine; Setubal, et al. (eds 1997) Introduction to Computational Molecular

Biology; Misener and Krawetz (eds, 2000) Bioinformatics: Methods and Protocols; Higgins and Taylor (eds., 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical

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Approach; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the

Internet; Han and Kamber (2000) Data Mining: Concepts and Techniques (2000); and

Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

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In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for lung cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may

be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

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The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results.

Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC,

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MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

Characteristics of lung cancer-associated proteins

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Lung cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In one embodiment, the lung cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes (see, e.g., Alberts (ed. 1994) Molecular Biology of the Cell (3d ed.). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2

domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden (see, e.g., Bateman, et al (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420; Bateman, et al. (1999) Nuc. Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-322).

In another embodiment, the lung cancer sequences are transmembrane proteins.

Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels, pumps, and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the

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localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site http://psort.nibb.ac.jp/).

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, hormones, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they may mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains may also associate with the extracellular matrix and contribute to the maintenance of the cell

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structure.

Lung cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for extracellular immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins in situ or in histological analysis. Alternatively, antibodies can also label intracellular proteins, in which case analytical samples are typically permeablized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful lung markers of disease.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the lung cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit

signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, sax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Lung cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.

Use of lung cancer nucleic acids

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As described above, lung cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the lung cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

The lung cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1A-16, can be fragments of larger genes, i.e., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the lung cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, et al., *supra*. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, http://www.ncbi.nlm.nih.gov/UniGene/).

Once a lung cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire lung cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant lung cancer nucleic acid can be further-used as a probe to identify and isolate

other lung cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant lung cancer nucleic acids and proteins.

The lung cancer nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the lung cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, RNAi, vaccine, and/or antisense applications. Alternatively, the lung cancer nucleic acids that include coding regions of lung cancer proteins can be put into expression vectors for the expression of lung cancer proteins, again for screening purposes or for administration to a patient.

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In a preferred embodiment, nucleic acid probes to lung cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the lung cancer nucleic acids, i.e., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under appropriate reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally complements of ORFs or whole genes are not used. In some embodiments, nucleic acids of lengths up to hundreds of bases can be used.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a

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particular target. The probes can be overlapping (i.e., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is typically meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to a biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. Often the substrate may contain discrete individual sites appropriate for ndivitual partitioning and identification. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in US application entitled Reusable Low Fluorescent Plastic Biochip, U.S.

Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

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In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized, and then attached to the surface of the solid support. Either the 5' or 3' terminus may be attached to the solid support, or attachment may be via linkage to an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized *in situ*, using known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GeneChipTM technology.

Often, amplification-based assays are performed to measure the expression level of lung cancer-associated sequences. These assays are typically performed in conjunction with

reverse transcription. In such assays, a lung cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of lung cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols, A Guide to Methods and Applications.

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560, Landegren, et al. (1988) Science 241:1077, and Barringer, et al. (1990) Gene 89:117), transcription amplification (Kwoh, et al. (1989) Proc. Natl. Acad. Sci. USA 86:1173), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Nat. Acad. Sci. USA 87:1874), dot PCR, and linker adapter PCR, etc.

Expression of lung cancer proteins from nucleic acids

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In a preferred embodiment, lung cancer nucleic acids, e.g., encoding lung cancer proteins, are used to make a variety of expression vectors to express lung cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known to those of skill in the art (see, e.g., Ausubel, supra, and Fernandez and Hoeffler (eds 1999) Gene Expression Systems) and are used to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the lung cancer protein. The term "control sequences" refers to DNA

sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

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Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the lung cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences may be either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector often contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating

vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art (e.g., Fernandez and Hoeffler, *supra*).

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

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The lung cancer proteins of the present invention are usually produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a lung cancer protein, under the appropriate conditions to induce or cause expression of the lung cancer protein. Conditions appropriate for lung cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaebacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the lung cancer proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral and adenoviral systems. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez and Hoeffler, *supra*). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived form SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

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In a preferred embodiment, lung cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the lung cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for Bacillus subtilis, E. coli, Streptococcus cremoris, and Streptococcus lividans, among others (e.g., Fernandez and Hoeffler, supra). The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, lung cancer proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, lung cancer protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for Saccharomyces cerevisiae, Candida albicans and C. maltosa, Hansenula polymorpha,

Kluyveromyces fragilis and K. lactis, Pichia guillerimondii, and P. pastoris, Schizosaccharomyces pombe, and Yarrowia lipolytica.

The lung cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the lung cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the lung cancer protein may be made as a fusion protein to increase expression for affinity purification purposes, or for other reasons. For example, when the lung cancer protein is a lung cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In a preferred embodiment, the lung cancer protein is purified or isolated after expression. Lung cancer proteins may be isolated or purified in a variety of appropriate ways. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the lung cancer protein may be purified using a standard anti-lung cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes (1982) Protein Purification. The degree of purification necessary will vary depending on the use of the lung cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the lung cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, therapeutic entities, for production of antibodies, as transcription or translation inhibitors, etc.

25 Variants of lung cancer proteins

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In one embodiment, the lung cancer proteins are derivative or variant lung cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative lung cancer peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at a particular residue within the lung cancer peptide.

Also included within one embodiment of lung cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three

classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the lung cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant lung cancer protein fragments having up to about 100-150 residues may be prepared by *in vitro* synthesis. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the lung cancer protein amino acid sequence. The variants typically exhibit a similar qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

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While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed lung cancer variants screened for the optimal combination of desired activity. Techniques exist for making substitution mutations at predetermined sites in DNA having a known sequence, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of mutants is often done using assays of lung cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be occasionally tolerated. Deletions generally range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. Larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of a lung cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution chart provided in the definition section.

Variants typically exhibit essentially the same qualitative biological activity and will elicit the same immune response as a naturally-occurring analog, although variants also are selected to modify the characteristics of lung cancer proteins as needed. Alternatively, the

variant may be designed or reorganized such that a biological activity of the lung cancer protein is altered. For example, glycosylation sites may be added, altered, or removed.

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Covalent modifications of lung cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a lung cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a lung cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking lung cancer polypeptides to a water-insoluble support matrix or surface for use in a method for purifying anti-lung cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimidate.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serinyl, threonyl or tyrosyl residues, methylation of the γ-amino groups of lysine, arginine, and histidine side chains (Creighton (1983) Proteins: Structure and Molecular Properties, pp. 79-86), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the lung cancer polypeptide encompassed by this invention is an altered native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended herein to mean adding to or deleting one or more carbohydrate moieties of a native sequence lung cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express lung cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to lung cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence lung cancer polypeptide (for O-linked glycosylation sites). The lung cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the lung cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the lung cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330, and in Aplin and Wriston (1981) CRC Crit. Rev. Biochem., pp. 259-306.

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Removal of carbohydrate moieties present on the lung cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al. (1987) Arch. Biochem. Biophys., 259:52 and by Edge, et al. (1981) Anal. Biochem., 118:131. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura, et al. (1987) Meth.. Enzymol., 138:350.

Another type of covalent modification of lung cancer comprises linking the lung cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192, or 4,179,337.

Lung cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a lung cancer polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a lung cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the lung cancer polypeptide. The presence of such epitope-tagged forms of a lung cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the lung cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a lung cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known and examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies

thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3(6):547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:6393-6397).

Also included are other lung cancer proteins of the lung cancer family, and lung cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related lung cancer proteins from primates or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include unique areas of the lung cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. PCR reaction conditions are well known in the art (e.g., Innis, PCR Protocols, supra).

Antibodies to lung cancer proteins

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In a preferred embodiment, when a lung cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the lung cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller lung cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are well known (e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 1A-16 or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal

being immunized. Immunogenic proteins include, e.g., keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Adjuvants include, e.g., Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art.

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The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of the tables, or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if nonhuman mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding (1986) Monoclonal Antibodies: Principles and Practice, pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovin, or primate origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are typically monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of the tables or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to lung cancer protein are capable of reducing or eliminating a biological function of a lung cancer protein, in a naked form or conjugated to an effector moiety. That is, the addition of anti-lung cancer protein antibodies (either polyclonal or preferably monoclonal) to lung cancer tissue (or cells containing lung cancer) may reduce or eliminate the lung cancer. Generally, at least a 25% decrease in activity, growth, size or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

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In a preferred embodiment the antibodies to the lung cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Medarex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of a human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. A humanized antibody optimally also will typically comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596). Humanization can be performed following the method of Winter and co-workers (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeyen, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by corresponding sequence from a non-human species.

Human-like antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom and Winter (1991) J. Mol. Biol. 227:381; Marks, et al. (1991) J. Mol. Biol. 222:581). The techniques of Cole, et al. and Boerner, et al. are also available for the preparation of human monoclonal antibodies (Cole, et al. (1985) Monoclonal Antibodies and Cancer Therapy, p. 77 and Boerner, et al. (1991) J. Immunol. 147(1):86-95). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in nearly all respects, including gene rearrangement, assembly, and antibody repertoire. This 10 approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Fishwild, et al. (1996) Nature Biotechnology 14:845-51; Neuberger (1996) Nature Biotechnology 14:826; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 15 13:65-93.

By immunotherapy is meant treatment of lung cancer with an antibody raised against a lung cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

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In a preferred embodiment the lung cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, may bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted lung cancer protein.

In another preferred embodiment, the lung cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment may bind the extracellular domain of the lung cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The

antibody may cause down-regulation of the transmembrane lung cancer protein. The antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the lung cancer protein. The antibody may be an antagonist of the lung cancer protein or may prevent activation of a transmembrane lung cancer protein, or may induce or suppress a particular cellular pathway. In some embodiments, when the antibody prevents the binding of other molecules to the lung cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF-α, TNF-β, IL-1, INF-γ, and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody may belong to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, lung cancer may be treated by administering to a patient antibodies directed against the transmembrane lung cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be various molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of a lung cancer protein. In another aspect the therapeutic moiety may modulate an activity of molecules associated with or in close proximity to a lung cancer protein. The therapeutic moiety may inhibit enzymatic or signaling activity such as protease or collagenase activity associated with lung cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to lung cancer tissue or cells results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with lung cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, saporin, auristatin, and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against lung cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane lung cancer proteins not only serves to increase the local concentration of therapeutic moiety in the lung cancer

PCT/US02/12476 WO 02/086443 afflicted area, but also serves to reduce deleterious side effects that may be associated with the untargeted therapeutic moiety.

In another preferred embodiment, the lung cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein or other entity which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the lung cancer protein can be targeted within a cell, i.e., the nucleus, an antibody theretomay contain a signal for that target localization, i.e., a nuclear localization signal.

The lung cancer antibodies of the invention specifically bind to lung cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a Kd of at least about 0.1 mM, more usually at least about 1 µM, preferably at least about 0.1 µM or better, and most preferably, 0.01 µM or better. Selectivity of binding to the specific target and not to related other sequences is also important.

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Detection of lung cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the lung cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing lung cancer), in lung cancer tissue (and in some cases, for varying severities of lung cancer that relate to prognosis, as outlined below), or in non-malignant disease are evaluated to provide expression profiles. A gene expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can

qualitatively have its expression altered, including an activation or inactivation, in, e.g.,

"Differential expression," or grammatical equivalents as used herein, refers to

PCT/US02/12476 WO 02/086443 normal versus lung cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; i.e., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart (1996) Nature Biotechnology 14:1675-1680, hereby 10 expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e., upregulation or downregulation) is typically at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

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Evaluation may be at the gene transcript or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the RNA or DNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the lung cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to lung cancer genes, e.g., those identified as being important in a lung cancer or disease phenotype, can be evaluated in a lung cancer diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes.

The lung cancer nucleic acid probes may be attached to biochips as outlined herein for the detection and quantification of lung cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity. Multiple protein expression monitoring can be performed as well. Similarly, these assays may be performed on an individual basis as well.

In a preferred embodiment nucleic acids encoding the lung cancer protein are detected. Although DNA or RNA encoding the lung cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a lung cancer protein is detected.

Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed *in situ*. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxygenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a lung cancer protein is detected by binding the digoxygenin with an anti-digoxygenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

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In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, lung cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as markers of lung cancer, e.g., for prognostic or diagnostic purposes. Detection of these proteins in putative lung cancer tissue allows for detection, prognosis, or diagnosis of lung cancer or similar disease, and perhaps for selection of therapeutic strategy. In one embodiment, antibodies are used to detect lung cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the lung cancer protein is detected, e.g., by immunoblotting with antibodies raised against the lung cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the lung cancer protein find use in *in situ* imaging techniques, e.g., in histology (e.g., Asai (ed. 1993) Methods in Cell Biology:

Antibodies in Cell Biology, volume 37. In this method cells are contacted with from one to many antibodies to the lung cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label, e.g., multicolor fluorescence or confocal imaging. In another method the primary antibody to the lung cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of lung cancer proteins. Many other histological imaging techniques are also provided by the invention.

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In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing lung cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of lung cancer proteins. Antibodies can be used to detect a lung cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous lung cancer protein or vaccine.

In a preferred embodiment, in situ hybridization of labeled lung cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including lung cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to lung cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple

genes may be useful in various combinations. As above, lung cancer probes may be attached to biochips for the detection and quantification of lung cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

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Assays for therapeutic compounds

In a preferred embodiment, the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, et al. (1998) Science 279:84-8; Heid (1996) Genome Res. 6:986-94.

In a preferred embodiment, the lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified lung cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the lung cancer phenotype or an identified physiological function of a lung cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, *supra*.

Having identified differentially expressed genes herein, a variety of assays may be performed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene with altered regulation in lung cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the lung cancer protein. "Modulation" thus includes an increase or a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing lung cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in lung cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in lung

WO 02/086443 PCT/US02/12476 cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in

cancer tissue compared to normal tissue often provides a target value of a 10-fold increase expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the lung cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

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In a preferred embodiment, gene or protein expression monitoring of a number of entities, i.e., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the lung cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of lung cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more lung cancer-associated sequences, e.g., a polynucleotide sequence set out in the tables. Generally, in a preferred embodiment, a test compound is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate lung cancer, modulate lung cancer proteins, bind to a lung cancer protein, or interfere with the binding of a lung cancer protein and an antibody, substrate, or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the lung cancer phenotype or the expression of a lung cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles of nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a lung cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induces a lung cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

In one aspect, a modulator will neutralize the effect of a lung cancer protein. By "neutralize" is meant that activity of a protein and the consequent effect on the cell is inhibited or blocked.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a lung cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

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In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks (Gallop, et al. (1994) J. Med. Chem. 37(9):1233-1251).

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature, 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Nat. Acad. Sci. USA 90:6909-6913), vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et

al. (1992) J. Amer. Chem. Soc. 114:9217-9218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661), oligocarbamates (Cho, et al. (1993) Science 261:1303), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14(3):309-314, and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, Baum (1993) C&EN, Jan 18, page 33; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

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Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual synthetic operations performed by a chemist. The above devices, with appropriate modification, are suitable for use with the present invention. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening.

Preferred assays thus detect modulation of lung cancer gene transcription, polypeptide expression, and polypeptide activity.

High throughput assays for evaluating the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins,

U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (i.e., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

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In addition, high throughput screening systems are commercially available (see, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate procedures, including sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that the nucleic acid or peptide consists of essentially random sequences of nucleotides and amino acids, respectively. Since these random peptides (or nucleic acids, discussed below) are often chemically synthesized, they may incorporate a nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. In a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc.

Modulators of lung cancer can also be nucleic acids, as defined above.

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As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. Digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After a candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence is analyzed. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an *in vitro* transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

Nucleic acid assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos.

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5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670,
5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

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A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allow formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the lung cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state,

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reens are performed to identify agents that bind and/or modulate the biological activity of

screens are performed to identify agents that bind and/or modulate the biological activity of the gene product, or evaluate genetic polymorphisms.

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Genes can be screened for those that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress a lung cancer expression pattern leading to a normal expression pattern, or to modulate a single lung cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated lung cancer tissue reveals genes that are not expressed in normal tissue or lung cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for lung cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated lung cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of lung cancer cells, that have an associated lung cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once a test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., lung cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress a lung cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on lung cancer activity. By defining such a signature for the lung cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

Measure of lung cancer polypeptide activity, or of lung cancer or the lung cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the metastatic polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of lung cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian lung cancer polypeptide is typically used, e.g., mouse, preferably human.

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Assays to identify compounds with modulating activity can be performed *in vitro*. For example, a lung cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the lung cancer polypeptide levels are determined *in vitro* by measuring the level of protein or mRNA. The level of protein is typically measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the lung cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNAse protection, dot blotting, are preferred. The level of protein or mRNA is typically detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using a lung cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed

genes are sometimes referred to herein as "lung cancer proteins." The lung cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

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In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the lung cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a lung cancer protein and a candidate compound, and determining the binding of the compound to the lung cancer protein. Preferred embodiments utilize the human lung cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative lung cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the lung cancer protein or the candidate agent is non-diffusably bound to an insoluble support, preferably having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflonTM, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is typically not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition, and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation

sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

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In a preferred embodiment, the lung cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the lung cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled *in vitro* protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the lung cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the lung cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ¹²⁵I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor may be a binding moiety known to bind to the target molecule (i.e., a lung cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between 4 and 40° C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically

between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

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In a preferred embodiment, the competitor is added first, followed by a test compound. Displacement of the competitor is an indication that the test compound is binding to the lung cancer protein and thus is capable of binding to, and potentially modulating, the activity of the lung cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the lung cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the lung cancer protein.

In a preferred embodiment, the methods comprise differential screening to identity agents that are capable of modulating the activity of the lung cancer proteins. In one embodiment, the methods comprise combining a lung cancer protein and a competitor in a first sample. A second sample comprises a test compound, a lung cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the lung cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the lung cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native lung cancer protein, but cannot bind to modified lung cancer proteins. The structure of the lung cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a lung cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results.

Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

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A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a lung cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising lung cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a lung cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate lung cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the lung cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting lung cancer cell division is provided. The method comprises administration of a lung cancer inhibitor. In another embodiment, a method of inhibiting lung cancer is provided. The method may comprise administration of a lung cancer inhibitor. In a further embodiment, methods of treating cells or individuals with lung cancer are provided, e.g., comprising administration of a lung cancer inhibitor.

In one embodiment, a lung cancer inhibitor is an antibody as discussed above. In another embodiment, the lung cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, viability, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

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Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of lung cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described in Freshney (1994) <u>Culture of Animal Cells a Manual of Basic Technique</u> (3rd ed.), herein incorporated by reference. See also, the methods section of Garkavtsev, et al. (1996), *supra*, herein incorporated by reference.

20 Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (³H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (1994), supra. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (³H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a lung cancer-associated sequence and are grown for 24 hours at saturation density in

WO 02/086443 PCT/US02/12476 non-limiting medium conditions. The percentage of cells labeling with (³H)-thymidine is

determined autoradiographically. See, Freshney (1994), supra.

Growth factor or serum dependence

Transformed cells typically have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) <u>J. Natl. Cancer Insti.</u> 37:167-175; Eagle, et al. (1970) <u>J. Exp. Med.</u> 131:836-879); Freshney, *supra*. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

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Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g., Gullino, "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) Biological Responses in Cancer, pp. 178-184). Similarly, Tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) "Angiogenesis and Cancer" in Sem Cancer Biol.).

Various techniques which measure the release of these factors are described in Freshney (1994), *supra*. Also, see, Unkeless, et al. (1974) <u>J. Biol. Chem.</u> 249:4295-4305; Strickland and Beers (1976) <u>J. Biol. Chem.</u> 251:5694-5702; Whur, et al. (1980) <u>Br. J. Cancer</u> 42:305-312; Gullino, "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) <u>Biological Responses in Cancer</u>, pp. 178-184; Freshney Anticancer Res. 5:111-130 (1985).

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Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate lung cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), *supra*, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by prelabeling the cells with ¹²⁵I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), *supra*.

Tumor growth in vivo

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Effects of lung cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the lung cancer gene is disrupted or in which a lung cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous lung cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous lung cancer gene with a mutated version of the lung cancer gene, or by mutating the endogenous lung cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi, et al. (1989) Science 244:1288). Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manual, Cold Spring Harbor Laboratory and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach, IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) <u>J. Natl. Cancer Inst.</u> 52:921), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) <u>Br. J. Cancer</u> 38:263; Selby, et al. (1980) <u>Br. J. Cancer</u> 41:52) can be used as a host. Transplantable tumor cells (typically about 10⁶ cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a lung cancer-associated sequences are injected subcutaneously. After a suitable length of time,

preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

5 Polynucleotide modulators of lung cancer

Antisense and RNAi Polynucleotides

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In certain embodiments, the activity of a lung cancer-associated protein is downregulated, or entirely inhibited, by the use of antisense or an inhibitory polynucleotide, i.e., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a lung cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or intersugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the lung cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized *in vitro*. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by binding to the antisense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for lung cancer molecules. A preferred antisense molecule is for a lung cancer sequence in the tables, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein

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is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659 and van der Krol, et al.
(1988) BioTechniques 6:958).

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) Sciencexpress (21March2002); Sharp (1999) Genes Dev. 13:139-141; and Cathew (2001) Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

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Ribozymes

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of lung cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25: 289-317 for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparing are well known to those of skill in the art (see, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-45; Leavitt, et al. (1995) Proc. Natl. Acad. Sci. USA 92:699-703; Leavitt, et al. (1994) Human Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126).

Polynucleotide modulators of lung cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of lung cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by

formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

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Thus, in one embodiment, methods of modulating lung cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-lung cancer antibody that reduces or eliminates the biological activity of an endogenous lung cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a lung cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the lung cancer sequence is down-regulated in lung cancer, such state may be reversed by increasing the amount of lung cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous lung cancer gene or administering a gene encoding the lung cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, e.g., when the lung cancer sequence is up-regulated in lung cancer, the activity of the endogenous lung cancer gene is decreased, e.g., by the administration of a lung cancer antisense or RNAi nucleic acid.

In one embodiment, the lung cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to lung cancer proteins. Similarly, the lung cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify lung cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a lung cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The lung cancer antibodies may be coupled to standard affinity chromatography columns and used to purify lung cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the lung cancer protein.

Methods of identifying variant lung cancer-associated sequences

Without being bound by theory, expression of various lung cancer sequences is correlated with lung cancer. Accordingly, disorders based on mutant or variant lung cancer genes may be determined. In one embodiment, the invention provides methods for

identifying cells containing variant lung cancer genes, e.g., determining all or part of the sequence of at least one endogenous lung cancer genes in a cell. In a preferred embodiment, the invention provides methods of identifying the lung cancer genotype of an individual, e.g., determining all or part of the sequence of at least one lung cancer gene of the individual.

This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced lung cancer gene to a known lung cancer gene, i.e., a wild-type gene.

The sequence of all or part of the lung cancer gene can then be compared to the sequence of a known lung cancer gene to determine if any differences exist. This can be done using known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the lung cancer gene of the patient and the known lung cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the lung cancer genes are used as probes to determine the number of copies of the lung cancer gene in the genome.

In another preferred embodiment, the lung cancer genes are used as probes to determine the chromosomal localization of the lung cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the lung cancer gene locus.

Administration of pharmaceutical and vaccine compositions

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In one embodiment, a therapeutically effective dose of a lung cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques (e.g., Ansel, et al. (1992) Pharmaceutical Dosage Forms and Drug Delivery; Lieberman, Pharmaceutical Dosage Forms (vols. 1-3), Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding; and Pickar (1999) Dosage Calculations). Adjustments for lung cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration,

drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

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The administration of the lung cancer proteins and modulators thereof of the present invention can be done in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the lung cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a lung cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose,

lactose, com and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

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The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that lung cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise a lung cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., Remington's Pharmaceutical Science (15th ed., 1980) and Hardman, et al. (eds. 1996)

Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent to those skilled in the art, e.g., Remington's Pharmaceutical Science and Goodman and Gilman, The Pharmacologial Basis of Therapeutics, supra.

The compositions containing modulators of lung cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

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It will be appreciated that the present lung cancer protein-modulating compounds can be administered alone or in combination with additional lung cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in the tables, such as antisense or RNAi polynucleotides or ribozymes, will be introduced into cells, *in vitro* or *in vivo*. The present invention provides methods, reagents, vectors, and cells useful for expression of lung cancer-associated polypeptides and nucleic acids using *in vitro* (cell-free), *ex vivo*, or *in vivo* (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors and other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (see, e.g.,

Berger and Kimmel, <u>Guide to Molecular Cloning Techniques</u>, <u>Methods in Enzymology</u> volume 152 (Berger), Ausubel, et al. (eds. 1999) <u>Current Protocols</u> (supplemented through 1999), and Sambrook, et al. (1989) <u>Molecular Cloning - A Laboratory Manual</u> (2nd ed., Vol. 1-3).

In a preferred embodiment, lung cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, lung cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the lung cancer coding regions) can be administered in a gene therapy application. These lung cancer genes can include antisense or inhibitory applications, e.g., as inhibitory RNA or gene therapy (e.g., for incorporation into the genome) or as antisense compositions.

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Lung cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses.. Such vaccine compositions can include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) J. Clin. Invest. 95:341), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in immune stimulating complexes (ISCOMS) (see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin Exp Immunol. 113:235-243), multiple antigen peptide systems (MAPs) (see, e.g., Tam (1988) Proc. Natl. Acad. Sci. U.S.A. 85:5409-5413; Tam (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p. 379 In: Kaufmann (ed. 1996) Concepts in vaccine development; Chakrabarti, et al. (1986) Nature 320:535; Hu, et al. (1986) Nature 320:537; Kieny, et al. (1986) AIDS Bio/Technology 4:790; Top, et al. (1971) J. Infect. Dis. 124:148; Chanda, et al. (1990) Virology 175:535), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25; Eldridge, et al. (1993) Sem. Hematol. 30:16; Falo, et al. (1995) Nature Med. 7:649), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369; Gupta, et al. (1993) Vaccine 11:293), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585; Rock (1996) Immunol. Today 17:131), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745; Robinson, et al. (1993) Vaccine 11:957; Shiver, et al., p. 423 In: Kaufmann (ed. 1996) Concepts in vaccine development; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923 and Eldridge, et al. (1993) Sem. Hematol. 30:16). Toxin-targeted

delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

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Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bortadella pertussis* or *Mycobacterium tuberculosis* derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff, et. al. (1990) Science 247:1465 as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivicaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode lung cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors useful for therapeutic administration or immunization e.g., adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the

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like, will be apparent to those skilled in the art from the description herein (see, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85).

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Methods for the use of genes as DNA vaccines are well known, and include placing a lung cancer gene or portion of a lung cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a lung cancer patient. The lung cancer gene used for DNA vaccines can encode full-length lung cancer proteins, but more preferably encodes portions of the lung cancer proteins including peptides derived from the lung cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a lung cancer gene. For example, lung cancer-associated genes or sequence encoding subfragments of a lung cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the lung cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment lung cancer genes find use in generating animal models of lung cancer. When the lung cancer gene identified is repressed or diminished in metastatic tissue, gene therapy technology, e.g., wherein antisense or inhibitory RNA directed to the lung cancer gene will also diminish or repress expression of the gene. Animal models of lung cancer find use in screening for modulators of a lung cancer-associated sequence or modulators of lung cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the lung cancer protein. When desired, tissue-specific expression or knockout of the lung cancer protein may be necessary.

It is also possible that the lung cancer protein is overexpressed in lung cancer. As such, transgenic animals can be generated that overexpress the lung cancer protein.

Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene.

Animals generated by such methods will find use as animal models of lung cancer and are additionally useful in screening for modulators to treat lung cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

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For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In diagnostic and research applications such kits may include at least one of the following: assay reagents, buffers, lung cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, RNAi, dominant negative lung cancer polypeptides or polynucleotides, small molecule inhibitors of lung cancer-associated sequences, etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing instructions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. A medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of lung cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a lung cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing lung cancer-associated activity. Optionally, the kit contains biologically active lung cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes typically will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

WO 02/086443 PCT/US02/12476 EXAMPLES

Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

Tables 1A and 1B were previously filed on April 18, 2001 in USSN 60/284,770 (18501-001500US) and on November 29, 2001 in USSN 60/334,370 (18501-001520US)

5	Table 1A					
	Pkey	ExAccn	UnigenelD	Unigene Titte	70% chron/90% NL	70% SQAD/90% NL
	100134	D13264	Hs.49	macrophage scavenger receptor 1	1.61	0.74
	100780	HG3731-HT4001		Immunoglobulin Heavy Chain, Vdjrc Reg	2.68	3.28
10	100971	J02874	Hs.83213	fatty acid binding protein 4; adipocyte	1.96 0.79	0.14 0.07
10	101088	L05568 L07594	Hs.553 Hs.79059	solute carrier family 6 (neurotransmitte transforming growth factor; beta recepto	2.55	1
	101102 101168	L15388	Hs.211569	G protein-coupled receptor kinase 5	0.88	0.27
	101277	L38486	Hs.118223	microfibrillar-associated protein 4	0.89	0.26
	101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	0.59	0.29
15	101336	L49169	Hs.75678	FBJ murine osteosarcoma viral oncogene h	1.15	0.41
	101345	L76380	Hs.152175	calcitonin receptor-like	0.81	0.31
	101578	M62505	Hs.2161	complement component 5 receptor 1 (C5a I	1.31	0.77 0.82
	101764	M80563	Hs.81256	S100 calcium-binding protein A4 (calcium	1.44 0.96	0.45
20	101771 101842	M81750 M93221	Hs.153837 Hs.75182	myeloid cell nuclear differentiation ant mannose receptor; C type 1	1.27	0.37
20	102283	U31384	Hs.83381	guanine aucleotide binding protein 11	1.04	0.3
	102363	U39447	Hs.198241	arnine oxldase; copper containing 3 (vasc	0.96	0.26
	102507	U52154	Hs.193044	potassium inwardly-rectifying channel; s	2.81	3.45
0.5	102698	U75272	Hs.1867	progastricsin (pepsinogen C)	0.95	0.23
25	103025	X54131	Hs.123641	protein tyrosine phosphatase; receptor t	1.62	0.21 0.41
	103280	X79981	Hs.76206	cadherin 5; VE-cadherin (vascular epithe flavin containing monooxygenase 2	0.9 1.27	0.49
	103496 103541	Y09267 Z11697	Hs.132821 Hs.79197	CD83 antigen (activated B lymphocytes; i	1.86	1
	103554	Z18951	Hs.74034	caveolin 1; caveolae protein; 22kD	1.27	0.47
30	104212	AB002298	Hs.173035	KIAA0300 protein	1.17	0.16
	104691	AA011176	Hs.37744	ESTs	1.08	0.35
	104825	AA035613	Hs.141883	ESTs	0.75	0.27
	104857	AA043219	Hs.19058	ESTs	26	3.3
35	104865	AA045136	Hs.22575	ESTs ESTs	1.23 0.63	0.49 0.32
22	104989	AA102098	Hs.118615 Hs.3807	ESTS; Weakly similar to PHOSPHOLEMMAN PR	0.86	0.34
	105729 105847	AA292694 AA398606	Hs.32241	ESTs	1.32	0.4
	105894	AA400979	Hs.25691	calcitonin receptor-like receptor activi	0.78	0.28
	106490	AA451861	Hs.115537	ESTs; Weakly similar to dipeptidase prec	1.2	0.47
40	106536	AA453997	Hs.23804	ESTs	0.82	0.15
	106605	AA457718	Hs.21103	Homo saplens mRNA; cDNA DKFZp5648076 (fr	0.99	0.07
	106667	AA461086	Hs.16578	ESTs	1.17 1.46	0.4 0.43
	106773 106797	AA478109 AA478962	Hs.188833 Hs.169943	ESTs ESTs	1.18	0.32
45	106844	AA485055	Hs.158213	sperm associated antigen 6	0.98	0.51
	106870	AA487576	Hs.26530	serum deprivation response (phosphatidy)	1.05	0.14
	106954	AA496980	Hs.204038	ESTs	1.25	0.33
	107054	AA600150	Hs.14366	ESTs	1.11	0.4
50	107292	T30407	Hs.4789	ESTs; Wealdy similar to oxidative-stress	1.07 0.7	2.58 0.21
20	107994 107997	AA036811 AA037388	Hs.165030 Hs.82223	ESTs Human DNA sequence from clone 141H5 on c	1.02	0.48
	108041	AA041552	Hs.61957	ESTs	1.44	0.51
	108087	AA045709	Hs.40545	ESTs	1.98	1
	108382	AA074885	Hs.67726	macrophage receptor with collagenous str	1.52	0.72
55	108435	AA078787	Hs.194101	ESTs .	2.53	1.53
	108480	AA081093	Hs.68055	ESTs	1.56	0.48
	109252	AA194830	Hs.85944 Hs.26981	ESTs .	2.69 1.19	3.18 · 0.65
	109550 109613	F01534 F03031	Hs.27519	ESTs ESTs	1.01	0.29
60	109837	H00656	Hs.29792	ESTs	0.81	0.15
•	109893	H04768	Hs.30484	ESTs	1.44	0.32
	109984	H09594	Hs.10299	ESTs	0.62	0.14
	110099	H16568	Hs.23748	ESTs	1.01	0.28
65	110837	N30796	Hs.17424	ESTs; Weakly similar to semaphorin F [H.	1.1	0.22 0.26
05	111247 111341	N69825 N80935	Hs.16762 Hs.22483	Homo sapiens mRNA; cDNA DKFZp584B2062 (f ESTs	1.26 1.57	0.52
	111510	R07856	Hs.16355	ESTs	3.96	1
	111737	R25410	Hs.9218	ESTs	0.97	0.24
	113195	T57112		"'yc20g11.s1 Stratagene lung (#937210) .	1.22	0.35
70	113238	T62979	Hs.189813	ESTs	2.27	0.45
		T90496	Hs.16757	ESTs	1.06 ·	0.22
	113552 113606	T90889 T93093	Hs.16026 Hs.17125	ESTs ESTs	1.16 1.48	0.42 0.7
	113695	T96965	Hs.17948	ESTs ESTs	1.54	0.28
75		W84753	Hs.37896	ESTs	1.79	0.72
	114251	Z39898	Hs.21948	ESTs	1.95	0.25
	114359	Z41589	Hs.153483	ESTs; Moderately similar to H1 chloride	1.42	0.13
	115230	AA278300	Hs.182980	ESTs	2.62	0.42
80	115279	AA279760	Hs.63671	ESTs	1.79 0.86	0.91 0.2
ou	115566 115965	AA398083 AA446661	Hs.43977 Hs.173233	ESTs ESTs	0.79	0.04
	116166	AA461556	Hs.202949	KIAA1102 protein	2.29	0.68
	116279	AA486073	Hs.57362	ESTs	2.27	0.78
	117023	H88157	Hs.41105	ESTs	1.36	0.16

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10112 228283 http://doi.org/1016/1016/1016/1016/1016/1016/1016/101		119861		11- 50350			
10 120467 AV25179 Hs.19726 EST6 1.91							
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15 12233 AMASSIDS H-34836 H-319325 STG AMASSIDS H-34836 H-319325 STG AMASSIDS H-34936							
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12931 CD2088 17007 Ri5380 Hz.2479 ESTs L.2479 ESTs L.2479 A0527559 Hz.12712 ESTs Weathy similar to plL2 hypothetica 1.01 C659 170797 A6227559 Hz.153712 ESTs L.55340 ESTs L.121 C32 L121 C32							
2.5 17707 A35387 ht. 2279 ESTs				Hs.22978			
25 177307 A3253567 115; 12712 ESTs; Weathy similar to plL2 hypothetica 1.01 0.65				Hr 2/070			
127699 AB02471 h. 130318 ESTs 1.27	25						
129455							
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128798	30						
128952 PS1076 Hs. 107361 ESTE, Highly similar to Rap2 Interacting 2.04 2.44 12910 AAA01654 Hs. 202549 Ms. 1365 Hs. 21747 CMVS2 antigon (CAMPATH-1 antigon) 1.77	50				chemokine (C-C motif) receptor-like 2		
1.282710 AA401654 Hs.202949 KIAA1102 grotelsh 1.11 1.11 0.38 1.29240 VVX/300 Hs.27868 VXX/300 Hs.27868 VXX/300 Hs.27868 VXX/300 Hs.27868 VXX/300 Hs.27868 VXX/300 Hs.2787777 Hs.198726 VXX/300 Hs.29811 Ks.20294 VXX/300 Hs.29811 Ks.20294 VXX/300 Hs.20295 AA487076 Hs.20296 AA487076 Hs.198726 VXX/300 Hs.1792 Ks.20296 AA487878 Hs.1712 Ks.20294 Ks.20296 VXX/300 Hs.1703 VXX/300 Hs.1703 Ks.2029 Ks.20		128952					
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131751 H18335	50						0.38
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100335 D53391 Hs.6793 platelet-activating factor acetythydrola 1 5.58 100360 078335 Hs.75939 Uridine monophosphate kinase 0.91 2.04 100370 D79997 Hs.184339 Uridine monophosphate kinase 0.91 2.04 100460 Hc61112-HT1112 Hc61112-HT1112 TiGR: ras-like protein TC4 1.09 1.93 100579 Hc62197-HT2267 *collagen, type VII, alpha 1* 0.97 3.6 100576 Hc62290-HT2366 *cataltanin/alpha-CGRP, all transcript 1 1 100906 Hc64716-HT5158 Suanosine 5-Monophosphate Synthase 1.18 2.29 100906 Hc64716-HT5158 Hc64716-HT5158 1.18 1.18 1.18 1.18 1.18 100906 Hc64716-HT5158 Hc64716-HT5158 1.18 1.18 1.18 1.18 1.18 1.18 100507 Hc64716-HT5158 Hc64716-HT51	75	100147	D13666	Hs.136348	Homo sapiens mRNA for osteoblast specifi		
100360 078335 Hs.75939 Uridine monophosphate kinase 0.91 2.04							
80 100372 079997 Hs.184339 KIAA0175 gene product 0.75 2.03 100486 HG1112-HT1112 TIGR: ras-like protein TC4 1.09 1.93 1.93 100559 HG2197-HT286 "collagen, type VII, atpha 1" 0.97 3.6 HG293-HT2386 "calcitonivalpha-CGRP, alt. transcript 1 1 1 100668 HG2981-HT3938 "TIGR: CD44 (epican, alt. transcript 12 0.85 1.9 100906 HG4716-HT5158 Gyanosine 5-Monophosphate Synthase 1.18 2.29						•	
80 100486 HG1112+HT1112 TIGR: ras-like protein TC4 1.09 1.93 100559 HG2197-HT2267 'collagen, type VII, alpha 1' 0.97 3.6 100576 HG2290-HT2386 'calcitonityalpha-CGRP, alt transcript 1 1 100668 HG2981-HT3938 'TIGR: CD44 (epican, alt transcript 12 0.85 1.9 100906 HG4716-HT5158 Guanosine 5-Monophosphate Synthase 1.18 2.29						0.75	
100559 HG2197-HT2267 *collagen, type VII, alpha 1* 0.97 3.5 100576 HG2290-HT2286 *calcitanitralpha-CGRP, all, transcript 1 1 1 100668 HG2981-HT3938 *TIGR: CD44 (epican, all, transcript 12 0.85 1.9 100906 HG4716-HT5158 Suanosine 5-Monophosphate Synthase 1.18 2.29	80	100486			TIGR: ras-like protein TC4	1.09	
100668 HG2981-HT3938 **TIGR: CI044 (epican, all transcript 12 0.85 1.9 100906 HG4716-HT5158 Guanosine 5-Monophosphate Synthase 1.18 2.29							
100906 HG4716-HT5158 Guanosine 5'-Monophosphate Synthase 1.18 2.29							
85 100930 HG721-HT4827 "TIGR: placental protein 14, endometrial 1 1.45					Guanosine 5'-Monophosphate Synthase	1.18	2.29
	85				"TIGR: placental protein 14, endometrial	1	1.45

	W	O 02/086	443			
	100960	J00124	Hs.117729	keratin 14 (epidermolysis bullosa simple	0.84	2.6
	101031	J05070	Hs.151738	"Matrix metalloproteinase 9 (gelatinase	0.77	1.52
	101111	L08424	Hs.1619	Achaete-scute complex (Drosophila) horrol	1	1
-	101124	L10343	Hs.112341	Protease inhibitor 3, skin-derived (SKA	0.62	2.67
5	101175	L18920	Hs.36980	Melanoma antigen, family A, 2	1	1.
	101204	L24203	Hs.82237	Atada-telangiectasia group D-associated	0.74	4.1 2.51
	101431	M19888	Hs.1076	Small proline-rich protein 18 (cornilin)	0.85 . 0.61	8.83
	101448	M21389	Hs.195850	keratin 5 (epidermolysis bullosa simplex Endogenous retroviral protease	1.03	1.13
10	101511	M27826 M29540	Hs.267319 Hs.220529	Carcinoembryonic antigen-related cell ad	1.07	4.61
10	101526 101548	M31328	Hs.71642	*Guanine nucleofide binding protein (G p	0.97	1.13
	101625	M57293	16.11042	"Human parathyroid hormone-related pepti	1	1
	101649	M60047	Hs.1690	Heparin-binding growth factor binding pr	1	2.7
	101724	M69225	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	1	8.98
15	101748	M76482	Hs.1925	Desmoglein 3 (pemphigus vulgaris antigen	1	2.78
	101759	M80244	Hs.184601	"Solute carrier family 7 (cationic amino	1.07	2.45
	101804	M86699	Hs.169840	TTK protein kinase	1	1
	101806	M86757	Hs.112408	S100 calcium-binding protein A7 (psorias	0.74	1.76 7
20	101809	M86849	11 70003	"Homo sapiens connexin 26 (GJB2) mRNA, c	1	í
20	101845	M93426	Hs.78867	*Protein tyrosine phosphatase, receptor-	1.13	2.6
	101851	MS4250 U10323	Hs.82045 Hs.75117	Midkine (neurite growth-promoting factor *Interleukin enhancer binding factor 2,	1.03	1.61
	102083 102154	U17760	Hs.75517	Laminin, beta 3 (nicein (125kD), kalini	0.94	3.52
	102193	U20758	Hs.313	secreted phosphoprotein 1 (osteopontin;	0.34	4.59
25	102305	U33286	Hs.90073	chromosome segregation 1 (yeast homolog)	1.45	2.97
	102348	U37519	Hs.87539	Aldehyde dehydrogenase 8	0.52	2.25
	102581	U61145	Hs.77256	Enhancer of zeste (Orosophila) homolog 2	0.91	2.46
	102610	U65011	Hs.30743	Preferentially expressed antigen in mela	1	3.88
20	102623	U66083	Hs.37110	"Melanoma antigen, family A, 9 (MAGE-9)"	1	1
30	102669	U71207	Hs.29279	Eyes absent (Drosophila) homolog 2	1 1.06	2.77
	102696	U74612	Hs.239	Forkhead box M1 Neurotensin	1	ī
	102829	U91618 X04741	Hs.80962 Hs.76118	Ubiquifin carboxyl-terminal esterase L1	1.13	2.59
	102888 102913	X07696	Hs.80342	kerafin 15	0.7	4.72
35	102915	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin	1.15	3.35
50	102963	X15943	Hs.37058	"Calcitonin/calcitonin-related polypepti	1	1
	103021	X53587	Hs.85266	*Integrin, beta 4*	1.38	2.34
	103036	X54925	Hs.83169	Matrix metalloprotease 1 (interstitial c	1	14.93
40	103058	X57348	Hs.184510	Stratifin	1.25	4.17 1.72
40	103060	X57766	Hs.155324	matrix metalloproteinase 11 (stromelysin	1 1.16	7.38
	103119	X63629	Hs.2877	"Cadherin 3, P-cadherin (placental)"	0.71	1.48
	103206 103242	X72755 X76342	Hs.77367 Hs.389	monokine induced by gamma interferon *Alcohol dehydrogenase 7 (class IV), mu	1	1
	103242	X82693	Hs.3185	"Lymphocyte antigen 6 complex, locus D;	0.92	1.28
45	103478	Y07755	Hs.38991	S100 calcium-binding protein A2	1.05	5.81
	103558	Z19574	Hs.2785	keralin 17	0.65	6.68
	103576	Z26317	Hs.2631	Desmoglein 2	0.79	1.73
	103587	Z29083 .	Hs.82128	5T4 Oncofetal antigen	1	3.93
50	103594	Z31560	Hs.816	SRY (sex determining region Y)-box 2, p	0.71	7.23
50	103768	AA089997	11 0400	*ESTs, Highly similar to integral membra	0.99 0.96	1.8 1.29
	104158	AA454908	Hs.8127	KIAA0144 gene product Human DNA sequence from clone 967N21 on	1.23	7.23
	104558 104689	R56678 AA010665	Hs.88959	ESTs	0.96	2.11
	104733	AA019498	Hs.23071	ESTs	1.18	1.88
55	104906	AA055809	Hs.26802	Protein kinase domains containing protei	1.11	3.15
	104978	AA088458	Hs.19322	ESTs; Weakly similar to !!!! ALU SUBFAMI	1.64	2.89
	105012	AA116036	Hs.9329 -	"Homo sapiens mRNA for fls353, complete	1.19	3.91
	105175	AA186804	Hs.25740	ESTs; Wealdy similar to unknown (S.cerev	0.9	4.63
60	105263	AA227926	Hs.6682	ESTs	0.95 1	2.87 1.13
60	105298	AA233459	Hs.26369	ESTs S-phase kinase-associated protein 2 (p45	1.32	3.01
	105312 105719	AA233854 AA291644	Hs.23348 Hs.36793	Hypothetical protein FLJ23188	1.28	2.31
	105743	AA293300	Hs.9598	FSTs	1	1
		AA411621	Hs.8895	ESTs; same as BFH6?	0.94	2.04
65	106231	AA429571	Hs.38002	KIAA1355 protein	1.04	1.5
	106540	AA454607	Hs.38114	Hypothetical protein FLJ11100	1.26	2.26
	106575	AA456039	Hs.105421	ESTs	1	2
	105632	AA459897	Hs.11950	GPI-anchored metastasis-associated prote	0.87	1.32 1.59
70	106727	AA465342	Hs.34045	Hypothetical protein FLJ20764	0.87 0.61	1.6
70	106906	AA490237 AA608545	Hs.222024 Hs.23044	Transcription factor BMAL2 (cycle-like f RAD51 (S. cerevislae) homolog (E coli Re	0.48	2.67
	107059 107104	AA609786	Hs.15243	Nucleolar protein 1 (120kD)	1.01	1.44
	107151	AA621169	Hs.8687	ESTs; procollagen I-N proteinase	0.97	2.89
	107284	S74039	Hs.291904	Accessory proteins BAP31/BAP29	1,15	3.65
75	107901	AA026418	Hs.91539	ESTs	0.72	3.44
	107922	AA028028	Hs.61460	lg superfamily receptor LNIR precursor	1	2.48
	107932	AA029317	Hs.18878	Hypothetical protein FLJ21620	1	1 252
	108695	AA121315	Hs.70823	KIAA1077 protein	0.91	3.53
80	108857	AA133250	Hs.62180	ESTs EST-	1 0.73	1 7.3
60	108860	AA133334	Hs.129911 Hs.72045	ESTs ESTs	1	1.3
	108990 109166	AA152296 AA179845	Hs.73625	*RAB6 interacting, kinesin-like (rabkine	i	4.55
	109424	AA227919	Hs.85962	Hyaluronan synthase 3	i	1.28
_	109665	F05012	Hs.27027	Hypothetical protein DKFZp762H1311	1.42	2
85	109970	H09281	Hs.13234	ESTs	1.13	2.16
					-	

	W	O 02/086	443			
	110015	H10998	Hs.7164	A disintegrin and metalloproteinase doma	0.84 0.94	1.55 1.41
	110156 110561	H18957 H59617	Hs.4213 Hs.5199	ESTs HSPC150 protein similar to ubiquifin-con	0.91	3.18
	111223	N68921	Hs.34306	ESTs; Wealdy similar to neogenin [H.sapi	0.91	3.13
5	111345	N89820	Hs.14559 Hs.293246	Hypothetical protein FLJ 10540	1 0.83	1.25 1.27
	111876 111902	R38239 R39191	Hs.109445	"ESTs, Weakly similar to putative p150 (KIAA1020 protein	0.91	0.91
	112244	R51309	Hs.70823	KIAA1077 protein	0.77	3.01
10	112973	T17271	Hs.89981	"cDNA FLJ13308 fis, ctone OVARC1001436, "Diacylglycerol kinase, zeta (104kD)"	1 0.55	1 1.03
10	112989 113047	T23482 T25867	Hs.7549	ESTs	0.87	2
	113095	T40920	Hs.126733	ESTs	1 0.42	1 1.44
	113531 113970	T90345 W86748	Hs.16740 Hs.8109	Hypothetical protein FLJ11036 ESTs	1.17	1.73
15	114346	Z41450	Hs.130489	*ATPase, aminophospholipid transporter-I	0.86	0.82
	114407	AA010188	Hs.103305	ESTs	0.8 1.06	1.88 1.34
	114471 114509	AA028074 AA043551	Hs.104613 Hs.101799	RP42 homolog KIAA1350 protein	1.82	2.32
	115060	AA253214	Hs.198249	'Gap junction protein, beta 5 (connexin	0.79	1.49
20	115091	AA255900	Hs.184523	KIAA0965 protein	0.72 0.59	1.92 1.97
	115123 115291	AA256642 AA279943	Hs.236894 Hs.122579	*ESTs, High sim to LRP1_hu low density I ESTs	1	1.25
	115506	AA292537	Hs.45207	Hypothetical protein KIAA1335	1.15	1.48
25	115522	AA331393	Hs.47378	ESTs ESTs	0.5 1	3.29 1
25	115536 115697	AA347193 AA411502	Hs.62180 Hs.63325	Homo sapiens type II membrane serine pro	i	6.53
	115909	AA436666	Hs.59761	ESTs	1	6.98
	115978	AA447522	Hs.69517 Hs.42644	Differentially expressed in Fanconi anem thioredoxin-like	1 0.99	2.31 1.68
30	116028 116107	AA452112 AA456968	Hs.92030	ESTs	1.14	1.8
•	116134	AA460246	Hs.50441	CGI-04 protein	1.11	1.85 1.9
	116157	AA461063	Hs.44298 Hs.61762	Hypothetical protein Hypoxia-inducible protein 2	0.99 0.44	0.86
	116158 116335	AA461187 AA495830	Hs.87013	"Homo sagiens cDNA FLJ10238 fis, clone H	0.62	3.89
35	116483	C14092	Hs.76118	Ubiquitin carboxyl-terminal esterase L1	1.04	2.36 0.64
	117320	N23239	Hs.211092 Hs.44532	LUNX protein; PLUNC(palate lung & nasal Diubiquitin	0.51 1.11	2.63
	117557 117693	N33920 N40939	Hs.112110	PTD007 protein	0.98	1.79
40	117881	N50073	Hs.260622	Butyrate-induced transcript 1	1 0.67	1.43 2.86
40	118368 118566	N64339 N68558	Hs.48956 Hs.42824	ESTs Hypothetical protein FLJ10718	1.21	0.83
	118695	N71781	Hs.50081	KIAA1199 see CVA7.doc	0.88	1.63
	119780	W72967	Hs.191381	ESTs; Weakly similar to hypothetical pro	1	1
45	119845 120102	W79920 W95428	Hs.58561 Hs.132927	G protein-coupled receptor 87 "ESTs, Moderately similar to p53 regulat	i	i
13	120104	W95477	Hs.180479	ESTs	0.69	3.07
	120486	AA253400	Hs.137569	Turnor protein 63 kDa with strong homolog Achaete-scute complex (Drosophila) homol	1.08 1	12.05 1
	120859 120880	AA350158 AA360240	Hs.1619 Hs.97019	EST	1	1
50	120948	AA397822	Hs.104650	Hypothetical protein FLJ 10292	1.04	2.15 1
	120983 121352	AA398209 AA405500	Hs.97587 Hs.97932	EST Chondromodulin I precursor	1	i
	121369	AA405657	Hs.128791	CGI-09 protein	i	1.8
	121791	AA423978	Hs.293317	'ESTs, Weakly similar to JM27 (H.sapiens	1	1
55	123005 123044	AA479726 AA481549	Hs.105577 Hs.130881	ESTs B-cell CLL/lymphoma 11A (zinc finger pro	0.95	1.88
	123160	AA488687	Hs.284235	ESTs	1.59	4.98
	123479	AA599469	Hs.135056	clone RP5-850E9 on chromosome 20	1.19 1.03	1.64 1.14
60	123571 123829	AA608956 AA620697	Hs.112619 Hs.112208	*ESTs, Weakly similar to PQ0109 Purkinje XAGE-1 protein	1.39	2.2
00	124006	D60302	Hs.108977	ESTs	1	4.85
	124059	F13673	Hs.99769	ESTs Seizure related gene 6 (mouse)-tike	1.49 0.76	8.62 0.77
	124960 125218	T15386 W73561	Hs.194766 Hs.110024	NADH:ubiquinone oxidoreductase MLRQ subu	1.33	1.77
65	125453	R05041	Hs.18048	"Melanoma antigen, family A, 10"	0.8	1.42
	125759	AA425587	Hs.82226 Hs.35406	Glycoprotein (transmembrane) nmb "ESTs, Highly similar to unnamed protein	1.52 1.05	2.26 2.48
	125972 125994		Hs.270799	EST	1	1.95
70	126395	N70192	Hs.278956	Hypothetical protein FLJ 12929 .	1	1.35 2.23
70	126645 127221		Hs.61635 Hs.72365	STEAP1 (Homo sapiens BAC clone RG041D11 ESTs	1 0.73	3.27
	127479		Hs.179729	collagen; type X; alpha 1 (Schmid metaph	0.51	1.94
	128192	A1204246	U- 40047	KIAA1085 protein	1.8 0.89	3.16 0.97
75	128610 128777	L38608 U46006	Hs.10247 Hs.10526	activated leucocyte cell adhesion molecu Cysteine and glycine-rich protein 2	1	1
, 5	128924		Hs.26557	Plakophilin 3	1.3	2.97
	129041	H58873	Hs.169902	"Solute carrier family 2 (facilitated gl	0.84 0.87	2.04 1.04
	129099 129404		Hs.108660 Hs.111128	*ATP-binding cassette, sub-family C (CFT ESTs	1	1
80	129466	L42583		"Genbank Homo sapiens keratin 6 isoform	0.72	12.67
	129605		Hs.115947	Keratin 16 (focal non-epidermolytic palm *Cyclin-dependent kinase inhibitor 2A (m	0.92 0.85	1.5 1.93
	129628 130023		Hs.1174 Hs.239600	Calmodulin-like 3	0.84	1.22
0.5	130080	X14850	Hs.147097	"H2A histone family, member X"	0.98	1.96
85	130385		Hs.155223	stanniocalcin 2	1	1

	W	O 02/08644	43			
	130410	V01514	Hs.155421	Alpha-fetoprotein	0.63	0.63
	130441	U35835	Hs.301387	"Human DNA-PK mRNA, partial cds"	1.15	3.65
	130482	1.32866	Hs.1578	Baculoviral IAP repeat-containing 5 (sur	1 0.92	1.88 1.95
5	130553 130577	AA430032 M35410	Hs.252587 Hs.162	Piblitary tumor-transforming 1 Insufin-like growth factor binding prote	1.17	4.7
,	130627	L23808	Hs.1695	Matrix metalloproteinase 12 (macrophage	0.69	4.05
	130800	AA223386	Hs.19574	ESTs; Weakly similar to katanin p80 subu	1.13	241
	130939	AA598689	Hs.21400	ESTs	0.8	0.89
10	131046	X02530	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN PRECURS	0.8 1.13	1.15 1.85
10	131244 131877	D38076 J04088	Hs.24763 Hs.156346	RAN binding protein 1 Topoisomerase (DNA) II alpha (170kD)	1.13	1
	131927	AA461549	Hs.34780	*Doublecortex; Issencephaly, X-linked (0.81	0.62
	131965	W90145	Hs.35962	ESTs	0.74	3.27
1.5	131978	D80008	Hs.36232	KIAA0186 gene product	1	1
15	132354	L05187	Hs.211913	Small proline-rich protein 1A	0.69 0.79	1.43 4.27
	132543 132632	AA417152 N59764	Hs.5101 Hs.5398	ESTs; Highly similar to protein regulati guanine-monophosphate synthetase	1	1.08
	132653	U31201	Hs.54451	"taminin gamma2 chain gene (LAMC2), exon	i	1
	132659	Z75190	Hs.54481	*Low density lipoprotein receptor-relate	0.89	0.89
20	132710	W93726	Hs.55279	"Serine (or cysteine) proteinase Inhibit	0.64	4.41
	132758	W52432	Hs.56105	"ESTs, Weakly similar to WDNM RAT WDNM1	1.55 0.83	2.08 1.66
	132767 132816	L05188 M74542	Hs.231622 Hs.575	Small proline-rich protein 2B Aldehyde dehydrogenase 3	0.55	0.55
	132990	AA458761	Hs.18387	transcription factor AP-2 alpha (activat	1	3.53
25	133070	U69611	Hs.64311	"A disintegrin and metalloproteinase dom	1.16	2
	133282	U52960	Hs.285145	*SRB7 (suppressor of RNA polymerase B, y	1	2.7
	133317	AA215299	Hs.70830	U6 snRNA-associated Sm-like protein LSm7	0.95	1.42 2.55
	133370	AA156897	Hs.72157	Homo sapiens mRNA; cDNA DKFZp56411922 H.sapiens activin beta-A subunit (exon 2	1.12 1.65	1.76
30	133391 133832	X57579 H03387	Hs.727 Hs.241305	estrogen-responsive B box protein (EBBP)	1.02	1.39
50	134032	Z81326	Hs.78589	"Serine (or cysteine) proteinase inhibit	1	1
	134168	AA398908	Hs.181634	"Homo sapiens cDNA: FLJ23602 fis, clone	0.95	1.53
	134218	AA227480	Hs.80205	Pim-2 oncogene	1.36	2.48
35	134405	R67275	Hs.82772	***Collagen, type XI, alpha 1***	0.76 1.89	2.86 3.78
33	134453 134470	X70683 X54942	Hs.83484 Hs.83758	SRY (sex determining region Y)-box 4 CDC28 protein kinase 2	1.82	4.11
	134645	U87459	Hs.167379	*Cancerhestis antigen (NY-ESO-1, CTAG1,	0.82	0.83
	134781	M17183	Hs.89626	Parathyroid hormone-like hormone	1	1
40	135002	U19147	Hs.272484	Gantigen 6	1	1
40	100040	M97935	11- 0050	AFFX control: STAT1	0.92 2.92	1.25 8.5
	101201 101664	L22524 M60752	Hs.2256 Hs.121017	matrix metalloproteinase 7 (matrilysin; H2A histone family; member A	1	1
	102025	U03911	Hs.78934	mutS (E. coli) homolog 2 (colon cancer;	0.8	1.61
	102031	U04898	Hs.2156	RAR-related orphan receptor A	1	1
45	102221	U24576		LIM domain only 4	1	1
	102270	U30255	Hs.75888	phosphogluconate dehydrogenase	1.08 0.88	1.43 1.32
	102339 102391	U37022 U41668	Hs.95577 Hs.77494	cyclin-dependent kinase 4 deoxyguanosine kinase	1.07	1.58
	103000	X51956	Hs.146580	enolase 2; (gamma; neuronal)	0.91	1.49
50	103395	X94754	Hs.119503	methionine-tRNA synthelase	0.89	1.32
	105638	AA281599	Hs.20418	Homo sapiens mRNA for for histone H2B; c	0.91	1.25
	105726	AA292328	Hs.9754	activating transcription factor 5	0.94 0.78	1.48 1.56
	114841 115206	AA234722 AA262491	Hs.55408 Hs.186572	ESTs; Moderately similar to CALCIUM-DEPE ESTs	1	1
55	115906	AA436616	Hs.82302	ESTs	0.74	2.52
	119132	R49046	Hs.107911	ATP-binding cassette; sub-family 8 (MDR/	1.1	1.51
	124163	H30539	Hs.189838	ESTs	1	1
	126487	AA482505	Hs.184601 Hs.75478	solute carrier family 7 (cationic amino	1.01 0.85	1.46 1.4
60	127141 128034	AA307960 AA905754	Hs.75103	KIAA0956 protein tyrosine 3-monooxygenase/tryptophan 5-mo	1	1.18
00	128609	AA234365	Hs.102456	survival of motor neuron protein interac	1	1.5
	128895	R37753	Hs.106985	ESTs	1.7	2
	130199	Z48579	Hs.172028	a disintegrin and metalloprotease domain	1	1
65	130524	U89995	Hs.159234 Hs.62402	forkhead box E1 p21/Cdc42/Rac1-activated kinase 1 (yeast	1	1
UJ	133000 133658	U24152 M25756	Hs.75426	secretogranin II (chromogranin C)	1	i
	135047	AA460466	Hs.93597	ESTs	i	1
	100053	M27830		AFFX control: 28S ribosomal RNA	0.88	1.53
70	100114	D00596	Hs.82962		0.68	1.86
70	100128	D11094	Hs.61153	proteasome (prosome; macropain) 26S subu	1.29 0.71	2.03 4.26
	100154 100161	D14657 D14694	Hs.81892 Hs.77329	KIAA0101 gene product phosphatidylserine synthase 1	1.02	1.56
	100168	D14874	Hs.394		0.46	1.17
	100187	D17793	Hs.78183	aldo-keto reductase family 1; member C3	1	1
75	100188	D21063	Hs.57101		0.97	1.4
	100217	D26600	Hs.89545	proteasome (prosome; macropain) subunit;	1.13	1.9
	100220 100287	D28364 D43950	Hs.1600	"Human mRNA for annexin II, 5'UTR (seq chaperonin containing TCP1; subunit 5 (e	1.11 1.13	1.53 2.09
	100297	D43930 D49489	Hs.182429		0.92	1.78
80	100330	D55716	Hs.77152	minichromosome maintenance deficient (S.	1.07	1.61
	100355	D78129		"Homo sapiens mRNA for squalene epoxid	0.96	1.87
	100364	D78586	Hs.154858	carbamoyi-phosphate synthetase 2; aspart	1.49	2.46
	100368	D79987 D84557	Hs.153479		0.59 1.08	1.32 1.9
85	100398 100438	D84557 D87448	Hs.155462 Hs.91417	topoisomerase (DNA) Il binding protein	1.00	2.15
	- 50 700					

	w	O 02/0864	143			
	100455	D87953	Hs.75789	N-myc downstream regulated	0.91	1.48
	100491	HG1153-HT11		Nucleoside Diphosphate Kinase Nm23-H2s	0.99	1.41
	100518	HG174-HT174		Desmoptakin I	1.28	3.17
_	100528	HG1828-HT18		Nexin, Glia-Derived	0.68 1.1	1.9 5.44
5	100661	HG2874-HT30 HG2981-HT31		Ribosomal Protein L39 Homolog "Epican, Alt. Splice 11""	0.8	1.97
	100667 100830	HG4074-HT43		Rad2	1.01	2.12
	101061	K03515	Hs.944	glucose phosphate isomerase	0.91	1.79
	101131	L10838	Hs.167460	splicing factor, arginine/serine-rich 3	1.23	1.87
10	101162	L14595	Hs.174203	solute carrier family 1 (glutamate/neutr	1.35 1.03	2.73 1.78
	101181	L19686 L19779	Hs.73798 Hs.795	macrophage migration inhibitory factor (H2A histone family; member O	0.57	1.3
	101183 101216	1.25876	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDX	0.7	2.2
	101228	L27706	Hs.82916	chaperonin containing TCP1; subunit 6A (0.99	1.99
15	101233	L29008	Hs.878	sorbital dehydrogenase	0.82	211
	101247	L33801	Hs.78802	glycogen synthase kinase 3 beta	1.2 0.69	1.91 2.78
	101332	L47276 L76191	Hs.182018	"Homo sapiens (cell line HL-5) alpha t interleukin-1 receptor-associated kinase	1.04	1.84
	101342 101396	M15796	Hs.78996	proliferating cell nuclear antigen	0.95	3.55
20	101423	M18391	Hs.89839	EphA1	1	1.5
	101445	M21259	Hs.1066	small nuclear ribonucleoprotein polypept	1.21	1.96
	101505	M27396	Hs.75692	asparagine synthetase	0.93 1.19	1.6 1.93
	101525	M29536 M30448	Hs.12163 Hs.251669	eukaryotic translation initiation factor casein kinase 2; beta polypeptide	0.96	1.42
25	101535 101607	M38690	Hs.1244	CD9 antigen (p24)	1.11	1.25
	101624	M55998		"Human alpha-1 collagen type I gene, 3	1.17	1.98
	101758	M77836	Hs.79217	pyrroline-5-carboxylate reductase 1	1.77	3.45 1.45
	101839	M93036	Hs.692	membrane component; chromosomal 4; surfa	0.71 0.84	1.19
30	101853	M94362	Hs.76084	lamin B2 "putative Rab5-interacting protein (cl	0.89	1.9
30	101977 101992	\$83364 U01038	Hs.77597	polo (Drosophia)-like kinase	0.66	1.46
	102009	U02680	Hs.82643	protein tyrosine kinase 9	1.23	3.35
	102012	U03057	Hs.118400	singed (Drosophila)-like (sea urchin fas	0.85	1.88
25	102039	U05861	Hs.201967	aldo-keto reductase family 1; member C1	0.93 1	2.32 4.28
35	102123	U14518	Hs.1594	centromere protein A (17kD) small nuclear ribonucleoprotein D3 polyp	0.89	1.42
	102130 102148	U15009 U16954	Hs.1575 Hs.75823	ALL1-fused gene from chromosome 1q	0.8	2.95
	102210	U23028	Hs.2437	eukaryotic translation initiation factor	1.01	1.34
	102220	U24389	Hs.65436	lysyl oxidase-like 1	1.15	2.34
40	102260	U28386	Hs.159557	karyopherin alpha 2 (RAG cohort 1; Impor	1.14 1.05	2.69 1.7
	102330	U35451	Hs.77254	chromobox homolog 1 (Drosophila HP1 beta small nuclear RNA activating complex; po	1.14	2.99
	102423 102455	U44754 U48705	Hs.179312 Hs.75562	discoldin domain receptor family; member	1.05	2.01
	102499	U51478	Hs.76941	ATPase; Na+/K+ transporting; beta 3 poly	1.27	1.92
45	102522	U53347	Hs.183556	solute carrier family 1 (neutral amino a	0.84	1.31
	102590	U62136		"Homo sapiens enterocyte differentiati	1.11 1.04	1.6 2.17
	102676	U72514	Hs.12045 Hs.93002	putative protein ubiquitin carrier protein E2-C	0.86	2.28
	102687 102704	U73379 U76638	Hs.54089	BRCA1 associated RING domain 1	1.12	1.63
50	102781	U83843		""Human HIV-1 Nef Interacting protein (0.9	1.39
	102784	U85658	Hs.61796	transcription factor AP-2 gamma (activat	0.98	2.16 1.62
	102827	U91327	Hs.6456	chaperonin containing TCP1; subunit 2 (b	0.96 1,21	4.2
	102935 102972	X13482 X16662	Hs.80506 Hs.87268	small nuclear ribonucleoprotein polypept annexin A8	1.25	2.32
55	102983	X17620	Hs.118638	non-metastatic cells 1; protein (NM23A)	1.03	1.83
• •	103023	X53793	Hs.117950	multifunctional polypeptide similar to S	1.58	5.44
	103038	X54941	Hs.77550	CDC28 protein kinase 1	1.32	3.79 2.58
	103075	X59543	Hs.2934	ribonucleotide reductase M1 polypeptide glutathione peroxidase 2 (gastrointestin	1.11 0.75	3.05
60	103168 103185	X68314 X69910	Hs.2704 Hs.74368	transmembrane protein (63kD); endoplasmi	1.01	1.97
oo	103212	X73874	Hs.2393	phosphorylase kinase; alpha 1 (muscle)	0.95	1.72
	103223	X74801	Hs.1708	chaperonin containing TCP1; subunit 3 (g	0.97	1.77
	103260	X78416	Hs.3155	casein; alpha	1 1 <i>.2</i> 3	3.09
65	103262 103330	X78565	Hs.204133 Hs.77496	hexabrachion (tenascin C; cytotactin) small nuclear ribonucleoprotein polypept	1.12	2.25
UJ	103354	X85373 X90872	Hs.75854	SULT1C sulfotransferase	2.85	4.62
	103375	X91868	Hs.54416	sine oculis homeobox (Drosophila) homolo	1	2.48
	103391	X94453	Hs.114366	pyrroline-5-carboxylate synthetase (glut	1	1.53
70	103404	X95586	Hs.78596	proteasome (prosome; macropain) subunit;	0.92 0.92	1.53 1.54
70	103437	X98260 X99133	Hs.82254 Hs.204238	M-phase phosphoprotein 11 lipocalin 2 (oncogene 24p3)	0.55	0.96
	103448 103605	Z35402	Hs.194657	cadherin 1; E-cadherin (epitheliai)	1.32	2.51
	103646	Z68228	Hs.2340	junction plakoglobin	0.88	1.28
95	103658	Z74615	Hs.172928	collagen; type t; alpha 1	1.06	2.98 4.66
75	103774	AA092898	Hs.92918	ESTs; Weakly similar to R07G3.8 [Celega	1.88 0.87	2.17
	104261 104276	AF008442 C02193	Hs.5409 Hs.85222	RNA polymerase I subunit ESTs; Weakly similar to R27090_2 [H.sapi	1.4	2.49
	104276	C16281	Hs.75478	KIAA0956 protein	1.15	1.68
	104434	L02870	Hs.1640	collagen; type VII; alpha 1 (epidermolys	1.04	1.49
80	104453	M19169	Hs.123114	cystafin SN	0.38	0.76 2.25
	104611	R98280	Hs.125845	ribulose-5-phosphate-3-epimerase	1.08 1.14	1.65
	104758		Hs.7010	ESTs; Weakly similar to ACYL-COA DEHYDRO adenosine A2b receptor pseudogene	0.91	1.38
	105114 105132		Hs.11801 Hs.247280	HBV associated factor	1.08	1.7
85	105174		Hs.34744	ESTs	0.95	2.05

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	105280	AA232215	Hs.14600	ESTs	1 0.72	1.4 2.02
	105344 105516	AA235303 AA257971	Hs.8645 Hs.21214	ESTs ESTs	1.35	3.56
	105515	AA280865	Hs.6375	Homo sapiens mRNA; cDNA DKFZp564KD222 (f	1.23	1.82
5	105698	AA287393	Hs.15202	ESTs; Weakly similar to oligodendrocyte-	0.98	1.28
	105705	AA290767	Hs.101282 Hs.22934	Homo sapiens mRNA; cDNA DXFZp434B102 (fr ESTs; Weakly similar to ZINC FINGER PROT	0.92 0.99	1.32 1.41
	105724 105782	AA292098 AA350215	Hs.21580	ESTs TREADY SAILING IN ENCOUNTRICE TROOP	1	1
	105799	AA372018	Hs.24743	ESTs	1.08	1.78
10	105807	AA393803	Hs.16869	ESTs; Moderately similar to COLLAGEN ALP	0.95 0.87	1.34 2.25
	105891 105936	AA400768 AA404338	Hs.26662	ESTs; Wealthy similar to turnor necrosis f ESTs	1.14	1.46
	106069	AA417741	Hs.29899	ESTs; Weakly similar to ZINC FINGER PROT	1	1
1.5	106103	AA421104	Hs.12094	ESTs	1.04 1.23	1.44 2.11
15	106140 106149	AA424524 AA424881	Hs.14912 Hs.256301	KIAA0286 protein ESTs	0.83	1.48
	106154	AA425304	Hs.6994	ESTs	0.77	2.05
	106182	AA426609	Hs.10862	ESTs	0.74 0.97	2.23 1.99
20	106220 106228	AA428582 AA429290	Hs.32196 Hs.17719	ESTs; Moderately similar to metargidin p ESTs	0.99	1.54
20	106318	AA436570	Hs.9605	pre-mRNA cleavage factor lm (25kD)	0.95	2.09
	106341	AA441798	Hs.5243	ESTs; Moderately similar to pll.2 hypothe	0.93 0.95	2.66 1.93
	106432 106474	AA448850 AA450212	Hs.17138 Hs.42484	ESTs Homo sapians mRNA; cDNA DKFZp564C053 (fr	1	1
25	106483	AA451676	Hs.30299	IGF-II mRNA-binding protein 2	1.4	2.29
	106599	AA457235	Hs.12842	ESTs; Moderately similar to non-function	1	1.82 2.78
	106611	AA458904	Hs.26267 Hs.3784	ESTs; Weakly similar to torsinA (H.sapie ESTs; Highly similar to phosphoserine am	1,49 1	1.4
	106654 107076	AA460449 AA609145	Hs.21143	ESTs; Weakly similar to fos39554_1 [H.sa	1.11	1.49
30	107115	AA610108	Hs.27693	ESTs; Highly similar to CGI-124 protein	1	1.03
	107129	AA620553	Hs.4756	flap structure-specific endonuclease 1	1.13 1.05	3.63 2.09
	107159 107444	AA621340 W28391	Hs.10600 Hs.5181	ESTs; Wealdy similar to ORF YKR081c [S.c proliferation-associated 2G4; 38kD	1.18	1.9
	107481	W58247	Hs.27437	Homo sapiens kinesin superfamily motor K	0.99	2.74
35	107516	X56597	Hs.99853	fibrillarin	0.94 1.05	1.77 2.29
	107529 107531	Y12065 Y13936	Hs.5092 Hs.17883	nucleolar protein (KKE/O repeat) protein phosphatase 1G (formerly 2C); ma	1.06	1.62
	107801	AA019433	Hs.173100	ESTs	1.03	1.4
40	107957	AA031948	Hs.57548	ESTs	0.95 0.59	1.46 1.35
40	108565 108780	AA085342 AA128561	Hs.1526 Hs.117938	ATPase; Ca++ transporting; cardiac muscl collagen; type XVII; alpha 1	1	7.63
	108828	AA131584	Hs.71435	DKFZP564O0463 protein	1.33	2.56
	109060	AA160879	Hs.241551	chloride channel; calcium activated; fam	0.67 1.03	1.42 2.31
45	109112 109344	AA169379 AA213696	Hs.72865 Hs.86559	ESTs poly(A)-binding pratein-like 1	0.97	1.55
٠,	109412	AA227145	Hs.209473	ESTs; Weakly similar to REGULATOR OF MIT	0.76	1.87
	110780	N23174	Hs.22891	solute carrier family 7 (cationic amino	0.9 1.17	0.95 2.26
	110958 111018	N50550 N54067	Hs.24587 Hs.3628	signal transduction protein (SH3 contain mitogen-activated protein kinase kinase	1.21	1.85
50	111337	N79612	Hs.16607	ESTs; Highly similar to Myosin heavy cha	1	1.45
	112305	R54822	Hs.26244	ESTs	1 1.24	1 1.64
	112401 112853	R61279 T02843	Hs.237536 Hs.4351	ESTs; Weakly similar to F25B5.3 [C.elega EST	1.56	1.96
	112869	T03313	Hs.4747	dyskeratosis congenita 1; dyskerin	1.03	1.57
55	112992	T23513	Hs.7147	ESTs	1 1.37	1 2.26
	113048 113063	T25895 T32438	Hs.184008 Hs.5027	ESTs; Weakly similar to RNA-binding prot ESTs	1	1
	113179	T55182	Hs.152571	ESTs; Highly similar to IGF-II mRNA-bind	1.33	2.7
<i>د</i> ۸	113573	T91166	Hs.15990	ESTs	0.76 0.79	1.47 1.51
60	113811 114086	W44928 Z38266	Hs.4878 Hs.12770	ESTs Homo sapiens PAC clane DJ0777023 from 7p	0.9	1.34
	114587	AA070827	Hs.180320	ESTs; Weakly similar to GOLGI 4-TRANSMEM	1.02	1.76
	114846	AA234929	Hs.44343	ESTs	1.32 1.1	2.36 1.84
65	114964 115047	AA243873 AA252627	Hs.82184 Hs.22554	ring finger protein 3 homeo box B5	1.01	2.36
03	115166		Hs.198907	myelin protein zero-like 1	1.05	2.31
	115167	AA258421	Hs.43728	hypothetical protein	1.52	2.52 2.57
	115239 115278	AA278650 AA279757	Hs.73291 Hs.67466	ESTs; Weakly similar to similar to the b ESTs; Weakly similar to BACN32G11.d [D.m	0.7 1.14	2.12
70	115652		Hs.38178	ESTs	0.82	4.67
	115875	AA433943	Hs.43946	ESTs; Weakly similar to Weak similarity	1.2	1.98 1.31
	116004 116121		Hs.76086 Hs.48855	ESTs; Highly similar to small zinc finge ESTs	0.96 0.97	1.55
	116129		Hs.49163	ESTs; Highly similar to putative ribonuc	1.08	2.73
75	116190	AA464963	Hs.67776	ESTs	0.8	1.57 2.65
	116312		Hs.65403 Hs.165909	ESTs ESTs	1.37 0.92	1.8
	116732 117602		Hs.44685	ESTs; Weakly similar to GOLIATH PROTEIN	1.15	1.84
00	117950	N51394	Hs.75478	KIAA0956 protein	1.04	2.36
80	117992		Hs.172089 Hs.111857	Homo sapiens mRNA; cDNA DKFZp58680222 (f GLI-Kruppel family member GLI2	0.62 1	1.29 1
	118785 119717		Hs.57987	ESTs	1	1.4
	119814	W74069	Hs.58350	ESTs	0.78	1.77
85	120128		Hs.91448	MKP-1 like protein tyrosine phosphatase ESTs	0.86 0.83	1.46 2.01
05	120242	Z98443	Hs.86366	Loid		

	W	O 02/086	443			4.01
	120483	AA252994	Hs.1578	apoptosis inhibitor 4 (survivin)	0.74 1.05	1.64 1.93
	121054	AA398604	Hs.97387 Hs.97031	ESTs ESTs; Weakly similar to Similar to phyto	0.98	1.3
	121326 121376	AA404246 AA405699	Hs.166232	ESTS; Moderately similar to SODIUM- AND	0.91	1.83
5	121457	AA411448	Hs.208985	ESTs	0.91	1.59
-	121780	AA422086	Hs.124660	ESTs	0.46	0.55 1.54
	121781	AA422150	Hs.98370	cytochrome P540 family member predicted	1.07 0.94	1.4
	121844 122059	AA425732 AA431737	Hs.98485 Hs.98749	gap junction protein; beta 2; 26kD (com EST	1.93	2.33
10	122338	AA443311	Hs.98998	ESTs	1	1
	122354	AA443772	Hs.186692	ESTs	88.0	1.39 2.93
	122591	AA453265	Hs.99311	ESTs; Wealdy similar to MRJ (H.sapiens)	2.28 0.88	1.3
	122790 123398	AA460156 AA521265	Hs.99556 Hs.105514	ESTs ·	1	1.93
15	123518	AA508531	Hs.170313	ESTs	1	1
••	123673	AA609471	Hs.112712	ESTs	1	1.15 1.12
	124000	D57317	Hs.74861	activated RNA polymerase II transcriptio	0.74 0.67	1.12
	124367 124447	N24006 N48000	Hs.99348 Hs.140945	distal-less homeo box 5 Homo sapiens mRNA; cDNA DKFZp586L141 (fr	1.19	1.7
20	125756	W25498	Hs.81634	ATP synthase; H+ transporting; mitochond	0.93	1.59
	125769	A1382972	Hs.82128	5T4 oncofetal trophoblast glycoprotein	1.65	6.76 2.26
	125852	H09290	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	0.72 1.22	2.25
	125924 126037	AA526849 M85772	Hs.82109 Hs.6066	syndecan 1 KIAA1112 protein	1.36	1.63
25	126214	N29455	Hs.74316	desmoplakin (DPI; DPII)	1.93	3.55
	126414	N78770	Hs.223439	ESTs	1.21	1.66 1
	126737	AA488132	Hs.62741	ESTs poly(A)-binding protein; cytoplasmic 1	1 1.3	2.16
	126743 126926	AA179253 AA179546	Hs.172182 Hs.832	ESTs; Highly similar to INTEGRIN BETA-8	2.53	2.8
30	127432	AA501734	Hs.170311	heterogeneous nuclear ribonucleoprotein	1.57	2.12
•••	128218	H02682	Hs.99189	ESTs; Moderately similar to recombinatio	1.24	2.09 1.78
	128527	M31523	Hs.101047	transcription factor 3 (E2A immunoglobul	1.08 1.23	3.48
	128568 128584	X60573 M11433	Hs.247568 Hs.101850	adenylate kinase 3 retinol-binding protein 1; cellular	0.87	2.42
35	128628	C14037	Hs.251978	EST	1.22	1.9
	128691	W27939	Hs.103834	ESTs	1.1	1.73 1.17
	128714	V00599	Hs.179661	Homo sapiens clone 24703 beta-tubulin mR	0.92 1.34	1.94
	128733 128781	AA328993 X85372	Hs.104558 Hs.105465	ESTs small nuclear ribonucleoprotein polypept	0.9	1.34
40	129052		Hs.182740	ribosomat protein S11	2.59	3.19
	129095	L12350	Hs.108623	thrombospondin 2	1.04	3.2 1.61
	129241	AA435665	Hs.109706	ESTs; Moderately similar to HN1 (M.muscu KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	0.95 1.28	2.63
	129665 129703	M88458 AA401348	Hs.118778 Hs.179999	ESTs	0.97	1.63
45	129720	AA476582	Hs.12152	ESTs; Moderately similar to SIGNAL RECOG	1.09	1.79
	129850	N20593	Hs.56845	GDP dissociation inhibitor 2	0.74 1.43	1.68 4.19
	129896	AA043021 AA055896	Hs.13225 Hs.146428	UDP-Gal:betaGtcNAc beta 1;4- galactosylt collagen; type V; alpha 1	1.17	1.98
	130069 130405	H88359	Hs.155396	nuclear factor (erythroid-derived 2)-lik	1.26	1.79
50	130541	X05608	Hs.211584	neurofilament; light polypeptide (68kD)	1	1
	130599	M91670	Hs.174070	ubiquitin carrier protein	1.07 1	1.66 4.8
	130867 131009	J04093 AA063596	Hs.2056 Hs.22142	UDP glycosyltransferase 1 ESTs; Weakly similar to NADH-CYTOCHROME	0.93	1.05
	131028	U20240	Hs.2227	CCAAT/enhancer binding protein (C/EBP);	1	1.23
55	131083	U66661	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.1	1.8 1.98
	131091	T35341	Hs.22880	ESTs; Highly similar to dipeptidyl pepti	1,28 1,43	2.06
•	131144 131148	C14412 C00038	Hs.23528 Hs.23579	ESTs; Highly similar to HSPC038 protein ESTs	0.88	3.38
	131164	Y00503	Hs.182265	keratin 19	1.19	2.77
60	131185		Hs.23960	cyclin B1	0.86 0.66	3.84 2.96
	131219 131454		Hs.24395 Hs.2699	small inducible cytokine subfamily B (Cy glypican 1	0.99	1.54
	131687	AA455896 L11066	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	1	1.18
	131689		Hs.30696	transcription factor-like 5 (basic helix	1	1.95 2.39
65	131692		Hs.30736	KIAA0124 protein	1.55 1	1.33
	131786		Hs.32125 Hs.184062	ESTs ESTs; Moderately similar to putative Rab	0.83	1.63
•	131843 131860		Hs.334	Oncogene TIM	1.08	2.2
	131884		Hs.3463	ribosomal protein S23	1.23	1.24
70	131903		Hs.3436	deleted in oral cancer (mouse; homolog)	0.91 1	1.18 2.8
	131945 131958		Hs.35120 Hs.3566	replication factor C (activator 1) 4 (37 ESTs; Highly similar to phosphorylation	0.87	1.36
	131964		Hs.3593	ESTs	1	1.25
	132001	J00277	Hs.37003	v-Ha-ras Harvey rat sarcoma viral oncoge	1.12	1.43 1.55
75	132040		Hs.172894 Hs.211594	BH3 interacting domain death agonist proteasome (prosome; macropain) 26S subu	1 0.89	1.27
	132065 132109		Hs.40098	ESTs	1	1.05
	132112		Hs.40154	jumonji (mouse) homolog	0.99	1.44
00	132123	AA447123	Hs.250705	ESTs	1.06 1.08	2.46 2.46
80	132162		Hs.41241 Hs.418	ESTs fibroblast activation protein; alpha; se	1.02	4.56
	132180 132309		Hs.2780	jun D proto-oncogene	1.16	1.8
	132371	AA235448	Hs.46677	ESTs	0.8	1.26
95	132618	AA253330	Hs.5344	adaptor-related protein complex 1; gamma	0.5 1.21	1.49 1.81
85	132736	U68019	Hs.211578	MAD (mothers against decapentaplegic; Dr		

	W	O 02/0864	143			
	132771	AA488432	Hs.56407	phosphoserine phosphatase	1	1.3
	132833	U78525	Hs.57783	enkaryotic translation initiation factor	0.91	1.43
	132922	T23641	Hs.6066	KIAA1112 protein	1.16	1.53
	132959	AA028103	Hs.61472	ESTs: Wealty similar to unknown (S.cerev	1.02	1.88
5	132994	AA505133	Hs.7594	solute carrier family 2 (facilitated glu	0.72	2.97
_	133005	C21400	Hs.103329	KIAA0970 protein	0.88	1.34
	133065	X62535	Hs.172690	diacytotycerol kinase; alpha (80kD)	0.93	1.23
	133083	N70633	Hs.6456	chaperonin containing TCP1; subunit 2 (b	1.14	1.76
	133086	L17131	Hs.139800	high-mobility group (nonhistone chromoso	0.97	1.43
10	133134	T89703	Hs.65648	RNA binding motif protein 8	1.1	1.8
	133195	AA350744	Hs.181409	KIAA1007 protein	2.29	2.69
	133313	AA249427	Hs.70704	ESTs	1.07	1.68
	133331	T62039	Hs.158675	ribosomal protein L14	0.85	1.18
	133438	D13370	Hs.73722	APEX nuclease (multifunctional DNA repail	0.91	1.45
15	133445	T99303	Hs.73797	guanine nucleolide binding protein (G pr	0.94	1.68
	133483	X52426	Hs.74070	keratin 13	0.85	1.14
	133492	L40397	Hs.74137	transmembrane trafficking protein	1.1	1.69
	133504	W95070	Hs.74316	desmoplakin (DPI; DPII)	0.7	6.21
	133517	X52947	Hs.74471	gap junction protein; alpha 1; 43kD (con	0.95	1.3
20	133540	D78151	Hs.74619	proteasome (prosome; macropain) 26S subu	0.91	1.25
	133594	L07758	Hs.172589	nuclear phosphoprotein similar to S. cer	0.84	1.29
	133627	U09587	Hs.75280	glycyl-tRNA synthetase	1.09	1.99
	133671	T25747	Hs.75471	zinc finger protein 146	1.02	1.5
	133859	U86782	Hs.178761	26S proteasome-associated pad1 homolog	1.11	3.33
25	133865	F09315	Hs.170290	discs; large (Drosophila) homolog 5	1.84	6.7
	133913	W84712	Hs.7753	calumenin	1.15	1.86
	133963	L34587	Hs.184693	transcription elongation factor B (SIII)	1.3	1.91
	133982	U47621	Hs.207251	nucleolar autoantigen (55kD) similar to	1.3	1.99
	134100	L07540	Hs.171075	replication factor C (activator 1) 5 (36	0.72	1.65
30	134110	U41060	Hs.79136	LIV-1 protein; estrogen regulated	1.04	1.62 1.55
	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	1 0.82	1.95
	134161	U97188	Hs.79440	IGF-II mRNA-binding protein 3	0.98	1.48
	134193	F09570	Hs.7980	ESTs	1	2.8
25	134367	X54199	Hs.82285	phosphoribosylglycinamide formyltransfer	1.26	2
35	134402		Hs.82712	fragile X mental retardation; autosomal	1.20	1.47
	134457	D86963	Hs.174044	dishevelled 3 (homotogous to Drosophila	0.94	1.57
	134469	X17567	Hs.83753	small nuclear ribonucleoprotein polypept	1.2	2.64
	134498	M63180	Hs.84131	threonyl-tRNA synthetase	0.84	1.36
40	134501	W84870	Hs.211568	eukaryotic translation initiation factor	1.7	293
40	134507	M63488	Hs.84318	replication protein A1 (70kD)	1.46	273
	134548	U41515	Hs.85215	Deleted in split-hand/split-foot 1 regio	1.36	2.22
	134599	X99226	Hs.86297	Fanconi anemia; complementation group A a disintegrin and metalloproteinase doma	0.77	1.64
	134692		Hs.8850		1.09	1.82
45	134693	N70361	Hs.8854	ESTs	0.98	1.35
43	134806	Z49099	Hs.89718 Hs.198382	spermine synthase plakophilin 1 (ectodermal dysplasia/skin	0.99	1.4
	134821	Z34974		actin related protein 2/3 complex; subun	0.95	1.42
	134864	Y08999	Hs.90370 Hs.91093	chitinase 1 (chitotriosidase)	1.16	1.29
	134914		Hs.91747	profilin 2	0.95	1.76
50	134953 134993	L10678 AA282343	Hs.9242	purine-rich element binding protein B	0.98	1.73
50	134993	C15324	Hs.93668	ESTs	1.35	2.11
	135158	U51711	12.53000	Human desmocollin-2 mRNA; 3' UTR	0.86	1.16
	133130	031711		CHILDRIC OCCUPANICS IN BALL O. C		

Table 18 shows the accession numbers for those pkeys in Table 1A lacking uniqueelD's. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the Accession oclumn.

60	Pkey: Unique Eas probeset identifier number
UU	CAT number: Gene cluster number
	According: Contract accession numbers

	Pkey	CAT	Accessions
65	100661 100667	23182_1 26401_3	BE623001 L05096 AA383604 AW966416 N53295 AA460213 AW571519 AA603655 L05424 X56794 S66400 X55150 W60071 AW351820 X55938 M83326 BE005289 BE070059 M83324 BE005248 BE069717 BE181648 BE069700 AW606203 BE069721 AW382138 AW803776 BE463954 BE005334 BE005274 T27386 AA932714 AA972595 AW377728 AI632506 T29066 AJ763934 AW377727 BE163715 AL047291 AA279047 AA523003 BE008048 BE440141 W23614 BE090519 BE092193 N29181 N20358 N44153
70			BE546944 T69231 AW377441 AA907406 H50799 AW051416 AI420712 BE620922 AI279161 AA992549 WA7198 BE005241 AI342896 H50700 AI969974 AI863955 AA374490 AW130675 AI959633 AV46687 H99482 X55150 BE005414 B1096 AI867806 AI887800 AW804171 AI675961 AW804172 AA778841 AL048050 AI127757 AI095568 AW204955 AW468978 W31898 AI05295 AI278771 BE464018 AI051903 AI824196 AA513211 AA411062 AW064376 N46752 AA703209 N35580 AW059918 AA054653 AI280942 T27619 BE621435 N56010 AW589527 AI160414 AA283090 AA962536 H82726 W52115 W45432 W60433 AA577548 AA146714 BE150994 AA054615 AW796025 AW382768 BE565671 C00444
75	100668	26401_3	AAD54555 L05424 X56794 \$66400 X55150 W60071 AW351820 X55938 M83326 BE005289 BE070059 M83324 BE005248 BE069717 BE181648 BE069700 AW606203 BE069721 AW382138 AW803776 BE463954 BE005334 BE005274 T27386 AA932714 AA972695 AW377728 AI632506 T29068 A1783934 AW377727 BE163715 AL047291 AA279047 AA523003 BE008048 BE440141 W23614 BE090519 BE092193 N29181 N20358 N44153
80			BES46944 T69231 AW377441 AA907406 H50799 AW051416 AI420712 BE620922 AI279161 AA992549 W47198 BE005241 AI342696 H50700 AI969974 AI863855 AA374490 AW130675 AI950633 AA146687 H99482 X55150 BE005414 BE005339 N28294 AI673068 AI887890 AW804171 AI675961 AW804172 AA776841 AL048050 AI127757 AI095568 AW204985 AW468978 W31898 AI052595 AI278771 BE464018 AI081503 AI824196 AA513211 AA411062 AW084376 N48752 AA703209 N35580 AW059918 AA054563 AI280942 T27619 BE621435 N56010 AW589527 AI160414 AA283090 AA962536 H82726 W52115 W45432 W60433 AA577548 AA146714 BE150994 AA054615 AW796025 AW382768 BE565571 C00444 AA054555
85	101332	25130_1	D4088 NM_001067 AF071747 AJ011741 N85424 AL042407 AA218572 BE296748 BED83981 AL040877 AW499918 AW675045 H17813 BE081283 AA670403 AW504327 BE094229 AA104024 A1471482 A1970337 AA737616 A1827444 AW003286 A1742333 A1344044 A1765634

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A948838 AW235336 AW172827 AA095289 BED45383 AI734240 W16699 AI660329 AI289433 AA933778 AV1469242 AA68838 AA906983

APAGE ARABATA AA196573 AIC74790 AA69673 AIC7479 AM994319 AI731824 AI377434

			AI948838 AW235336 AW172827 AA095289 BE045383 AI734240 W16699 AI660329 AI289433 AA933778 AW469242 AA68838 AA930953 AA625873 W78031 BE206307 AA550803 AI743147 AI990075 AA948274 AA129533 AI635399 AA655313 AI624669 AW594319 AI221834 A1337434
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			R94438 N73126 H33466 AAU9026 AAU90261 12902 H34591011 2471 C4121 AV262710 A1076594 AA583483 AW973194 AW575166 A1128799 H34033 N57027 AA544348 AA327563 AW959913 N53767 AA543715 A145347 AW263710 A1076594 AA583483 AW973194 AW575166 A1128799 A803319 A1042776 AW074313 AB587722 A1032284 AA447521 A1123885 N29334 A1354911 AW970687 AA326753 AA355353 AA335573 AA365757
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			AAR34316 AW591901 AW063876 AW294770 AI300266 AI336094 AI560380 AA721755 RU9976 D20305 D25155 ATT621755 BE155554
			A4457474 AW466316 AA550969 AA630768 BE561958 BE561728 BE397612 BE514391 BE269037 BE514207 BE562381 BE514256 BE514403 BE514250 BE397832 BE269598 BE559865
15	100780	458_127	
13	100830	4002_1	
	100000	4002_1	
			BE548530 AW747547 AC (6062 BE35/362 ANG601 10111
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			A1358774 RE243487 AA620553 AA653297 AA292690 T10110 Z38906 AA908544 AA340930 A1155438 105328 126644 A667010 A664385
0.5	100905	4312_1	AIB72575 BE388740 156780 AW373138 BE286717 A0059971 AU076916 BE298110 AW239395 AW672700 NM, 003875 U10860 AW651755 BE297958 C03806 AI795876 AA644165 T36030 AW392852 AA446421 AW881865 AI469428 BE548103 T96204 R94457 N78225 AI564549 AW0004984 AW780423 AW675448 AW087890 AA971454 AA305698
25			
	100930	16865_1	
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30			AA708816 AI826712 AW296294 AA293419 AI276361 AW044134 AW49128 AA21247 AA36220 AL047797 M34046 N42277 AA228076 W02698 AI420297 AI804952 AA479874 AI59761 AI427671 AI479738 AA421247 AA421247 AA436220 AL047797 M34046 N42277 AA228076 W02698 AI420297 AI804952 AA479878 AI479738 AA421247 AA421247 AA436220 AL047797 M34046 N42277 AA228076 W02698 AI420297 AI804952 AA479878 AI479738 AA421247 AA436220 AL047797 M34046 N42277 AA228076 W02698 AI420297 AI804952 AA479878 AI804978 AI80
		0004 4	AA434011 AI35997 AA479731 AI865541 AI418020 AA421246 AA452764 AL048051 NM_006769 U24576 AW161961 AW160473 AW160465 AW160472 AW161069 AI824831 AW162635 AI990356 AW162477 AW162571 AI520836 NM_006769 U24576 AW161961 AW160473 AW160465 AW160472 AW161069 AI824831 AW162635 AI990356 AW162477 AW162571 AI520836
	102221	3861_1	
35			AW356451 T34489 D65106 D6351 AW30357 AW05251 F4 AW165236 AH315242 D45274 AW263991 AA442920 AA129965 ALD35713 AI923255 AI949082 AI952998 AA912579 AI143356 AW902211 R64717 AW157235 AI915242 D45274 AW263991 AA442920 AA129965 ALD35713 AI923255 AI949082 AI942526 AI684160 AI701987 AI678954 AI827349 BE463635 AW628092 AW302281 AA4923203 BE3484856 BE536419 AW193969 AW673661 AI442826 AI684160 AI701987 AI678954 AI827349 BE463635 AW628092 AW302281 AA492303 BE34976 AI69791 AIR74704 AI7072 AI7072 AIR74704 AI7072 AI7
			A 104 (CON A A 07200 S AT 0.4720 S AT 1200 S S AT 0.4720 S AT 1708
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	101809	32963_1	A1186756 A1273778 AA610487 A179746 AA639937 A199593 AA59151 A21607 A199784 A189784 A19958 AW383155 AA490688 AW117930 AW384563 AW384544 M86849 AA315289 NM A00400 AA315269 BE142653 AA461400 AW802042 BE152893 AW383155 AA490688 AW117930 AW384563 AW384564 AW378307 AW378307 AW378323 AW839085 AA257102 AW378317 AW276060 AW271245 AW378238 AW384457 A198114 AW264544 A1018136 AW378307 AW378307 AW378323 AW839085 AA257102 AW378317 AW276060 AW271245 AW378238 AW384457 A198114 AW264544 A1018136 AW378307 AW378307 AW378323 AW839085 AA257102 AW378317 AW276060 AW27104 AW378317 AW378307 AW378323 AW839085 AA257102 AW378317 AW276060 AW27104 AW378317 AW378317 AW26460 AW378317 AW378317 AW378317 AW378317 AW378317 AW378317 AW378317 AW378317 AW278517 AW278517 AW278517 AW378317 AW37831 AW378317 A
45			
			AD00737 A418400 AA947181 AA9527 10 A120033 A1912481 AA9500714 BE465701 NB4149 C00523 NB4240 AA677120 AD076554 AW511702 NB5923 HB8912 AA257017 A1952506 HB8913 AB912481 AA500714 BE465701 NB4149 C00523 NB4240 AA677120 AD076554 AW511702 NB592506 HB8913 AB912481 AA500714 BE466701 NB4149 C00523 NB4240 AA677120 AD076554 AW511702 AW5
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			AA297/163 AA218550 AA21 1005 A02550 1005 A025100 A025100 A025100 A02510
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60	101977	250/3_1	10 COOK 11 COOKER ALADORA COOKER AMERICAN ALECTRIC AMERICAN AMERICAN ALECTRICAN ALECTRIC
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			AW028742 BE088442 AA65/742 AA74436 AW1 1008 Al03522 WA2575 A 1093341 A1278762 BE092517 N74204 H06158 T58149 A1129303 N58366 A1375014 A1125547 A1348244 A13460477 A1748952 N26915 A1753574 A1093341 A1278762 BE092517 N74204 H06158 T58149 A1129303 N58366 A354456 BE122661 AA542925 A1246120 A1735203 AA706829 AA877544 A1082289 AA926687 N92840 AW249798 AA934763 AW998563 AA524456 BE122661 AA542925 A1246120 A1735203 AA706829 AA877544 A1082289 AA926687 N92840 AW249798 AA934763 AW998563 AA524456 BE122661 AA542925 A1246120 A1735203 AA706829 AA877544 A1082289 AA926687 N92840 AW249798 AA934763 AW998563 AA524456 BE122661 AA542925 A1246120 A1735203 AA706829 AA877544 A1082289 AA926687 N92840 AW249798 AA934763 AW998563 AA54456 BE122661 AA542925 A1246120 A1735203 AA706829 AA877544 A1082289 AA926687 N92840 AW249798 AA934763 AW998563 AA54456 BE122661 AA542925 A1246120 A1735203 AA706829 AA877544 A1082289 AA926687 N92840 AW249798 AA934763 AW998563 AA54456 BE122661 AA542925 A1246120 A1735203 AA706829 AA877544 A1082289 AA926687 N92840 AW249798 AA934763 AW998563 AA54456 BE122661 AA542925 A1846120 A1735203 AA706829 AA87754 A1082289 AA926687 N92840 AW249798 AA934763 AW998563 AA54456 BE122661 AA542925 A1846120 A1735203 AA706829 AA87754 A1082289 AA926687 N92840 AW249798 AA934763 AW998563 AA54456 BE122661 AA542925 A1846120 A1735203 AA706829 AA97654 A1846120 A18461
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			AA125112 AI800091 AI551215 H17902 AI4013512 AI6013503 AI6502 AI791212 AI6504091313 AI674584 AA292533 AI079471 AA642325 AA719050 AA159174 AI827966 F30305 F30309 AA806662 AI091923 AW878722 AA583430 AW571913 AI674584 AA292533 AI079471 AA642325 AA719050 AW793172 AA305476 AW103745 T23459 N79525 AI784438 AA534551 AW193751 AI074560 BE281214 T32229 W25065 W01725 T63086 AW793172 AA305476 AW103745 T23459 N79525 AI784438 AA534551 AW193751 AI074560 BE281214 T32229 W25065 W01725 T63086 AW793172 AA305476 AW103745 T23459 N79525 AI784438 AA534551 AW193751 AI074560 BE281214 T32229 W25065 W01725 T63086 AW793172 AA305476 AW103745 T23459 N79525 AI784438 AA534551 AW193751 AI074560 BE281214 T32229 W25065 W01725 T63086 AW793178 AA305476 AW103745 T23459 N79525 AI784438 AA534551 AW193751 AI074560 BE281214 T32229 W25065 W01725 T63086 AW793178 AA305476 AW103745 T23459 N79525 AI784438 AA534551 AW193751 AI074560 BE281214 T32229 W25065 W01725 T63086 AW793178 AW10375 AI78460 AW7937 AW10375
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, ,			AA737921 AA873274 RE241546 RE241540 AA484058 AW468970 AA127876 AA159120 AWUU1568 AW795213 AW795236 AW795236 AW795236
			BE387572 AA910895 AA161217 BE250380 W31500 T95167 AI719306 AI359224 BE258778 BE281230 BE410044 T33723 AW672694 AW410439 NM_006429 AF026292 T35505 BE542333 T08940 AU076737 AW247471 BE258778 BE281230 BE410044 T33723 AW672694 AW410439 NM_006429 AF026292 T35505 BE542333 T08940 AU076737 AW247471
	102781	20812_1	0500004 6 ALMOOCA DECADAD TOOATO DECOSAA TOLOGE DECOSER RECTOLISMO (NO. 17/10/10 MEANDAYO BEZODA DE DOCOSO DECADOS DECADOS DE CADOS DE CAD
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			AA315781 AA192212 N84547 BE292737 BE259631 AA232179 A133144 E37467 BE249739 BE249739 BE249739 BE249739 BE249739
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			4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
			AW073674 BE296033 BE467326 AB28796 AB16578 AW511604 A921213 AW152427 A1797/87 ABU1016 AW100806 A022144 A030533 AW073674 BE296033 BE467326 AB28796 AB16578 AW515404 A921213 AW152427 A1797/87 AB211016 AW100806 A022144 A030543
85			AW173690 AW511540 BE535520 AA383014 BE301 TO4 AL66696 AW514969 AA66650 AW129146 AW615672 BE394507 AA483902 AW475032 BE378532 AW615636 AW732207 AW377638 AA521784 AA641629 AA633105 AA527640 AW129146 AW615672 BE394507 AA483902 AW475032 BE378532
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5			AA911505 AA148762 AW674535 AL587329 BE328328 AW707348 AA153225 AW717705 AV474997 AW9191919 AA614797 AW604535 AU60507 AW530973 AU76711 AA192213 N88741 BE454552 AW1072679 AL53706 AA152165 AA605924 AL557078 AU767818 AW173484 AU561980 BE300766 AU59598 AU56792 AW247333 AW272851 AA078818 AA150012 AA551232 AA67821 AW873869 AW768266 AU660315 AA319210
			AWZ48898 AT51830 AA907816 R08898 AWX87989 AUZ23300 AA148595 AUZ25977 133425 AA213571 AB73201 A4066279 R43512 AB73201 AA76202 AWX199762 AWX10088 AW759566 AU522097 A475204 D57490 AW517531 BE245270 AW470008 T33427 AWX05731 A1795795 T23753 AWZ72981 T15747 AA552875 T23644 AW361289 A1755558 BE207435 AA876958 T33561 AA883569 F37533 AA582321 AW082524 R42212 AA973847 A49705 AA976570 AM76570 T37670 T37724 T37727 RF671568 D57489 D25906 BE621151 F16510 C05966
10			T35127 AAS30427 AB333481 AA309426 AI918440 BE551854 BE51856 BE394675 BE296173 AW951687 BE383739 BE616141 BE312730 BE535351 AW080575 BE313330 BE616664 AI354390 AA847315 BE544509 BE515212 BE297833 BE278808 BE54484 AW090178 AI896664 BE546708 AW189943 BE274412 BE382399 BE266392 BE254949 BE280596 BE383237 BE261575 BE257721 BE312683 BE275476 BE514850 BE546708 AW189943 BE276412 BE386591 BE264813 AW592575 AI336332 AI278641 AI795791 BE222662 AW249316 AA314361 AL036012 AW402923 BE266845 AA075945 AA314436 BE384640 AW731759 AW957077 AA552234 AA573560 AW367038 AA313399 AI983873 BE410159 BE263803 BE514339 BE409073 BE281296 BE543396 BE395387 BE088360 BE546946 BE546570 BE390626 AA074638 AA301821 AW845230
15	119221	102947_1	AW582379 AI949222 AW029572 AA515843 AW272394 BE259234 C14322 W74060 AI074232 AA595624 BE048955 AI148417 AI583145 AI473460 AI801688 AW573593 AI950741 AI628140 AW467921 R98105 AI149258 AI247584 AI078378 AI139850 AA489411 W24744 R98104 AI033825 AA699589 AI033120 N55544 W88984 AW970771 AA703362 AA099138 AA706792 AA046150 H98381 AI916574 AA953018 AI972749 AI921343 AA909044 AA094751 AI203124 AA582143 AI446654
20			AW235415 R70377 AA099236 F20703 AA524436 R69484
	125831	1522905_1	H04043 D60988 D60337
	128192	45743_3	AI204246 AI204250 AI194050
25	113195	178688_1	AZZUZZG AZZUZZU AT19400 AT9400 THE AZZUZZI A
25			AA564433 AA774503 AA367671 T59757 W78816 AI720806 AI633854 AI632086 AI668663 N70894 AW571809 AI383592 AI201348 W80715 N91880 AW963101 AA339011
30	119861 112973	238266_1 4868_1	AB033023 BE391906 BE275965 BE277872 BE003882 AA313774 BE019159 BE288024 BE299/27 BE390011 BE39027 BE394764 NO7535 BE409419 BE408652 BE408197 AL 119332 AA622427 AB16265 AA610118 T07318 AA019839 AA31430 BE205794 BE049461 AI042322 AI552711 AI917645 AA630045 AW191969 AI817882 T17271 AI803663 AI095533 H46019 AW592438 AI652436 AI675552 D51149 AW132058 AI652711 AI917645 AA630045 AW191969 AI817882 T17271 AI803663 AI095533 H46019 AW592438 AI652436 AI675552 D51149 AW132058 AI67545 AA630045 AW191969 AI817882 T17271 AI803663 AI095533 H46019 AW592438 AI652436 AI675552 D51149 AW132058 AI67545 AA630045 AW191969 AI817882 T17271 AI803663 AI095533 H46019 AW592438 AI652436 AI675552 D51149 AW132058
20			AW875926 AW875645 AW875647 AW938037 AL138042 AW892619 BE243018 AW995454 BE240381 BEUU9U82 BE276921 AW997642 AW87642 AW87692 AL138042 AW87692 AL13803 T63772 AL13804 AW87642 AW87642 AW87642 AW87692 AL13803 T63772 AL13804 AW87642 AW8
	129402	47367_1	A 1070 TOC 11404 TO DA 404 A 104 4040 A 4006 797 LINROND H1041R AWGS (778 A 135NI) 71 AA5H (35) A 1450 25 LINROND H1041 039
35	105936	260931_1	AISO474 H73776 W74397 AA579604 AI131018 W72331 AI719085 AA569348 AI859045 AI814819 AI888714 BE467470 AW131268 H19419 H27694 AI342165 AI914155 AA534872 BED18176 R60206 H11647 R45641 AI860466 BE301656 AI125453 AI498120 AA593735 AA879110 AI016404 T33018 AA588397 AW449767 AA470365 BE501139 AA588354 AI337500 AW078532 Z41279 AI125449 AA335725 AA404338 L42583 NM_005554 L42601 BE183076 AI541221 BE140557 L42610 V01516 J00269 AW275792 AW383052 AW380143 AI541102 BEE12846
	129466	2094_50	
40			A1040004 A1640000 ANDODO01 AA640000 A1640863 A1608860 AWR60564 AWR60725 AWR60903 AWR60904 AA640000 AW/094721 AVV/09011
			AL591181 BE182523 AW794644 AW794620 AI935224 AI608903 AI608623 AW797060 AW084935 BE182517 BE182517 AIGUNDA AW369396 AW797012 BE182522 AW794838 AI608794 AW36289 AA147193 AA595995 AW381128 AW366270 AA589718 AI828416 BE122864 AW368343 AA431080 AW082039 AW380976 AA587144 AA443636 AW872937 AW794448 AW378382 AW085761 AW794718 AW2653895 AA583587 AA482670 AA587004 AA58
45			ABS1095 AW263554 AW378391 AW378415 AW378381 AA036990 AW278395 AZ265446 BEZ08279 BEL99526 AG25300 AG25310 AW36091 AW36091 AW36091 BEL29835 AA55820 AW268264 AZ265712 AA582875 AW59376 BEL29835 AA558276 BEL59636 AA16328 AL51454 AL655930 AA583700 AA169275 AW253427 AL287474 AA912569 AA582700 AA169275 AW253427 AL287474 AA912569 AA582720 AAV253427 AW253427 AA582720 AA583710 AA169275 AW253427 AA582720 AA58270 AA169275 AW578542 AW378114 AA147179 AA584239 AA150532 AW168862 AW085999 AW082480 AA659742 AW079703 AW57273 AA583981 AW25471 AW3781414 AA147179 AA584239 AA150532 AW168862 AW085999 AW082480 AA659742 AW079703 AW57273 AA585981 AW25471 AW378346 AW578114 AA147179 AA584239 AA150532 AW168862 AW085999 AW082480 AA659742 AW079703 AW57273 AA585981 AW25471 AW378365 C00141 D29181 D29567
50			AW103359 W95238 A1991663 AA587298 BE184608 AA099833 W95121 W95150 D29584 A1934111 D29456 D29533 AW265380 D29290
50			AW2338463 AA121041 D29204 AA595925 D29441 AW081840 AA587018 D29323 AA582891 BE182433 BE182437 BE158295 BE182434
	100220	45374_1	AIAM4 EE2 A A A 24 A 36 G A A 2007 15 RESERERS AWE20404 D2R364 AW995678
	100355	40500 4	A1007444 A A500724 A1044045 A A404545 AA 121344 D7R130 NM 003129 AA341650 184166 AFUNSED AA13U9/D DEVOSOO
	100000	H05719 F134	10 T00400 ANNATCON F00044 A144 4700 D40000 A A404074 A A122202 D78120 AA132213 AW94R930 AW94R919 AA25355 AW940C95 AW940C95
55		103/13/10-	AAZ78558 R50895 N26940 N40818 AW021255 AA054851 AA653379 AW948795 AW94893 AA400345 AW948911 N503/4 W70544 AA341974 AI760182 AA286783 BE617763 BE617263 AW263690 BE049454 BE617928 AW515038 AW950584 AA601009 AI079194 AA147204 AW083163 A4320854 AA286783 BE617763 AB66787 AI550565 AA273718 AA575878 AW7515038 AW950584 AA601009 AI079194 AA147204 AW083163 A4320854 AA28678 AA667878 AB66787 AI550565 AA273718 AA275878 AIA71982 AA687834 AI143944 N30172 AA400196 AI769049 AI084342
			A1231390 AA948469 A1807240 AA113270 AA158138 AA076231 A1521024 A1810962 A1133616 AA805106 AA101516 R40052 R50778 A1231390 AA948469 A1807240 A4113270 AA158138 AA076231 A1521024 A1810962 A1133616 AA805106 AA101516 R40052 R50778 R43280 T65036 AW131924 AA114251 AA152331 F09650 AA580614 AA558927 C75491 Z38352 AA554595 C75606 W80742
60		0.000 4	D56165 M36981 X58965 NM_002512 BE379177 AA314836 BE256445 BE252016 AW248343 Al720933 AW085701 BE386050 BE619742
60	100491 BE27780	34803_1 5 AA147951 AA6	DS6158 M36581 X35983 MIC W2312 BEZ3717 AS 1142891 AB29101 A1123832 AW129670 AA471268 AW170242 AW873079 AA148011 A1608620 CM 1313 BEZ53293 A1246588 A183405 A1954174 A1126891 AI829101 A1123832 AW129670 AA471268 AW170242 AW873079 AA148011 A1608620 AA482961 A1003658 H43261 AA657978 A1735072 R83139 AA722002 AA626271 AW273877 BE464626 AA071483 AA429973 AA494342 AA6220436 AA775597 AA775601 AA826847 A1192585 AA826359 AA411159 A1193419 A1204013 AA705323 AA716255 A1784611 A1081144 A1128227 AA828464 A1148911 A1493446 A1626084 A189180 A1721196 A1190618 AA284987 A1128543 AA632064 A133073 A1278470 AA131688
65			ALADATCO A ADOTEDA A ACORDE A AROADET AWOADRAL AASROTAD ALORESTE AAND 1676 ALOBOU AADD 7618 AADD 4230 1143000 ALOUZDON
03			AA127545 AI609219 H20426 AI042292 AI056466 AA581836 W47002 AA422057 AA937673 F29757 AA92403 AW1327462 AA372039 W02144 AA036805 AA487365 AA961037 A1139946 AA487250 AA737118 AI952504 AI242293 AA650552 AI708401 AI633133 AA630848 AA654317 F24128 AI434165 WA6252 AWD43879 AI033763 F37228 AA687809 N49087 AA876981 AA506947 AI914572 AI833284 F22253 AA026222 R50166 AI434165 WA6252 AWD43879 AI033763 F37228 AA687809 N49087 AA876981 AA506947 AI914572 AI833284 F22253 AA026222 R50166 AI344165 WA6252 AWD43879 AI03763 AA96849 AA513466 AA57847 AA418700 F36771 AI880700 AI601170 AI652851 A1708633 AA524499
70			A 6 4 2 2 2 2 2 3 4 4 4 5 5 2 2 4 4 7 4 7 7 10 1 A 2 2 1 5 2 7 5 2 5 4 7 2 1 5 4 5 4 5 2 5 4 5 4 5 4 5 5 4 5 4 5 5 4 5 5 4 5 5 5 6 5 6
70			AI905958 AI318611 H45099 AI472604 T60667 AA373087 W32479 AA514034 BEE19183 AA134672 AA127494 H25942 BE330599 AW327461. AA422139 AW327357 AW327348 F33510 AI633382 AW827126 F27133 AI335189 AW517599 W80471 AA8858814 N89681 BE393173 AA617760 AA522629 AA66627 AA46734 B43625 B43625 B43627 B43627 AA071732 BE5A5409 AA306292 BE774447 AA380861 AA34038
			A 4 3 4 6 0 C. A 4 0 C C C 7 A 10 C C 2 A 4 17 C C 2 1 A 4 17 C C 2 A A 2 7 C C C A A 2 4 6 0 C C A 4 0 C C C A 4 C C C C C C C C C C C C C C C
75			DE0200 NE0014 NA721 AM051723 AA514798 AA418708 AW673377 AA379822 AA977995 AA708224 AA708216 ANJ18249 ANJ18233 AA411100
, 5	100518	13165_1	AA026221 AA316774 AA486908 AI500094 AA096362 AW583742 BE536422 BE618653 R70203 AA131732 AA345048 BE552720 126342 AND 00446 AL024069 177820 BE140760 AW752599 AW848723 AW376697 AW376697 AW376699 AW848371 AW376782 AW848789
			AMEGA 412 AMEGA 0074 AMEGO 7130 AMEGO 304 AW799304 RE077020 RE077017 RE185187 AW997195 BE156621 BE179915 BEW0001 BE143100
00			AW89085 BE002107 AW103521 AA857316 AW383133 BE011378 AW170253 BE185750 AW886475 BE160433 J05211 BE082576 BE082584 BE004047 AW507238 AW377700 AW377699 BE082526 BE082505 BE082507 BE082514 AW178000 AW177933 AI905935 AW747877 AW748114
80			BE004047 AW607238 AW377700 AW377699 BE082526 BE082507 BE082507 BE082517 AW17600 AW177750 ASSC535 AW74107 AW17608 BE148516 AW265328 AW847678 AW847688 AW365151 AW365148 AW365153 AW365156 AW365157 AW365154 AW0668840
			DEADESTS AMBRESAE DEADS DE 182166 RE144243 READS 23 AISS 1766 AI434518 RE184920 RE184933 AI284090 BE184941 AWOUND 4
			DE494024 COAT46 M20409 AMROS616 RE1R4948 RE159846 AWR06653 AA099891 AA131128 AA337270 AA340777 AW384371 AA852212
			DEDTAL AMPRESES AMPRAGED AAROSEST AAROS
85			AW609750 AW391912 AW849690 T87267 AW853812 AA852213 W74149 BE009090 AA056401 H91011 AW368529 AW390272 C18467
00			VIII QUANTI QUANTI CA LA TATA CANADA CA

	wo	02/0864	43 PCT/US02/12476 AW674920 N57176 AA026490 AW576767 H93284 AA026853 AY177787 AA026654 AY177786 BE092134 BE092137 BE092136 AW177784 AN022862 BE091653 AW376811 AV848592 AA040018 BE185331 BE182164 AA365E54 AW551576 T29918 AA131077 W95048 W25458 AW205789 H90899 N29754 W32490 R20904 BE167181 BE167165 N84767 H27408 H30145 A190590 C03378 AJ554403 AI20563 AA128470
5			AE392926 AF139055 AV370813 AW370827 AW798417 AW798780 AW798833 AW798569 R33557 AA149191 CE32/9 AVV177/83 AA069000 AW370829 AA247885 BE0022273 AL760816 AH259101 AW879451 AL700963 AA451923 AE340326 AL590957 548793 AL569896 A1442882 AA039975 AH70146 AA9446936 BE0677737 BE067786 W19287 AA644381 AA702424 AH417612 A1306554 AL668889 AL5668892 AW190555 AL571075 AL220573 AL470146 AA9446936 BE0677737 AB471874 AL971874 AL971
10			AM94059 AI911702 AA149191 AA026854 AI830049 AI887258 AW780435 AI910434 AI819984 AI858282 AI078449 AI025932 AI860584 AI635878 AA026047 AA703232 D12062 AW192085 AA658154 AW514597 AW791892 T87181 AA782066 AW243815 AW150038 AW266333 AW004633 AI97207 AA782109 AW473233 AI804485 AW169216 AI572669 AA602182 AW015480 AW771865 AI270027 AA961816 AA283207 AI076652 AI498487 AI348053 AI783914 H44405 AW799118 AA128330 AA515500 AA918281 W02156 AI905927 AA022701 W38382 R20795 T77861 AW850878
15	100528	45979_1	AW600576 BE336801 AU077729 AA143755 BE302747 AA853375 US0162 BE274163 BE277479 BE408180 BE274874 C15000 AA047476 N27099 AA391655 BE336801 AU077729 AA143755 BE302747 AA853375 US0162 BE274163 BE277479 BE408180 BE274874 C15000 AA047476 N27099 AA391649 AA151283 AI853925 AW644977 AI207392 AA931263 AA443112 R40139 AW068538 AA351008 AA676972 R62303 AA916492 AW01855 HA2334 H38280 AA121497 AA114137 AI750738 M17783 AA383786 BE274462 AI753182 C0535 AAW57404 AW069298 AI754351 AI756404 AA188808 AA186879 AA585243 AU040655 AA456177 AI750722 AA045756 AA213580 C16936 AW578747 AW753731 H41632 N44761 R58560 R61260 AA039902 N99721 AW992543 R68380 AA149686 T29017 H03739 BE383822 BE387105 BE408251 BE410425 H41550 AA247591
20	100559	2260_1	BE389677 A1752233 AI556195 AA856004 AI424523 AW753720 AA852159 BE385803 NM, 000094 L02870 D13594 S51236 M95984 AW946290 M55158 AI285422 D29523 AL119886 AW630655 L06662 AI884355 AW168737 T29085 AW797005 AW801340 AI355504 AW079048 AW801337 AI690455 AI972063 AW265565 W66588 AA567326 AA863493 A1033523 AW510336 AW591998 H98463 AL043852 AI150055 AI566233 AI624803 AA844717 H40670 AA922334 AI864424 AW615094 AW451233 AI302203 F31221 AW591998 H98463 AL043852 AI150055 AI566233 AI624803 AA844717 H40670 AA922334 AI864424 AW615094 AW451233 AI302203 F31221 AW591998 H98463 AA904478 AI917631 AW014208 AW450759 AA847625 AI284033 AA848176 AA5985507
25	100576 124357 101624 101625 135158	9986_1 genbank_N22 entrez_M559 entrez_M572 57963_1	98 M55998

Table 2A shows 504 genes down-regulated in lung tumors relative to normal lung and chronically diseased lung. Chronically diseased lung samples represent chronic non-mailgnant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 5980 probesets on the Eos/Afrymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

•			•									
	Pkey: ExAcon: UnigenelD	Exempla	ar Accession of	identifier number number, Genbank accession number								
10		itle: Unigene 90th per	centile of Al fo	or normal lung samples divided by the 80th percen								
	R2:			al lung samples divided by 90th percentile of Al for al lung samples minus the 15th percentile of Al for								
15	R3:	the 90th	percentile of	Al for adenocarcinoma and squamous deli calcili	oma lung tumo	r samples	minus the	15th perc	entite of A	li for all no	rmal	
••		lung, ch	ronically disea	ased tung and tumor samples.	nus cell carcine	oma and a						
	R4: R5:	median	of Al for norm	al lung samples divided by the 90th percentile of A	I for adenocar	cinomas.	the discour	rad hma ar	d himor	samnles di	ided by th	a 90th
20	R6:	median	of Al for norm	al lung samples minus the 15th percentile of Al for	all normal tuno	a, chronica		sed linuid su seen inniid su	d tumor s	amples.		
20	R7:	average	of All for norm	nal lung samples divided by the 90th percentile of	Al for squamo	us cell car	inomas.	and long as	vi himor	ih salomes	rided by th	ne 90th
	R8:			nal lung samples divided by the 90th percentile of al lung samples minus the 15th percentile of Al fo warnous cell carcinomas minus the 15th percentile				ly disease	lung and	tumor sar	nples.	
		percent	ac or Ar kar sq		R1	R2	R3	R4	R5	R6	R7	Ra
25	Pkey	ExAcon	UnigenelD	Unigene Title	KI	ΝZ	·w					
	100095	Z97171	Hs.78454	myocilin; trabecular meshwork inducible	40.20							3.46
	100115 100138	NM_002084 U83508	Hs.336920 Hs.2463	glutathione peroxidase 3 (plasma) angiopoietin 1			2.30					
30	100299	D49493	Hs.2171	growth differentiation factor 10		11.00				3.06		
	100305	U86749 NM_014767	Hs.80598	transcription elongation factor A (SII); KIAA0275 gene product								3.16
	100447 100458	S74019	Hs.247979	Vpre-B	42.40					4.13		
25	100862	AA005247	Hs.285754	Hepatocyte Growth Factor Receptor actin; alpha; cardiac muscle				125.60		4.10		
35	100959 101032	AA359129 BE206854	Hs.118127 Hs.46039	phosphoglycerate mutase 2 (muscle)	36.40			24.00				
	101081	AF047347	Hs.4880	armyloid beta (A4) precursor protein-bind				34.60 193.20				
	101088 101125	X70697 AJ250562	Hs.553 Hs.82749	solute carrier family 6 (neurotransmitte transmembrane 4 superfamily member 2						3.10		
40	101180	U1 1874	Hs.846	interleukin 8 receptor, beta	33.20			54.86				
	101308 101330	L41390 L43821	Hs.80261	"Homo sapiens core 2 beta-1,6-N-acetylgle enhancer of fitamentation 1 (cas-like do				36.40				
	101345	NM_005795	Hs.152175	Calcitonin receptor-like			2.29	70.55				
45	101346	A1738616 M26380	Hs.77348 Hs.180878	hydroxyprostaglandin dehydrogenase 15-(N lipoprolein lipase				, 0.00				3.54
43	101397 101414	NM_000066		complement component 8; beta polypeptide				34.60			3.81	
	101435	NM_001100	Hs.1288	actin; alpha 1; skeletal muscle interleukin 1 receptor; type I				37.60				
	101507 101530	X16896 M29874	Hs.82112 Hs.1360	cytochrome P450; subfamily IIB (phenobar			0.54					4.25
50	101537	Al469059	Hs.184915	zinc finger protein; Y-linked cytochrome P450; subfamily XVII (steroid		5.50	2.54					
	101542 101545	NM_000102 BE246154	Hs.154210	EDG1; endothelial differentiation, sphin	39.40							
	101554	BE207611	Hs.123078	thyroid stimulating hormone receptor Intercellular adhesion molecule 2, exon		13.00						3.38
55	101560 101574	AW958272 M34182	Hs.83733 Hs.158029	protein kinase; cAMP-dependent, catalyti						4.37		3.80
55	101605	M37984	Hs.118845	troponin C; slow	30.20							3.00
	101621 101680	BE391804 AA299330	Hs.62661 Hs.1042	guanylate binding protein 1; interteron- Sjogren syndrome antigen A1 (52kD; ribon	50.20					0.27	2.75	
	101829	AW452398	Hs.129763	solute carrier family 8 (sodium/calcium				38.20		3.37		
60	101842 101961	M93221 AW004056	Hs.75182 Hs.168357	mannose receptor, C type 1 "Hs-TBX2=T-box gene (T-box region) [huma			2.32	00.20				6.05
	101994	T92248	Hs.2240	uteroglobin			2.45					6.85
	102020	AU077315 BE280901	Hs.154970 Hs.83155	transcription factor CP2 aldehyde dehydrogenase 7			2.70					6.75
65	102091 102112	AW025430	Hs.155591	forkhead box F1	54.60							3.98
	102190	AA723157	Hs.73769	folate receptor 1 (adult) fructose-bisphosphatase 1								3.62
	102202 102241	NM_000507 NM_007351	Hs.268107	Multimerin		7.00	2.32					
70	102310			Accession not listed in Genbank "Human sodium cotransporter RKST1 mRNA,	29.40	7.00						
70	102397 102571	U41898 U60115	Hs.239069	"Homo sapiens skeletal muscle LIM-protei						3.07		3.75
	102620	AA976427	Hs.121513	Human clone W2-6 mRNA from chromosome ? "Human ataxia-tetangiectasia locus prote	(2.40			3.07		
	102636 102667	U67092 U70867	Hs.83974	solute carrier family 21 (prostaglandin			3.15			3 55		
75	102675	U72512	Hs.7771	"Human B-cell receptor associated protei orogastricsin (pensinogen C)						3.56		4.51
	102698 102727	M18667 U79251	Hs.1867 Hs.99902	opioid-binding protein/cell adhesion mol				•	12.00			
	102852	V00571	Hs.75294	conficultación releasing harmone	37.40				13.00			
80	103026 103028	X54162 X54380	Hs.79386 Hs.74094	thyroid and eye muscle autoanligen D1 (6 gregnancy-zone protein	28.80							
00	103098	M86361		Human mRNA for T cell receptor, clone IG		6.00			10.00			
	103117 103241		Hs.295449	parvalbumin H.sapiens MAL gene exon 4		0.00	2.47					
	103241		Hs.76206	Cadherin 5 VE-cadherin (vascular epithe			2.69				2.16	
85	103360		Hs.73082	keratin; hair, acidic; 5								

										РСТ/І	1502/1	2476
		O 02/086	443 Hs.132821	flavin containing monooxygenase 2							1302/1	5.97
	103496 103508	Y10141	ns. 132021	"H.sapiens DAT1 gene, partial, VNTR"			0.40			3.27		
	103561	NM_001843		contactin 1			2.40 2.99					
5	103569 103575	NM_005512 Z26256	HS.151041	glycoprotein A repetitions predominant "H.sapiens isoform 1 gene for L-type cal						4.18		
,	103627	Z48513		H.sapiens XG mRNA (clone PEP6)						3.44	2.25	
	103767	BE244667	Hs.296155 Hs.213194	CGI-100 protein Hypothetical protein MGC10895; sim to SR				46.55				
	103850 104078	AA187101 AA402801	Hs.303276	ESTs						3.05 3.54		
10	104326	AW732858	Hs.143067	ESTs						3.16		
	104352 104398	BE219898 AI423930	Hs.173135 Hs.36790	dual-specificity tyrosine-(Y)-phosphoryl ESTs; Weakly similar to putative p150 (H	64.80							3.38
	104473	A1904823	Hs.31297	ESTs			2.47					3.30
15	104493	AW960427 AW975587	Hs.79059 Hs.292979	ESTs; Moderately similar to TGF-BETA REC ESTs	28.60		241					
13	104495 104595	A1799603	Hs.271568	ESTs		c 00				3.42		
	104597	Al364504	Hs.93967	ESTs; Weakly similar to Slit-1 protein [34.00	6.00						
	104659 104686	AW969769 AA010539	Hs.105201 Hs.18912	ESTs ESTs		11.00						
20	104691	U29690	Hs.37744	ESTs; Beta-1-adrenergic receptor	56.80			60.40				
	104764 104776	A1039243 AA026349	Hs.278585	ESTs ESTs	34.20							
	104776	AA035613	Hs.141883	ESTs	44.00		3.03					
25	104865	T79340	Hs.22575	Homo sapiens cDNA: FLJ21042 fis, clone C ESTs	41.20							3.27
25	104942 104989	NM_016348 R65998	Hs.285243	ESTs				40.00				3.20
	105062	AW954355	Hs.36529	ESTs	34.20							0.20
	105101 105173	H63202 U54617	Hs.38163 Hs.8364	ESTs ESTs	54.25							4.17
30	105194	R06780	Hs.19800	ESTs		16.00	2.34					
	105226	R58958	Hs.26608 Hs.16529	ESTs transmembrane 4 superfamily member (tetr			2.72					
	105256 105394	AA430650 BE245812	Hs.8941	ESTs			2.61					
25	105647	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	33.60							3.59
35	105789 105817	AF106941 AA397825	Hs.18142	arrestin; beta 2 synaptopodin						4.46		
	105847	AW964490	Hs.32241	ESTs			3.43	35.40				
	105894	A1904740 BE268786	Hs.25691 Hs.21543	calcitonin receptor-like receptor activi ESTs		7.00	3.70					
40	105999 106075		Hs.25930	ESTs				42.60				
	106178	AL049935	Hs.301763	KIAA0554 protein ESTs	34.80				12.00			
	106381 106467		Hs.24106 Hs.154162	ADP-ribosylation factor-like 2				00.40		3.69		
4.0	106536	AA329648	Hs.23804	ESTs				96.40 47.20		•		
45	106569 106605		Hs.300741 Hs.21103	sorcin Homo sapiens mRNA; cDNA DKFZp564B076 (fr				220.40				
	106842	AF124251	Hs.26054	novel SH2-containing protein 3	39.20		2.55					
	106844 106870		Hs.158213 Hs.26530	sperm associated antigen 6 serum deprivation response (phosphatidy)	35.20		2.28					
50	106943		Hs.9973	ESTs								4,28 4.32
	106954		Hs.204038	ESTs ESTs					10.45			1.02
	107106 107163		Hs.28482 Hs.27018	ESTS			2.57			2.04		
55	107201	D20378	Hs.30731	EST		8.00				3.84		
55	107238 107376		Hs.330777 Hs.327179	EST solute carrier family 17 (sodium phospha		10.67						
	107530	Y13622	Hs.85087	tatent transforming growth factor beta b			2.32	34.60				
	107688 107706		Hs.60536 Hs.29276	ESTs ESTs	28.40			54.00				
60	107723			EST				80.80		3.29		
	107727		Hs.173091	DKFZP434K151 protein				51.40				
	107750 107751		Hs.60781 Hs.235390	ESTs ESTs						3.14		
	107873	AK000520	Hs.143811	ESTS		9.00				3.65		
65	107899 107994		Hs.83869 Hs.48469	ESTs; Weakly similar to IIII ALU SUBFAMI ESTs				44.60				
	107997	AL049176	Hs.82223	Human DNA sequence from clone 141H5 on c				32.00 30.80				
	108041 108048		Hs.61957 Hs.165195	ESTs ESTs				00.00			4.75	
70	108338		113,103,50	*zm53g11.s1 Stratagene fibroblast (#9372			2.33				2.92	
	108434			"zm94b1.s1 Stratagene colon HT29 (#93722 "zm92a11.s1 Stratagene ovarian cancer (#						3.06	2.02	
	108447 108480		Hs.68055	ESTs				34.00				2 20
-	108499	AA083103		"zn1b12.s1 Stratagene hNT neuron (#93723					19.00			3.36
75	108535 108550		Hs.226440	Homo sapiens clone 24881 mRNA sequence "zn11f6.s1 Stratagene hNT neuron (#93723					12.00			
	108604		Hs.49696	ESTs			2.33					5.82
	108625	AW972330	Hs.283022	ESTs "zn24c6.s1 Stratagene neuroepithelium NT							3.42	u.uz
80	108629 108655			"zm65c6.s1 Stratagene fibroblast (#93721		7.00						
-	108756	AA127221	Hs.117037		28.80	6.05						
	108864 108895		Hs.199957 Hs.62713	ESTs ESTs	32.80							
	108921	AI568801	Hs.71721	ESTs			•	57.80				
85	108967	AA142989	Hs.71730	ESTs	28.80							

	W	O 02/086	443						•	PCT/I	JS02/1	2476
	109001		Hs.72116	ESTs, Moderately similar to hedgehog-int			2.57					
	109003		Hs.71825	ESTs							2.11	
	109004	AA156235	Hs.139077	EST		5.60			10.00			
_	109065		Hs.252739	EST ESTs; Wealdy similar to PHOSPHATIDYLETHA					10.00		3.44	
5	109250	H83784 AA233416	Hs.62113 Hs.139202	ESTs Weakly Shillian to Price							292	
	109490 109510		Hs.87191	ESTs			2.40					
	109578	F02208	Hs.27214	ESTs		10.00		40.00				
	109601	F02695	Hs.311662	EST				40.80 54.40				
10	109613	H47315	Hs.27519	ESTs	31.20			34.40				
	109550	R31770	Hs.23540	ESTS	31.20	8.40						
	109682 109724	H18017 D59899	Hs.22869 Hs.127842	ESTs ESTs				29.40				
	109782	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene					8.00			
15	109833	R79864	Hs.29889	ESTs		10.00	c 10					
	109837	H00656	Hs.29792	ESTs			6.49				2.75	
	109977	T64183	Hs.282982	ESTs				107.00				
	109984	AI796320	Hs.10299 Hs.31581	ESTs: Moderately similar to SYNTAXIN 18							2.22	
20	110146 110271	H41324 H28985	Hs.31330	ESTS						3.48		
20	110280	AW874263	Hs.32468	ESTs	44.20			00.00				
	110420	R93141	Hs.184261	ESTs	00.40			32.00				
	110578	T62507	Hs.11038	ESTs	28.40				20.00			
25	110634	R98905	Hs.35992	ESTs potassium voltage-gated channel; shaker-								4.15
25	110726	AW961818 H03109	Hs.24379 Hs.108920	ESTs; Weakly similar to semaphorin F [H.				56.80				
	110837 110875	N35070	Hs.26401	tumor necrosis factor (ligand) superfami			3.13					
	110894	R92356	Hs.66881	ESTs; Moderately similar to cytoplasmic		5.33		44.60				
	110971	AI760098	Hs.21411	ESTs	32.40			44.00				
30	111023	AV655386	Hs.7645	ESTs	32.40				17.14			
	111057	T79639	Hs.14629	ESTs Homo sapiens mRNA; cDNA DKFZp554B2062 (f							4.58	
	111247	AW058350 BE247767	Hs.16762 Hs.18166	KIAA0870 protein								3.42
	111330 111374	BE250726	Hs.283724	ESTs; Moderately similar to HYA22 [H.sap								3.91
35	111442	AW449573	Hs.181003	ESTS				33.20				
-	111737	H04607	Hs.9218	ESTs	46.20			53.00				
	111747	AI741471	Hs.23666	ESTs	40.20	16.00						
	111807	R33508	Hs.18827	ESTs EST		10.00				3.91		
40	111862 112045	R37472 A1372588	Hs.21559 Hs.8022	TU3A protein							2.74	
40	112057	R43713	Hs.22945	EST					42.00		4.92	
	112214	AW148652	Hs.167398	ESTs			2.43		13.00			
	112263	R52393	Hs.25917	ESTs		9.00	2,43					
45 .	112314	AW206093	Hs.748	ESTs limbic system-associated membrane protei		5.00			14.00			
45 ·	112324 112362	R55965 AW300887	Hs.26479 Hs.26638	ESTs; Weakly similar to CD20 receptor [H			2.49					
	112380	H63010	Hs.5740	ESTs			2.34					
	112425	AA324998	Hs.321677	ESTs; Weakly similar to IIII ALU SUBFAMI		8.00				4.53		
	112473	R65993	Hs.279798	pregnancy specific beta-1-glycoprotein 9				29.80		4.00		
50	112492	N51620	Hs.28694	ESTs ESTs				20.00		3.62		
	112541 112620	AF038392 R80552	Hs.116674 Hs.29040	ESTs			2.37					
	112623	AW373104	Hs.25094	ESTs			2.26					
	112867	T03254	Hs.167393	ESTs		0.50			12.00			
55	112894	T08188	Hs.3770	ESTs		6.50 7.00						
	112954	AA928953	Hs.6655	ESTs ESTs; Weakly similar to !!!! ALU SUBFAMI		7.00						4.39
	113029		Hs.7369 Hs.209100									4.47
	113086 113140	T50405	Hs.175967	ESTs					10.00			
60	113252	NM_004469		c-fos induced growth factor (vascular en		14.00				3.72		
	113257	Al821378	Hs.159367	ESTs						3.60		
	113394	T81473	Hs.177894	ESTS	35.00					0.00		
	113437	T85349	Hs.15923 Hs.16188	EST ESTs	W.00	6.00						
65	113454 113502	Al022166 T89130	AS. 10 100	ESTs	39.60							
0.5	113552		Hs.16026	ESTs							0.50	3.88
	113645		Hs.333181	ESTs				90 20			2.58	
	113691	T96935	Hs.17932	EST .				38.20		3.09		
70	113706		Hs.269192	ESTs oxidative 3 alpha hydroxysteroid dehydro			2.31					
70	113883 113924	U89281 BE178285	Hs.11958 Hs.170056		30.40							
	114035		Hs.269181	ESTs					13.00		-	- 00
	114058	AK002016	Hs.114727	ESTs				40.00				5.00
	114084	AA708035	Hs.12248	ESTs			2.31	40.60				
75	114121	H05785	Hs.25425	ESTS		7.00	2.31					
	114124		Hs.125019			6.00						
	114275 114297		Hs.306117 Hs.173091					48.80				
	114427		Hs.33532	ESTs; Highly similar to Miz-1 protein (H					40.00	3.45		•
80	114449	AA020736		"ze63b11.s1 Soares retina N2b4HR Homo sa		14.00			10.00			
	114452		Hs.243010	ESTs, Moderately similar to RTCO_HUMAN G		14.00				3.13		
	114609			"zm97a5.s1 Stratagene colon HT29 (#93722 "zn25b3.s1 Stratagene neuroepithelium NT				35.40		•		
	114648 114731		Hs.155651	and at a mile for board.								3.42
85	114762		Hs.288464		33.00							

	w	O 02/086	5443							PCT/	US02/1	2476
		AA151719	Hs.95834	ESTs	34.40							
	115009	AA251561	Hs.48689	ESTs: Weakly similar to hypothetical L1	30.20 32.60							
	115272 115279	AW015947 AW964897	Hs.290825	ESTs Weakly surran to hypothesiscal El		6.00			40.00			
5	115302	AL109719	Hs.47578	ESTs					12.00	3.32		
	115365 115559	AW976252 AL079707	Hs.268391 Hs.207443	ESTs ESTs				48.00				
	115556	A1142336	Hs.43977	ESTs				56.20				
10	115683	AF255910	Hs.54650	ESTs, Weakly similar to (defline not ava ESTs; Highly similar to dJ1178H5.3 [H.sa	31.40			33.60				
10	115744 115819	AA418538 AA486620	Hs.43945 Hs.41135	Endomucin 2				74.40		•		
	115949	A1478427	Hs.43125	ESTs			3.18	388.80				
	115965	AA001732	Hs.173233 Hs.184564	ESTs .				33.20				
15	116035 116049	AA621405 AA454033	Hs.41644	ESTs				45.80		3.57		
	116081	Al190071	Hs.55278	ESTs			3.06			3.37		
	116082 116213	AB029496 AA292105	Hs.59729 Hs.326740	ESTs leucine rich repeat (in FLII) interactin	50.60							
	116228	A1767947	Hs.50841	ESTs; Wealdy similar to tuffelin [M.musc		6.00	3.85					
20	116250	N76712 Al613480	Hs.44829 Hs.47152	ESTs ESTs; Weakly similar to testicular tekli		0.00		30.00				
	116419 116617	D80761	Hs.45220	EST		•	2.27					
	116784	AB007979	Hs.301281	tenascin R (restrictin; janusin)	47.20			41.20				
25	116835 116970	N39230 AB023179	Hs.38218 Hs.9059	ESTs KIAA0962 protein					11.00			
	117023	AW070211	Hs.102415	ESTs	49.40			91.00				
	117027 117036	AW085208 H88908	Hs.130093 Hs.41192	ESTs EST	40.40			32.60				
	117110	AA160079	Hs.172932	ESTs		8.67		30.60				
30	117209	W03011	Hs.306881	ESTs				30.00	9.29			
	117325 117454	N23599 N29569	Hs.43396 Hs.44055	ESTs ESTs						3.19		
	117475	N30205	Hs.93740	ESTs	44.00	16.00						
35	117543 117567	BE219453 AW444761	Hs.42722 Hs.44565	ESTs ESTs		10.00			12.00			
55	117570	N48649	Hs.44583	ESTs					11.00	3.74		
	117600	N34963	Hs.44676	EST ESTs		6.00				W.14		
	117730 117791	N45513 N48325	Hs.46608 Hs.93956	EST		9.00		00.00				
40	117929	N51075	Hs.47191	ESTs		8.00		29.20				
	117990 118224	AA446167 N62275	Hs.47385 Hs.48503	ESTs EST	31.40	0.00						
	118244	N62516	Hs.48556	ESTs	32.80		2.40			•		
45	118357 118446	AL109567 N66361	Hs.124154 Hs.269121	Homo sapiens mRNA full length insert cDN ESTs			2.28					
7.7	118447	N66399	Hs.49193	EST	30.80					3.10		
	118530	N67900	Hs.118446	ESTs EST						3.41		
	118549 118823	N68163 W03754	Hs.322954 Hs.50813	ESTs; Wealdy similar to long chain fally			3.94			2.00		
50	118862	W17065	Hs.54522	ESTS				33.00		3.58		
	118935 118944	A1979247 A1734233	Hs.247043 Hs.226142	KIAA0525 protein ESTs; Weakly similar to !!!! ALU SUBFAMI				00.00	11.43			
	118995	N94591	Hs.323056	ESTs		14.00		52.60				
55	119073 119268	BE245360 T16335	Hs.279477 Hs.65325	ERG-2/ERG-1; V-ets avian erythroblastosi EST	31.40			32.00				
33	119514	W37937	110.00000	Accession not listed in Genbank			0.75			3.50		
	119824	W74536	Hs.184	advanced glycosylation end product-speci DKFZP586L2024 protein			2.75					3.21
	119831 119861	AL117664 W78816	Hs.58419 Hs.49943	ESTs; Moderately similar to !!!! ALU SUB				33.80				
60	119889	W84346	Hs.58671	ESTs	29.00			30.03				
	119921 120082	W86192 H80286	Hs.58815 Hs.40111	ESTs ESTs	23.00					3.80		
	120094	AA811339	Hs.124049	ESTs		6.00		36.60				
65	120132		Hs.125019 Hs.285728	Human lymphoid nuclear protein (LAF-4) ESTs		12.00		30.00				
03	120378 120404			KIAA1013 protein	39.40				0.00			
	120504	AA256837		ESTs	33.00				8.00			
	120512 120667		Hs.194718 Hs.78335	ESTs microtubule-associated protein; RP/EB fa	30.00							4.18
70	120777	AA287702	Hs.10031	KIAA0955 protein				46.60 39.00				
	121082 121191		Hs.104447	ESTs ESTs	41.60			33.00				
	121248		Hs.97827	EST					40.00		5.08	
75	121363		Hs.97933	ESTs					12.00 20.00			
75	121366 121483		Hs.25274	ESTs ESTs; Moderately similar to putative sev						3.32		
	121518	AA412155		ESTs			2.29	30.20				
	121545 121622		Hs.98132 Hs.126065	ESTs ESTs		9.00	LU					
80	121665	AA416556	Hs.98234	ESTs		-		34.80				
	121709	A1338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f ESTs	34.80 38.80							
	121730 121740		Hs.98328 Hs.98334	EST		7.00						
0.5	121772	A1590770	Hs.110347	Homo sapiens mRNA for alpha integrin bin	36.20							3.61
85	121821	AL040235	Hs.3346	ESTs								

	W	A 02/086	3443							PCT/	US02/1	2476
		O 02/086 AB033030	Hs.300670	ESTs			2.34					
	121835 121841	AA427794	Hs.104864	ESTs			2.61					
	121885	AA934833	Hs.98467	ESTs							2.25	
_	121888	AA426429	Hs.98463	ESTs				40.00			2.92	
5	121938	AA428659	Hs.98610	ESTs				46.80 31.40				
	121950	AA429515	U- 00724	EST ESTs	34.40			31.40				
	122030 122054	AA431310 AA431725	Hs.98724 Hs.98746	EST	V1.10						3.58	
	122211	AA300900	Hs.98849	ESTs; Moderately similar to bithoraxoid-	49.40							
10	122233	AA436455	Hs.98872	EST	29.80			00.00				
	122247	AA436676	Hs.98890	EST		0.00		39.80				•
	122253	AA436703	Hs.104936	ESTs; Wealty similar to hypothetical pro		9.00				3.60		
	122266	AA435840	Hs.98907 Hs.121602	EST EST						3.14		
15	122285 122409	AA436981 AA446830	Hs.99081	ESTs	30.80							
15	122485	AA524547	Hs.160318	phospholemman			2.65					
	122697	AA420683	Hs.98321	Homo sapiens cDNA FLJ14103 fis, clone MA		15.00 6.67						
	122772	AW117452	Hs.99489	ESTs		0.07				3.37		
20	122831 122913	A1857570 A1638774	Hs.5120 Hs.105328	ESTs ESTs				32.20				
20	123049	BE047680	Hs.211869	ESTs				41.80				
	123076	Al345569	Hs.190046	ESTs	35.80						2.58	
	123136	AW451999	Hs.194024	ESTs					19.00		230	
25	123309	N52937	Hs.102679	ESTs ESTs				82.80	15.00			
25	123455 123691	AA353113 AA609579	Hs.112497 Hs.112724	ESTs					_	3.95		
	123756	AA509971	Hs.112795	EST	35.40				•			
	123802	AA620448		Homo sapiens clone 24760 mRNA sequence	58.00			32.40				
20	123837	AI807243	Hs.112893	ESTs			2.63	32.40				
30	123844	AA938905	Hs.120017 Hs.241519	olfactory receptor, family 7; subfamily ESTs	29.00		2.00					
	123936 123987	C21171	Hs.95497	ESTs; Weakly similar to GLUCOSE TRANSPOR				70.60				
	124013	AI521936	Hs.107149	ESTs: Weakly similar to PTB-ASSOCIATED S	28.40				12.00			
0.5	124150	R40290	Hs.124685	ESTs					13.00	4.74		
35	124205	H77570	Hs.108135	ESTs			2.35			4.14		•
	124226	AA618527 H67680	Hs.190266 Hs.270952	ESTs ESTs			2.55	29.40				
	124246 124348	AI796320	Hs.10299	ESTs		17.00						
	124358	AW070211	Hs.102415	"yw35g11.s1 Morton Fetal Cochlea Homo sa			3.07			3.14		
40	124409	Al814166	Hs.107197	ESTS			2.48			3.14		
	124442 124468	AW663632 N51413	Hs.285625 Hs.109284	TATA box binding protein (TBP)-associate ESTs			2.70	30.80				
	124479	AB011130	Hs.127436	calcium channet; voltage-dependent; alph								6.03
	124519	A1670056	Hs.137274	ESTs; Weakly similar to SPLICEOSOME ASSO			2.50					
45	124711	NM_004657		serum deprivation response (phosphatidy)	59.20	8.00						
	124866 124874	AI768289 BE550182	Hs.304389 Hs.127826	ESTs ESTs		0.00		37.60				
	125097	AW576389	Hs.335774	ESTs					10.00			
	125179	AW205468	Hs.103118	ESTs						3.12	2.79	
50	125200	AW836591	Hs.103156	ESTs				34.20			213	
	125299	T32982	Hs.102720	ESTs DKFZP586D0824 protein	29.00			34.20				
	125400 125810	AL110151 H00083	Hs.128797	aryl hydrocarbon receptor-interacting pr	32.20							
	126176	BE242256	Hs.2441	KIAA0022 gene product		12.00						
55	126303	D78841		HUM525A05B Human placenta polyA+ (TFuji	25.00			33.60				
	126403	AW629054	Hs.125976	ESTs; Weakly similar to metalloprotease/ ESTs; Weakly similar to HC1 ORF [M.muscu	35.80			29.80				
	126507 126773	AL040137 AA648284	Hs.23964 Hs.187584	ESTS. Weakly stilled to HOT ON [Milliasco	39.60							•
	127307	AW962712	Hs.126712	ESTs: Weakly similar to plL2 hypothetica	28.80							
60	127462	AA760776	Hs.293977	aa59b04.s1 NCI_CGAP_GCB1 Homo sapiens c				34.40				
	127486	AW002846	Hs.105468	ESTs ·		9.00	2.36					
	127572	AA594027	Hs.191788	ESTS			2.30	29.40				
	127609 127832	X80031 AW976035	Hs.530 Hs.292396	ESTs ESTs				37.20				
65	127898		Hs.128970	ESTs							4.42	
•••	128073	AW340720	Hs.125983	ESTs				38.40				
	128101	AA905730	Hs.128254	ESTs		7.33					2.58	
	128149 128212	NM_012214 W27411	Hs.177576 Hs.336920	mannosyl (alpha-1;3-)-glycoprotein beta- glutathione peroxidase 3 (plasma)			3.09					
70	128333	W68800	Hs.12126	ESTs: Weakly similar to LR8 [H.sapiens]				34.40				
	128364	N76462	Hs.269152	ESTs; Weakly similar to ZINC FINGER PROT		10.00					4.31	
	128426	Al265784	Hs.145197	ESTs	31.20						4.51	
	128598 128634	AA305407 AA464918	Hs.102308	potassium inwardly-rectifying channel; s ESTs; Moderately similar to !!!! ALU SUB	01.20			41.60				
75	128687	AW271273	Hs.23767	ESTs				87.00				4.00
	128726	AJ311238	Hs.104476	ESTs					0.00			4.02
	128773	NM_004131		granzyme B (granzyme 2; cytotoxic T-lymp					9.00			3.76
	128833		Hs.184581 Hs.75309	ESTs eukaryotic translation elongation factor			2.66					J., J
80	128870 128878	H39537 R25513	Hs.10683	ESTs						3.10		
	128885		Hs.180141	cofilin 2 (muscle)					11.00		2 24	
	128998		Hs.107761	ESTs; Weakly similar to PUTATIVE RHO/RAC							3.21	3.68
	129000 129038		Hs.107767 Hs.108124	ESTs; Moderately similar to CaM-KII inhi ribosomal protein L41						3.17		
85	129038	AW156903 AW580945			34.60							

	w	O 02/086	443							PCT/U	JS02/1	2476
	129210		Hs.202949	KIAA1102 protein								4.09
	129240	AA361258	Hs.237868	interleukin 7 receptor			2.29			0.00		
	129262		Hs.109843	ESTs						3.30		4.05
5	129301 129331		Hs.330780 Hs.279772	Human cytochrome P450-IIB (hIIB3) mRNA; ESTs; Highly similar to CGI-38 protein [4.09
3	129381		Hs.110903	claudin 5 (transmembrane protein deleted			293					
	129565	χππ	Hs.198726	vasoactive intestinal peptide receptor 1				160.80	10.00			
	129595	U09550	Hs.1154	oviductal glycoprotein 1; 120kD ESTs; Weakly similar to collagen alpha 1					10.00	3.40		
10	129613 129782		Hs.172847 Hs.104105	EST		9.00						
10	129950		Hs.1369	decay accelerating factor for complement				87.80				
	129958	R27496	Hs.1378	annexin A3			2.72	44.60				
	129959		Hs.274463	defensin; alpha 1; myeloid-retated seque UDP-GathetaGlcNAc beta 1;3-galactosyltr			212	42.20				
15	130160 130259	AA305688 NM_000328	Hs.267695 Hs.153614	retinitis pigmentosa GTPase regulator			2.54					
1.5	130273	AW972422	Hs.153863	MAD (mothers against decapentaplegic; Or				51.60		2.46		
	130312		Hs.15430	DKFZP586G1219 protein						3.16		4.11
	130436 130523	NM_001929 AA999702	Hs. 155597 Hs. 214507	D component of complement (adipsin) ESTs						4.77		
20	130799	AB028945	Hs.12696	ESTs		6.00						
	130885	NM_005883	Hs.20912	adenomatous polyposis coll like						3.54		3.50
	131002	AL050295	Hs.22039	KIAA0758 protein		20.00						0.00
	131012 131031	AL039940 NM_001650	Hs.202949 Hs 288650	KIAA1102 protein aquaporin 4	41.20	20.00						
25	131051	N64328	Hs.268744	ESTs; Moderately similar to KIAA0273 [H.				31.40				
	131066	AW169287		ESTs				29.60	9.00			
	131082	AJ091121	Hs.246218 Hs.22824	ESTs; Weakly similar to zinc linger prot ESTs; Weakly similar to p160 myb-binding					3.00			3.86
	131087 131161	AF147709 AF033382	Hs.23735	potassium voltage-galed channel; subfami						3.14		
30	131179	AA171388	Hs.184482	DKFZP586D0624 protein						3.80		3.67
	131182	AI824144	Hs.23912	ESTs			2.98					3.01
	131205 131277	NM_003102 AA131466	Hs.23767	superoxide dismutase 3; extraceflular ESTs			3.15					
	131281	AA251716	Hs.25227	ESTs				32.20				2.44
35	131282	X03350	Hs.4	alcohol dehydrogenase 3 (class I); gamma						6.40		3.44
	131285	AI567943	Hs.25274 Hs.25956	ESTs; Moderately similar to putative sev DKFZP564D206 protein		8.00				0.40		
	131355 131391	R52804 AW085781	Hs.26270	ESTs		10.00						
	131461	AA992841	Hs.27263	butyrate response factor 2 (EGF-response	28.80						4.03	
40	131487	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp56401763 (f	39.00						4.03	
	131517 131545	AB037789 AL137432	Hs.263395 Hs.28564	ESTs; Highly similar to semaphorin VIa [ESTs	33.00				11.00			
	131583	AK000383	Hs.323092	ESTs: Weakly similar to dual specificity					10.00			
4.5	131647	AA359615	Hs.30089	ESTs			2.47			3.06		
45	131675	H15205	Hs.30509	ESTs ESTs	45.80					0.00		
	131676 131708	Al126821 S50415	Hs.30514 Hs.30941	calcium channel; voltage-dependent; beta	10.00		2.28					
	131717	X94630	Hs.3107	CD97 antigen				40.50				3.78
50	131756	AA443966	Hs.31595 Hs.107767	ESTs ESTs; Moderately similar to CaM-KII inhi				40.60				3.67
30	131762 131821	AA744902 AA017247	Hs.164577	ESTs			2.87					
	131839	AB014533	Hs.33010	KIAA0633 protein							3.48	
	131861	AL096858	Hs.184245	KIAA0929 protein Msx2 Interacting nuclea	54.00			49.20				
55	132015 132070	AI418006 BE622641	Hs.3731 Hs.38489	ESTs ESTs				34.80				
22	132242	AA332697	Hs.42721	ESTs			2.68					
	132334	AW080704	Hs.45033	facrimal profine rich protein	34.20		4.66					
	132476 132490	AL119844 NM_001290	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi LIM binding domain 2	34.20		2.66					
60	132533	Al922988	Hs.172510	ESTs		13.00						
•••	132598	X80031	Hs.530	collagen; type IV; alpha 3 (Goodpasture				30.60		4.02		
	132619	H28855	Hs.53447	ESTs; Moderately similar to kinesin ligh						3.18		
	132652 132726	N41739 N52298	Hs.61260 Hs.55608	ESTs ESTs; Wealthy similar to cONA EST yk484g1					11.43	•		
65	133028	R51604	Hs.300842	ESTs			2.37					
	133071	BE384932	Hs.64313	ESTs			2.27 2.63				•	
	133120 133129	NM_003278 AA428580	Hs.65424 Hs.65551	tetranectin (plasminogen-binding protein ESTs			203					5.49
	133147	AA026533	Hs.66	interleukin 1 receptor-like 1			6.20					
70	133151	NM_014051		ESTs				24.40		3.69		
	133213	AA903424 AW978439	Hs.6786 Hs.69504	ESTs ESTs				31.40	9.00			
	133276 133377	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene famili	41.20				•••			
	133407	AF017987	Hs.7306	secreted frizzled-related protein 1	50.20					2.70		
75	133535	AL134030	Hs.284180	protocadherin 2 (cadherin-like 2)						3.72		3.35
	133537 133656	U41518 BE149455	Hs.74602 Hs.75415	aquaporin 1 (channel-forming integral pr Accession not listed in Genbank			2.65					
	133689	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)				90.80				
00	133779	T58486	Hs.222566	ESTs			2.92			3.05		
80	133978	AF035718 L34657	Hs.78061 Hs.78146	transcription factor 21 platelet/endothelial cell adhesion molec			2.32					3.45
	133985 134000	L34057 AW175787	Hs.334841	selenium binding protein 1								4.05
	134111	Al372588	Hs.8022	TU3A protein			4.49				3.27	
85	134185	AA285136	Hs.301914	Homo sapiens mRNA; cDNA DKFZp586K1220 (f ESTs; Weakly similar to CGI-69 protein (40.80			3.21	
63	134204	A1873257	Hs.7994	CO.0' MENTA STREET IN COLOR MOTOR (

IS02/12476							443	O 02/086	W	
	3.76	32.20				protein tyrosine phosphatase; non-recept ESTs	Hs.156114 Hs.177711	A1092634 AA251363	134641 134677	
			3.05	15.00		angiotensin receptor 1B	Hs.89472	NM_000685	134745	
		57.80	200			carbonic anhydrase IV angiopoietin 1 receptor; TEK tyrosine ki	Hs.89485 Hs.89640	T28499 T29618	134749 134786	5
3.73						thyroid transcription factor 1	Hs.197764	U33749	134825	,
		31.60	2.52			ficolin (collagen/fibrinogen domain-cont	Hs.333383	AI829008	134978	
	3.21	31.00								
404					28.80	RNA binding molif protein 6	Hs.173993	AF069517		10
4.24				9.00		ESTs	Hs.94367	AA493650	135091	
	4.31			0.00						
	•				43.00	ESTs				
6.42			2 02			Human mRNA for KIAA0328 gene; partial cd	Hs.97393	R41179	135266	15
						phospholipase AZ; group IB (pancreas)				
					37.20	elastase 2; neutrophil				
	A 24				38.60	EST	Hs.99865	W27965	135388	••
	4.41					dopamine receptor D4	Hs.99922	L12398	135402	20
4.3 6.42		31.50	3.82 4.15	8.00	43.00 37.20	ficolin (cottagen/fibrinogen domain-conl ESTs ESTs RNA binding motif protein 6 ESTs syntrophin; beta 1 (dystrophin-associate ESTs ESTs ESTs Human mRNA for KIAA0328 gene; partial od phosphofipase A2; group IB (pancreas) potassium voltage-golde channet; shaker- elastase 2; neutrophil	Hs.33383 Hs.92927 Hs.93678 Hs.17393 Hs.94367 Hs.95011 Hs.269386 Hs.96901 Hs.97393 Hs.9992 Hs.24379 Hs.99863	AI829008 N50465 AIV796190 AF069517 AA493650 AA775910 C15737 AI636208 R41179 NM_000928 AW961818 NM_001972 W27965	134978 135010 135053 135081 135091 135135 135203 135236 135266 135346 135378 135387	10 15 20

TABLE 2B shows the accession numbers for those primekeys lacking unigenelD's for Table 2A. For each probeset we have listed the gene cluster number from which the obgonucleotides were designed. Gene clusters were compiled using sequences derived from Cenbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Caldand California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

	Pkey:	Unique Eos probeset identifier number
	CAT	iber: Gene cluster number
30		
<i>3</i> 0	Accession	n: Genoalx accessin numbers
	Di	CAT number Accessions
	Pkey	CAT fluitget Accessions
	108447	434527 AA079126
35	108550	120073_1 AA084867 AA084996
	108655	127522 1 AA099960 AA113013
	102397	44371_1 U41898
	126303	1525933_1 D78841 D78880
	125810	1554054 1 H00083 R81062
40	103627	2615_2 Z48513 Z48512
40	121366	280401, 1 Al743515 AA405617 AW276706
	114509	11677_1 AA079505 AA079537
	115272	172113_1 AW015947 AA211890 AA279425
	108338	112186 1 AA070773 AA070774
45	108434	114012 1 A4078399 A4078788
43	123802	genbank_AA620448 AA620448
		MOT_FOUND_entrez_U33839 U33839
	102310	HOID OWN TANKED TO THE TANKED
	102636	entrez_U67092 U67092 cenbank AA026349 AA026349
50	104776	
50	120504	genbank_AA256837 AA256837
	113502	genbank_T89130TB9130
	108499	genbank_AA083103 AA083103
	101308	entrez_L41390 L41390
	108629	genbank_AA102425 AA102425
55	103098	221_215 M86361 Z26593 X02850 D13070 AE000659 M17649 M87869 M87871 X61077 M16286 AF018169 X61079 S59351 X60142 AF043169
	103241	entrez_X76223 X76223
	103508	entrez_Y10141 Y10141
	103575	entrez_Z26256 Z26256
	119514	NOT_FOUND_entrez_W37937 W37937
60	121082	genbank_AA398722 AA398722
	128634	AA464918_at
	105817	oenbank AA397825 AA397825
	121518	genbank AA412155 AA412155
	114449	genbank_AA020736 AA020736
65	114648	genbank_AA101056 AA101056
	121950	genbank AA429515 AA429515
	107723	genbank AA015967 AA015967
	10//20	Squarement and the same and the

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Table 3A shows 452 genes up-regulated in chronically diseased lung relative to normal lung. Chronically diseased lung samples represent chronic non-matignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 59660 probesets on the Eost/Affyrnetrix Hu03 Genechip array. Gene expression data for each probesed obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5 Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number ExAccn: Unigene number UninenelD: Unigena gene title Unigene Title: 80th percentile of Al for chronically diseased lung samples divided by the 90th percentile of Al for normal lung samples. 80th percentile of Al for chronically diseased lung samples divided by the 90th percentile of normal lung samples, squamous cell carcinomas and 10 R2: Toth percentile of AI for chronically diseased lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and turnor samples divided by the 90th percentile of normal lung samples, squamous cell carcinomas and adenocarcinomas minus the 15th percentile of AI for all normal lung, R3: chronically diseased lung and tumor samples 15 R3 R1 R2 ExAcon UnigenelD Unigene Title Pkey 12 40 Human BRCA2 region, mRNA sequence CG030 Hs.138751 135423 U50531 213 20 135378 AW961818 Hs.24379 MUM2 protein phospholipase A2, group IB (pancreas) NM_000928 135346 Hs 992 Hs.293507 12.40 AW298244 ESTS 135235 11.67 U90268 Hs.93810 cerebral cavernous malformations 1 135057 8.00 hypothetical protein 134951 BF305081 Hs.169358 GRO3 oncogene 25 134799 M36821 Hs.89690 8.20 TEK tyrosine kinase, endothelial (venous 134786 T29618 Hs.89640 29.80 glutamate receptor, ionotrophic, AMPA 4 NM_000829 BE246762 134772 134752 Hs.163697 1.93 Hs.89499 arachidonate 5-lipoxygenase 2.07 T28499 Hs.89485 carbonic anhydrase IV 134749 30 BF326276 **ESTs** 134696 Hs.8861 Hs.87205 lymphocyte antigen 64 (mouse) homolog, r 13.60 NM 005582 134636 1.92 134627 AI018768 Hs.12482 glyceronephosphate O-acyltransferase ESTs, Weakly similar to A55380 faciogeni 1.92 AW975159 Hs 293097 134622 SWI/SNF related, matrix associated, acti adenosine dearninase, RNA-specific, B1 (h Hs.172280 13 20 134570 U65615 1.78 35 134561 U76421 Hs.85302 CD33 antigen (gp67) 6.20 NM_001772 NM_006416 Hs 83731 134468 solute carrier family 35 (CMP-sialic aci transforming growth factor, beta recepto 134417 Hs.82921 134343 D50683 Hs.82028 deleted in liver cancer 1 Hs.8700 134323 RF170651 40 134300 NM_001430 Hs.8135 endothelial PAS domain protein 1 134299 AW580939 Hs.97199 complement component C1q receptor 20.60 siatophorin (gpL115, leukosialin, CD43) 134253 X52075 Hs.80738 Hs.7972 KIAA0871 protein platelet/endothelial cell adhesion molec 12.20 134182 D52059 133985 1.34657 Hs.78146 45 AF035718 transcription factor 21 Hs.78061 133978 Hs.76640 RGC32 protein 133835 A1677897 dihydropyrimidinase-like 2 nucleolar and ooiled-body phosphprotein 133651 Al301740 Hs 173381 15.20 D21262 Hs.75337 133633 ESTs, Moderately similar to ALU7_HUMAN A DNA segment, single copy probe LNS-CAI/L Hs.313500 Hs.178112 133565 AW955776 50 1.77 133548 AW946384 Hs.74120 adipose specific 2 AA335295 133488 2.08 Hs.31432 Hs.293676 133478 X83703 cardiac ankyrin repeat protein ESTs 9.60 133337 AF085983 hypothetical protein FLJ 10210 HSKM-B protein AB037715 Hs.183639 1.77 133200 30.60 55 133153 AF070592 Hs.66170 zinc finger protein 161 22.60 Al128606 Hs.6557 133130 Hs.65424 tetranectin (plasminogen-binding protein NM_003278

R52804 Hs.25956 DKFZP564D206 protein A AR 131355 R71802 Hs.24853 **ESTs** 15.00 131253 131207 AF104266 Hs.24212 latrophilin 80 Hs.323117 ESTs 1.84 AI472209 131156 3.54 AW169287 Hs.22588 **ESTs** 131066 Hs.268744 KIAA1796 protein 131061 N64328 guanine nucleotide binding protein (G pr hypothetical protein DKFZp564L0864 simil 1.93 AA348541 Hs.296261 131053 16.60 AA641767 Hs.21015 130895 85 130762 D84371 Hs.1898 paraoxonase 1

protein kinase C, alpha KIAA0960 protein

interleukin 6 receptor

ESTs

ESTs

ESTs

ESTs

ESTs

SAC2 (suppressor of actin mutations 2, ESTs, Weakly similar to T33468 hypotheti

Homo sapiens clone TUA8 Cri-du-chat regi

hypothetical protein DKFZp566A1524 KIAA0781 protein

ESTs, Moderately similar to A46010 X-li

sema domain, transmembrane domain (TM).

A kinase (PRKA) anchor protein 2

GRB2-associated binding protein 2

MHC class II transactivator

epithelial membrane protein 2

133120

132928 132836

132799 132742

132548

132476

132439

132240

132210

132199

131751

131745

131694

131686

131676

131629

131589

131536

131517

60

65

70

75

AW168082

AR023177

AA025480

AL119844

AK001942

AR018324

NM_007203

AL041299

T96555

AI828559

Al126821

245794

C18825

AA019201

AR037789

NM_000246 NM_012296

W73311

X12830

Hs.169449 Hs.29900

Hs.169407

Hs.292812

Hs.193400

Hs.49476

Hs.4863 Hs.42676

Hs.42322

Hs.165084 Hs.31562

Hs.31447

Hs 3076

Hs.30687

Hs.30514 Hs.238809

Hs.29191

Hs.269210 Hs.263395

13.80

41 60

40.40

21.20

15.20

27.80

21.40

7.20

476

4.00

6.20

9.40

3.59

1.88

1.99

1.76

	w	O 02/086	143				
	130657	AW337575	Hs.201591	ESTs			
	130555	AJ831962	Hs.17409	cysteine-rich protein 1 (intestinal)			2.03
	130589 130562	AL110226 D50402	Hs.16441 Hs.182611	DKFZP434H204 protein solute carrier family 11 (proton-coupled			1.91
5	130555	R69743	Hs.116774	integrin, alpha 1		9.60	
	130365	W56119	Hs.155103	eukaryotic translation initiation factor	11.60	6.60	
	130273 130259	AW972422 NM_000328	Hs.153863 Hs.153614	MAD (mothers against decapentaplegic, Or refinitis pigmentosa GTPase regulator		0.00	1.91
	130090	H97878	Hs.132390	zinc finger protein 36 (KOX 18)	21.20		
10	129958	R27496	Hs.1378	annexin A3		5.05	
	129898 129875	AI672731 AA181018	Hs.13256 Hs.13056	ESTs hypothetical protein FL/13920	18.60		
	129699	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas			
1.5	129626	F13272	Hs.111334	ferritin, light polypeptide	20.02		
15	129598 129593	N30436 A1338247	Hs.11556 Hs.98314	Homo sapiens cDNA FLJ12566 fis, clone NT Homo sapiens mRNA; cDNA DKFZp586L0120 (f	22.63		
	129565	X77777	Hs.198726	vasoactive Intestinal peptide receptor 1			2.53
	129527	AA769221	Hs.270847	delta-tubulin	39.20		2.11
20	129402 129385	W72052 AA172106	Hs.11112 Hs.110950	ESTs Rag C protein	15.20		2.11
20	129315	NM_014563	Hs.174038	spondyloepiphyseal dysptasia, tate	12.40		
	129312	T97579	Hs.110334	ESTs, Wealty similar to 178885 serine/th	20.83		1.95
	129240 129210	AA361258 AL039940	Hs.237868 Hs.202949	interleukin 7 receptor KIAA1102 protein			1.55
25	129122	AW958473	Hs.301957	nudix (nucleoside diphosphate linked moi		4.20	
	129057	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)		E 20	
	128946 128798	Y13153 AF015525	Hs.107318 Hs.302043	kynurenine 3-monooxygenase (kynurenine 3 chemokine (C-C motif) receptor-like 2		5.20	
	128789	AW368576	Hs.139851	caveolin 2			2.24
30	128778	AA504776	Hs.186709	ESTs, Wealdy similar to 138022 hypothet	12.20		
	128766	AW160432	Hs.296460 Hs.155546	craniofaciat development protein 1 K1AA 1080 protein; Golgi-associated, gamm	26.40		1.78
	128631 128624	R44238 BE154765	Hs.102647	ESTs, Weakly similar to TRHY_HUMAN TRICH			2.51
	128609	NM_003516	Hs.102456	survival of motor neuron protein interac	16.00		
35	128603	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT potassium inwardly-rectifying channel, s	12.80	4.00	
	128598 128458	AA305407 H55864	Hs.102308 Hs.56340	ESTs			
	128061	AF150882	Hs.186877	sodium channet, voltage-gated, type XII,	17.20		
40	127968	AA830201 Al302471	Hs.124347 Hs.124292	ESTs Homo sapiens cDNA: FLJ23123 fis, clone L	21.30		
40	127959 127944	AI557081	Hs.262476	S-adenosylmethionine decarboxylase 1	10.60		
	127925	AA805151	Hs.3628	mitogen-activated protein kinase kinase	13.40	7.00	
	127896	AI669586 AA761802	Hs.222194 Hs.291559	ESTs ESTs	14.00	7.00	
45	127859 127817	AA836641	Hs.163085	ESTs	14.00		•
	127742	AW293496	Hs.180138	ESTs	11.00		
	127628 127609	AI240102 X80031	Hs.322430 Hs.530	NDRG family, member 4 collagen, type IV, alpha 3 (Goodpasture	11.10		
	127582	AA908954	Hs.130844	ESTs	19.60		
50	127543	AK000787	Hs.157392	Homo saplens cDNA FLJ20780 fis, clone CO	15.40		
	127535 127404	AA558424 AJ379920	Hs.164450 Hs.270224	ESTs ESTs	17.50 14.60		
	127396	L31968	Hs.187991	DKFZP564A122 protein	15.40		
<i>e e</i>	127374	AA442797	Hs.312110	ESTs, Weakly similar to 138022 hypothet	14.60		
55	127346 127340	AA203616 BE047653	Hs.44896 Hs.119183	DnaJ (Hsp40) homolog, subfamily B, membe ESTs, Weakly similar to ZN91_HUMAN ZINC	21,00 15.80		
	127307	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	.0.00		
	127242	AW390395	Hs.181301	cathepsin S	22.60		
60	127167 127046	AA625690 AA321948	Hs.190272 Hs.293968	ESTs ESTs	21.40 41.20		
00	126928	AA480902	Hs.137401	ESTs	11.00		
	126900	AF137386	Hs.12701	plasmolipin		6.60	1.78
	126852 126816	AA399961 AA248234		gb:zu68c01.r1 Soares_testis_NHT Homo sap gb:zsg2228.seq.F Human fetal heart, Lamb	12.20	5.60	
65	126812	AB037860	Hs.173933	nuclear factor VA	17.19		
	126666	AA648886	Hs.151999	ESTs	13.57		
	126645 126592	AA316181 AI611153	Hs.61635 Hs.6093	six transmembrane epithelial antigen of Homo sapiens cDNA: FLJ22783 fis, clone K	15.40	4.67	
	126556	AF255303	Hs.112227	membrane-associated nucleic acid binding	18.00		
70	126433	AA325606		gb:EST28707 Cerebellum II Homo sapiens c	16.77		
	126299 126218	AW979155 AL049801	Hs.298275 Hs.13649	amino acid transporter 2 Novel human gene mapping to chomosome 13	14.60	3.50	
	126182	AA721331	Hs.293771	ESTs	13.40	4.30	
75	126177	AW752782	Hs.129750	hypothetical protein FLJ10546	18.20		
75	126142 126077	H86261 M78772	Hs.40568 Hs.210836	ESTs ESTs	14.00 16.59		
	125994	AI990529	Hs.270799	ESTs	17.40		
	125934	AA193325	Hs.32646	hypothelical protein FLJ21901	13.00		
80	125847 125831	AW161885 H04043	Hs.249034	ESTs gb:yj45c03.r1 Soares placenta Nb2HP Homo	49.57		
	125731	R61771	Hs.26912	ESTs	13.20		
	125676	BE612918	Hs.151973	hypothetical protein FLJ23511	11.20		
	125561 125552	F18572 H09701	Hs.22978 Hs.278366	ESTs, Weakly similar to ALU4_HUMAN ALU S ESTs, Weakly similar to 138022 hypotheti	12.60		
85	125489	H49193	Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A	33.40		

	WO 02/086443									
	125422	AA903229	Hs.153717	ESTs	38.00		1.80			
	125331 125309	AJ422996	Hs.161378 Hs.183745	ESTs hypothetical protein FLJ13456	18.20					
	125167	T12411 AL137540	Hs.102541	netrin 4			1.95			
5	125139	AW194933	Hs.9788	hypothetical protein MGC10924 similar to	24.00		1.84			
	125042	T78906	Hs.269432	ESTs, Moderately similar to ALU1_HUMAN serum deprivation response (phosphatidy)	21.80	10.60				
	124711 124631	NM_004657 NM_014053	Hs.26530 Hs.270594	FLVCR protein	23.20	10.00				
	124578	N68321	Hs.231500	EST	21.43		4.77			
10	124574	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2	37.20		1.77			
	124472	NS2517	Hs.102670 Hs.11090	EST membrane-spanning 4-domains, subfamily A	31.20					
	124438 124357	BE178536 N22401	H3.11030	gb:yw37g07.s1 Morton Fetal Cochlea Horno	14.64					
	124306	AW973078	Hs.293039	ESTs		4.00				
15	124214	H58608	Hs.151323	ESTS		27.20				
	124097 123978	AW298235 T89832	Hs.101689 Hs.170278	ESTS ESTs			2.03			
	123972	T46848	Hs.70337	immunoglobulin superfamily, member 4		6.00	4 70			
20	123961	AL050184	Hs.21610	DKFZP434B203 protein		15.80	1.79			
20	123936 123802	NM_004673 AA620448	Hs.241519	angiopoietin-like 1 gb:ae58c09.s1 Stratagene lung carcinoma		4.23				
	123734	AA609861	Hs.312447	ESTs		4.20				
	123619	AA602964		gb:no97c02.s1 NCI_CGAP_Pr2 Horno sapiens	33.60					
25	123596	AA421130	Hs.112640	EST	10.93		2.18			
25	123476 123340	AA384564 AA504264	Hs.108829 Hs.182937	ESTs peptidylprolyl isomerase A (cyclophilin	11.20					
	123190	AA489212	Hs.105228	EST	14.20	7.00				
	123136	AW451999	Hs.194024	ESTs	31.20	7.00				
30	123073 123055	AA485061 AA482005	Hs.105652 Hs.105102	ESTs ESTs, Weakly similar to reverse transcri	3120	4.80				
30	122699	AA456130	Hs.301721	KIAA1255 protein		5.00				
	122679	AA811286	Hs.192837	ESTs, Wealty similar to ALUS_HUMAN ALU S	14.40					
	122633	NM_001546	Hs.34853	Inhibitor of DNA binding 4, dominant neg ESTs	40.00					
35	122553 122544	AA451884 AW973253	Hs.190121 Hs.292689	ESTS	15.40					
55	122485	AA524547	Hs.160318	FXYD domain-containing ion transport reg		40.40	1.81			
	122211	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H		12.10	1.95			
	122127 122011	AW207175 AA431082	Hs.106771	ests gb:zw78a10.s1 Soares_testis_NHT Homo sap			1.89			
40	121992	AJ860775	Hs.98506	ESTs		3.60				
	121989	W56487	Hs.193784	Homo sapiens mRNA; cDNA DKFZp586K1922 (f			2.01 1.85			
	121835	AB033030 AF241254	Hs.300670 Hs.178098	KIAA1204 protein angiotensin I converting enzyme (peptidy	12.43		1			
	121726 121690	AF241234 AV660305	Hs.110286	ESTs Conversing Citations (proposa)			1.82			
45	121643	AA640987	Hs.193767	ESTs	44.00					
	121633	AA417011	Hs.98175 Hs.126065	EST ESTs	14.00	16.40				
	121622 121497	AA416931 AA412031	Hs.97901	EST	11.20					
	121351	AW206227	Hs.287727	hypothetical protein FLJ23132	12.20		1 00			
50	121314	W07343	Hs.182538	phospholipid scramblase 4	22.40		1.83			
	121242 121059	AA400857 AA393283	Hs.97509	ESTs gb:zt74e03.r1 Soares_testis_NHT Homo sap	14.80					
	120934	AA226198		gb:nc26a07.s1 NCI_CGAP_Pr1 Homo sapiens	21.20		4 70			
e e	120755	AA312934	Hs.190745	Homo saplens cDNA: FLJ21326 fis, clone	20.00		1.79			
55	120637 120484	AA811804 AA253170	Hs.96473	gb:ob39a05.s1 NCt_CGAP_GCB1 Homo sapiens EST	40.20					
	120336	N85785	Hs.181165	eukaryotic transtation elongation factor		6.60				
	120266	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	16.80	6 72				
60	120132	W57554	Hs.125019	ESTs ESTs		4.73	1.75			
00	120041 119996	AA830882 W88996	Hs.59368 Hs.59134	EST		7.20				
	119970	AA767718	Hs.93581	hypothetical protein FLJ10512	11.20	2 70				
	119861	W78816	Hs.49943	ESTs, Weakly similar to S65657 alpha-1C- advanced glycosylation end product-speci		3.78				
65	119824 119740	W74536 AW021407	Hs.184 Hs.21068	hypothetical protein	20.20					
05	119271	AI061118	Hs.65328	Fanconi anemia, complementation group F	15.20					
	119221	C14322	Hs.250700	tryptase beta 1	12.60					
	119126 119073	R45175 BE245360	Hs.117183 Hs.279477	ESTs ESTs	12.00					
70	118928	AA312799	Hs.283689	activator of CREM in testis		10.00				
	118901	AW292577	Hs.94445	ESTs		3.96				
	118661	AL137554	Hs.49927	protein kinase NYD-SP15	10.40	9.60				
	118507 118449	Al377444 · Al813865	Hs.54245 Hs.164478	ESTs, Weakly similar to S65824 reverse thypothetical protein FLJ21939 similar to			1.90			
75	118416	N66028	Hs.49105	FKBP-associated protein	16.20	4.00				
	118379	N64491	Hs.48990	ESTs gb:yy62f01.s1 Soares_multiple_sclenosis_		4.00 6.60				
	118329 118320		Hs.141600			3.80				
	118253		Hs.20887	hypothetical protein FLJ10392	17.60					
80	118124	N5696B	Hs.46707	chromosome 21 open reading frame 37	14.00		1.86			
	118056		Hs.42768 Hs.47544	hypothetical protein DKFZp761O0113 - EST		5.00	1.00			
	118032 117840		Hs.48802	Homo saplens clone 23632 mRNA sequence		4.00				
0.7	117404	N39725	Hs.15220	zinc finger protein 106	44.00		1.90			
85	117314	N32498	Hs.42829	ESTs	14.20					

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	117209	W03011	Hs.306881	MSTP043 protein			2.31
	117023 116814	AV/070211 H50834	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586ND121 (f gb:yp86a10.s1 Soares fetal liver spleen	20.20		201
	116784	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific		3.51	
5	116766	AIS08657	Hs.95097	ESTs	16.20	6.80	
	116712	AW901618 H10344	Hs.61935 Hs.49050	Homo sapiens mRNA; cDNA DKFZp7611071 (fr ESTs, Wealty similar to A Chain A, Human	18.60	0.00	
	116707 116351	AL133623	Hs.82501	similar to mouse Xm1 / Dtm2 protein	19.40		
10	116279	AW971248	Hs.291289	ESTs, Wealthy similar to ALU1_HUMAN ALU S			2.13
10	116166	AL039940	Hs.202949 Hs.15220	KIAA1102 protein zinc finger protein 106			1.75
	116152 116117	AL040521 8E613410	Hs.31575	SEC63, endoplasmic reticulum translocon	13.20		
	116107	AL133916	Hs.172572	hypothetical protein FLJ20093	30.11		2.36
15	115965 115955	AA001732 AF263613	Hs.173233 Hs.44198	hypothetical protein FLJ10970 intracellular membrane-associated calciu	18.20		2.00
13	115844	Al373062	Hs.332938	hypothetical protein MGC5370	18.57		
	115583	AF255910	Hs.54650	junctional adhesion molecule 2	11.82	23.00	
	115573 115672	AA406341 AB89110	Hs.269908 Hs.73251	Homo sapiens cDNA FLJ11991 fis, clone HE ESTs	10.60		
20	115566	Al142336	Hs.43977	Human DNA sequence from clone RP11-196N1			1.76
	115313	AA808001	Hs.184411	albumin	25.20	8.00	
	115279 115230	AW964897 AA278300	Hs.290825 Hs.124292	ESTs Homo sapiens cDNA: FLJ23123 fis, clone L		0.00	1.80
	115110	AK001671	Hs.11387	KIAA1453 protein	14.20		
25	114999	BE246481	Hs.87856	ESTs	19.20	5.60	
	114930 114922	AA237022 AA235672	Hs.188717 Hs.87491	ESTs ESTs		3.60	
	114837	BE244930	Hs.166895	ESTs	43.70		
20	114769	AA149060	Hs.296100	ESTs	11.00 14.00		
30	114761 114736	AA143781 Al610347	Hs.126280 Hs.103812	hypothetical protein FLJ23393 ESTs, Moderately similar to ALU1_HUMAN A	14.00	4.20	
	114596	AA310162	Hs.169248	cytochrome c	10.71		
	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like ESTs, Wealdy similar to ALU8_HUMAN ALU S	20.40 20.40		
35	114455 114452	H37908 Al369275	Hs.271616 Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE	20.10	17.20	
55	114359	NM_016929	Hs.283021	chloride intracellular channel 5	40.40		2.09
	114357	R41677	Hs.6107	Homo saptens cDNA FLJ14839 fis, clone OV ESTs	12.40		2.00
	114251 114138	H15261 AW384793	Hs.21948 Hs.15740	Homo sapiens mRNA; cDNA DKFZp434E033 (fr		11.40	
40	114124	W57554	Hs.125019	ESTs		6.04	1.82
	113946 113695	AW083883 T96965	Hs.37896 Hs.17948	Homo sapiens cDNA FLJ 13510 fis, clone PL ESTs, Weakly similar to ALUB_HUMAN [!]!			1.02
	113606	NM_013343	Hs.278951	NAG-7 protein			2.15
15	113590	R49642	Hs.142447	ESTs, Weakly similar to ALU1_HUMAN ALU S	32.00	3.60	
45	113560 113552	T91015 Al654223	Hs.268626 Hs.16026	ESTs hypothetical protein FLJ23191	02.00		
	113540	AW152618	Hs.16757	ESTs		0.25	
	113502	T89130	Hs.12967	gb:ye12d01.s1 Stratagene lung (937210) H ESTs	12,40	8.35	
50	113288 113252	A1076838 NM_004469	Hs.11392	c-fos induced growth factor (vascular en	12,10	4.27	
•	113238	R45467	Hs.189813	ESTs	04.00		
	113203	AA743563	Hs.10305 Hs.8881	ESTs ESTs, Weakly similar to S41044 chromosom	21.20		1.92
	113195 113089	H83265 T40707	Hs.270862	ESTs	14.33		
55	113076	AF033199	Hs.8198	zinc finger protein 204		6.00 9.40	
	113009 112937	T23699 A1694320	Hs.7246 Hs.6295	ESTs ESTs. Wealdy similar to T17248 hypotheti		12.20	
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-li	10.57		
۷٥	112794	R97018	Un 000647	gb:yq74b08.s1 Soares fetal liver spleen ESTs	26.60 15.33		
60	112691 112602	R88708 AW004045	Hs.220647 Hs.203365	ESTS	15.60		
	112366	AF035318	Hs.12533	Homo sapiens clone 23705 mRNA sequence	15.40		
	112210	R49645	Hs.7004 Hs.22689	ESTs Homo sapiens mRNA; cDNA DKFZp586O1318 (f	14.00 13.00		
65	112064 111998	AL049390 R42379	Hs.138283	ESTs	11.00		
05	111987	NM_015310	Hs.6763	KIAA0942 protein	22.40		1.77
	111803		Hs.325823 Hs.9218	ESTs, Moderately similar to ALU5_HUMAN A ESTs			1.86
	111737 111605	H04607 T91061	Hs.194178	ESTs, Moderately similar to PC4259 femi	23.00		
70	111510	R07856	Hs.16355	ESTs	11.02		1.88
	111341 111280		Hs.22483 Hs.19385	Homo sapiens mRNA; cDNA DKFZp762M127 (fr CGI-58 protein	18.40		1.00
	111247		Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f			
75	111232		Hs.16928	ESTs	27.60 14.80		
75	110942 110924		Hs.28419 Hs.12940	ESTs zinc-lingers and homeoboxes 1	24.71		
	110837	H03109	Hs.108920	HT018 protein			2.18
	110824 110776		Hs.26942 Hs.19545	ESTs frizzled (Drosophila) homolog 4	12.20		1.75
80	110776		Hs.37889	ESTs	13.00		
- •	110369	AK000768	Hs.107872			5.60	2.31
	110099 109984		Hs.23748 Hs.10299	ESTs Homo sapiens cDNA FLJ13545 fis, clone PL			6.01
	109958		Hs.133521	ESTs	11.25		
85	109893		Hs.30484	ESTs			2.68

	WO 02/086443						
	109842	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	23.83		3.91
	109837	H00656	Hs.29792 Hs.12024	ESTs, Weakly similar to 138022 hypotheti ESTs		17,20	J.31
	109796 109688	AI600515 R41900	Hs.22245	ESTs		9.60	
5	109648	H17800	Hs.7154	ESTs	22.80		
	109613	H47315	Hs.27519	ESTs ESTs			
	109550 109523	AW021488 AW193342	Hs.26981 Hs.24144	ESTs			1.89
	109472	AK001989	Hs.91165	hypothetical protein	45.00	6.00	
10	109355	AA524525	Hs.48297	DKFZP586C1620 protein	15.00 25.60		
	109260 108781	AW978515 AA128654	Hs.131915	KIAA0863 protein gb:zn98g07.s1 Stratagene fetal refina 93	14.20		
	108663	BE219231	Hs.292653	ESTs, Weakly similar to T26845 hypotheti	11.00		
1.5	108573	AA086005		gbzl84c04.s1 Stratagene colon (937204)	26.00		
15	108480 108382	AL133092 NM_006770	Hs.68055 Hs.67726	hypothetical protein DKFZp434l0428 macrophage receptor with collagenous str			1.83
	108174	AA055632	Hs.303070	ESTs	15.20		
	108138	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr	15.44	3.60	
20	108087 108048	AA045708 Al797341	Hs.40545 Hs.165195	ESTs Homo sapiens cDNA FLJ14237 fis, clone NT		11.40	
20	108041	AW204712	Hs.61957	ESTs		4 =0	
	107997	AL049176	Hs.82223	chordin-like		4.76	
	107994 107922	AA036811 BE153855	Hs.48469 Hs.61460	LIM domains containing 1 lg superfamily receptor LNIR	14.20		
25	107522	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	51.80		
	107666	AA010611	Hs.60418	EST PURE CERTAIN AND AND AND AND AND AND AND AND AND AN	29.20 10.73		
	107332 107292	T87750 BE166479	Hs.183297 Hs.4789	DKFZP566F2124 protein Homo sapiens serologically defined breas	32.00		
	107230	A1034467	Hs.34650	ESTs	17.40		
30	107168	W57578	Hs.237955	RAB7, member RAS oncogene family	10.43 11.40		
	107160 107054	AA314490 Al076459	Hs.27669 Hs.15978	KIAA1563 protein KIAA1272 protein	11.40		
	107029	AF264750	Hs.288971	myeloid/lymphoid or mixed-lineage leukem	21.40		
25	106999	H93281	Hs.10710	hypothetical protein FLJ20417	35.80		1.76
35	106954	AF128847	Hs.204038 Hs.26530	indolethylamine N-methyltransferase serum deprivation response (phosphatidy)			1.10
	105870 106865	A1983730 AW192535	Hs.19479	ESTs	13.40		
	106844	AA485055	Hs.158213	sperm associated antigen 6		7.13 7.00	
40	106820	NM_016831	Hs.12592	period (Drosophila) homolog 3 hypothetical protein FLJ11273	13.00	7.00	
40	105818 106797	AK002135 A1768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL			2.05
	106773	AA478109	Hs.188833	ESTs	40.60		
	106747	NM_007118	Hs.171957 Hs.21938	triple functional domain (PTPRF interact hypothetical protein FLJ12492	12,60 10.60		
45	106743 106667	8E613328 AW360847	Hs.16578	ESTs			
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr			2.40 1.78
	106567	AW450408 AL031846	Hs.86412 Hs.152151	chromosome 9 open reading frame 5 plakophilin 4			1.76
	106562 106536	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot			2.19
50	106533	AL134708	Hs.145998	ESTs	23.20		
	106507	AA259068 AA404265	Hs.267819 Hs.115537	protein phosphatase 1, regulatory (inhib putative dipeptidase	15.20		
	106490 106474	BE383668	Hs.42484	hypothetical protein FLJ10618	10.44		
e e	106211	AA428240	Hs.126083	ESTs		29.80 3.70	
55	105986 105894	AB037722 Al904740	Hs.8707 Hs.25691	KIAA1301 protein receptor (calcitonin) activity modifying		0.10	1.94
	105847	AW964490	Hs.32241	ESTs, Weakly similar to \$65657 alpha-1C-			1.75
	105803	AW747996	Hs.160999	ESTs, Moderately similar to A56194 throm	10.71		2.47
60	105731 105729	AA834664 H46612	Hs.29131 Hs.293815	nuclear receptor coactivator 2 Homo sapiens HSPC285 mRNA, partial cds	10.7 1		
00	105688	Al299139	Hs.17517	ESTs	23.40		
	105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	37.20	8.30	
	105101 104989	H63202 R65998	Hs.38163 Hs.285243	ESTs hypothetical protein FLJ22029		8.09	
65	104986	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1			1.92
	104969	A1670947	Hs.78406	phosphatidylinositol-4-phosphate 5-kinas		5.40 7.60	
	104903 104896	AI436323 AW015318	Hs.31141 Hs.23165	Homo sapiens mRNA for KIAA1568 protein, ESTs	13.80	7.00	
	104865	179340	Hs.22575	Homo sapiens cDNA: FLJ21042 fis, clone C			4 000
70	104825	AA035613	Hs.141883	ESTs			1.87 1.93
	104781 104776	AA099904 AA026349	Hs.21610	DKFZP434B203 protein gb:zj99f01.s1 Soares_pregnant_uterus_NbH		10.20	
	104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor		5.69	
75	104667	A1239923	Hs.30098	ESTS		3.82 4.20	
75	104404 104392	H58762 AA076049	Hs.274415	gb:EST00057 HE6W Homo sapiens cDNA clone Homo sapiens cDNA FLJ10229 fis, clone HE	27.20	7.20	
	104212		Hs.173035	KIAA0300 protein			1.91
	104074	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	11.20		
80	103749 103645		Hs.8768 Hs.7043	hypothetical protein FLJ 10849 succinate-CoA ligase, GDP-forming, atpha	10.86 12.00		
50	103554		Hs.323469	caveotin 1, caveolae protein, 22kD			· 1.80
	103541	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i			
	103496 103428		Hs.132821 Hs.78921	flavin containing monooxygenase 2 A kinase (PRKA) anchor protein 1	11.20		
85	103353		Hs.119274		19.80		

	w	O 02/0864	143					PCT/US02/1247	76
			Hs.2375	ent-like module containing, mucin-like,		3.60			
	103295 103280		Hs.76206	cadherin 5, type 2, VE-cadherin (vascula					
	103100		Hs.184585	LIM domain only 2 (rhombotin-like 1)			1.76		
	103025		Hs.123641	protein tyrosine phosphatase, receptor t			2.15		
5	102698		Hs.1867	progastricsin (pepsinogen C)					
•	102659	BE245169	Hs.211510	CUG triplet repeat, RNA-binding protein	11.00				
	102580	U60808	Hs.152981	COP-diacylglycerol synthase (phosphatida	25.40				
	102417	AA034127	Hs.153487	signal transducing adapter molecule (SH3	14.00				
	102363	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc	40.00				
10	102302	AA306342	Hs.69171	protein kinase C-like 2	10.86				
	102283	AW161552	Hs.83381	guanine nucleotide binding protein 11		7.40			
	102188	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	16.40	1.40			
	102151	T27013	Hs.3132	steroidogenic acute regulatory protein	15.40				
	101957	128824	Hs.74101	spleen tyrosine kinase	15.40				
15	101842	M93221	Hs.75182	mannose receptor, C type 1 myeloid cell mudear differentiation ant					
	101771	NM_002432	Hs.153837 Hs.81256	S100 calcium-binding protein A4 (calcium			1.78		
		A1198550	Hs.2563	tachykinin, precursor 1 (substance K, su	18.80				
	101716	AF050658 M62505	Hs.2161	complement component 5 receptor 1 (C5a)			2.22		
20	101678 101447	M21305	113.2101	ob:Human alpha satellite and satellite 3	504.80				
20	101383	NM_000132	Hs.79345	coamilation factor VIII, procoagulant co		31.00			
	101345	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N			1.75		
	101345	NM_005795	Hs.152175	calcitonin recentor-like			0.04		
	101336	NM_006732	Hs.75578	FBJ murine osteosarcoma viral oncogene h			2.24		
25		L43821	Hs.80261	enhancer of filamentation 1 (cas-like do					
	101277	BE297626	Hs.296049	microfibrillar-associated protein 4	19.00				
	101262			gb:Human dystrophin (dp140) mRNA, 5' end	19.00		201		
		NM_005308	Hs.211569	G protein-coupled receptor kinase 5			201		
••	101102	NM_003243	Hs.79059	transforming growth factor, beta recepto		7.52			
30	101088	X70597	Hs.553	solute carrier family 6 (neurotransmitte	19.38	7.04			
	101066	AW970254	Hs.889	Charot-Leyden crystal protein fatty acid binding protein 4, adipocyte	15.55		1.91		
	100971	BE379727	Hs.83213 Hs.180789	S164 protein	15.40				
		BE245294 W25797.comp		amyloid beta (A4) precursor protein (pro	11.20				
35	100770 100716		Hs.172350	HIR (histone cell cycle regulation defec	14.80				
22	100716	M69181	115.172550	gb:Human nonmuscle myosin heavy chain-8	33.00				
	100333	NM_014747	Hs.78748	KIAA0237 gene product	16.20				
	100428	D86640	Hs.56045	src homology three (SH3) and cysteine ri		4.00			
	100382		Hs.156007	Down syndrome critical region gene 1-lik		4.24			
40	100351	D64158				6.20			
	100299	D49493	Hs.2171	growth differentiation factor 10		21.20			
	100134	AA305746	Hs.49	macrophage scavenger receptor 1			1.79		
	100108		Hs.76873	hyaluronoglucosaminidase 2		5.40	1.73		
4.5	100095	Z97171	Hs.78454	myocilin, trabecular meshwork inducible	11.29	3,40			
45	100066			•	11.20				

TABLE 39 shows the accession numbers for those primekeys tacking unigenelD's for Table 3A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene duster number
Accession: Genbank accession numbers

60	Pkey	CAT number	Accessions	
oo	123619	371681_1	AA602964 A	A609200
		127143_1	AA325606 A	A099517 N89423
		1522905_1		988 D60337
	126816	122973_1	AA248234 A	A090985
65	126852	136135_1	AA399961 A	A128347
00	121059	273450_1	AA393283 A	A398628
	120637	200885 1	AAB11804 A	A809404 AA286907 AW977624
	122011	7617 -2	AA431082	
	120934	177521 1	AA226198 A	A226513 AA383773
70	123802	genbank_AA62	0448	AA62044B
, 0	116814	genbank_H508	34	H50834
	118329	genbank_N635	20	N63520
	104404			
		genbank AA02		AA026349
75	113502	genbank_T8913	30TB9130	
15	101262		L35854	
	108573			AA086005
	101447			
	124357			N22401
80	108781		8654	AA128654
	112794			R97018
	100351			15.0.0
	100555		M69181 M8	11051151039
	100555	MAT 11 5540	1100101110	

85

PCT/US02/12476 WO 02/086443

Table 4A shows 202 genes up-regulated in samples from patients treated with chemotherapy or radiotherapy. These genes were selected from 5960 probesets on the Eos/Alfymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the retainve level of mRNA expression.

Ptey: Unique Eos probeset identifier number

ExAcon: Exemplar Accession number, Genbank accession number

UnigenelD: Unique a number

Unique gene filte: Unique gene filte

R1: average of AI for samples from patients treated with chemotherapy or radiotherapy divided by the average of AI for normal lung samples. 5

4.0	R1:	average of	Al for samples	from patients treated with chemotherapy or radiother	apy divided
10	Pkey	ExAcon	UnigenelD	Unigene Title	R1
•	100113	NM_001269	Hs.84746	chromosome condensation 1	27.20
	100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3	20.60 20.40
15	100210	D26361	Hs.3104	KIAA0042 gene product glutamate receptor, matabotropic 5	20.60
	100225 100269	D28539 NM_001949	Hs.167185 Hs.1189	E2F transcription factor 3	29.40
	100233	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	23.50
	100877	X80821	Hs.27973	KIAA0874 protein	35.56
20	100893	BE245294	Hs.180789	S164 protein	43.40 21.80
	101273	Z11933 M21305	Hs.182505	POU domain, class 3, transcription facto gb:Human alpha satellite and satellite 3	193.60
	101447 101649	AW959908	Hs.1690	heparin-binding growth factor binding pr	38.40
	101724	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	198.80
25	101748	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	78.60 162.20
	101809	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn nuclear autoanligenic sperm protein (his	50.00
	101879 101915	AA176374 AF207881	Hs.243886 Hs.155185	cytosolic ovarian carcinoma antigen 1	26.00
	101973	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:potyp	37.20
30	102025	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	22.00
	102031	U04898	Hs.2156	RAR-related orphan receptor A	32.00 51.20
	102052 102391	NM_002202 AA296874	Hs.505 Hs.77494	ISL1 transcription factor, LIM/homeodoma deoxyguanosine kinase	13.90
	102420	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	28.80
35	102610	U65011	Hs.30743	preferentially expressed antigen in mela	110.60
	102829	NM_006183	Hs.80962	neurotensin	116.80 2.30
	103000	NM_001975	Hs.146580 Hs.83169	enolase 2, (gamma, neuronal) matrix metalloproteinase 1 (interstitial	181.40
	103036 103507	M13509 AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	49.20
40	103587	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	86.60
	104660	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	42.60 29.40
	104896 105038	AW015318	Hs.23165 Hs.9414	ESTs KIAA1488 protein	21.50
	105298	AW503733 BE387790	Hs.26369	hypothetical protein FLJ20287	32.80
45	105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	20.20
	105667	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	28.40 25.40
	105073 106205	AL157441 AW965058	Hs.17834 Hs.111583	downstream neighbor of SON ESTs, Weakly similar to 138022 hypotheti	32.00
	106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (40.60
50	106533	AL134708	Hs.145998	ESTs	59.80
	105575	AW970602	Hs.105421	ESTs	43.40 50.80
	106654 106851	AW075485 Al458623	Hs.286049	phosphoserine aminotransferase gb:tk04g09.x1 NCI_CGAP_Lu24 Homo sapiens	53.40
	106995	AB023139	Hs.37892	KIAA0922 protein	20.88
55	107332	T87750	Hs.183297	DKFZP566F2124 protein	23.60
	107532	AA443473	Hs.173684	Homo sapiens mRNA; cDNA DKFZp762G207 (fr	57.20 49.00
	107922 108609	BE153855 BE409857	Hs.61460 Hs.69499	lg superfamily receptor LNIR hypothetical protein	19.67
	108780	AU076442	Hs.117938	collagen, type XVII, alpha 1	48.17
60	109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	59.20
	109260	AW978515	Hs.131915	KIAA0863 protein	28.60 22.80
	109280 109292	AK001355 AW975746	Hs.279610 Hs.188662	hypothetical protein FLJ10493 KIAA1702 protein	22.00
	109292	AA219172	Hs.86849	ESTs	21.00
65	109415	U80736	Hs.110826	trinucleotide repeat containing 9	31.60
	109445	AA232103	Hs.189915	ESTs	24.20 21.40
	109502	AW967069	Hs.211556 Hs.170267	hypothetical protein MGC5487 ESTs	20.40
	109633 109786	AW003785 AI989482	Hs.146286	kinesin family member 13A	19.60
70 -	109958	AA001266	Hs.133521	ESTs	24.00
	110920	N47224	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	28.40
	110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1 PDZ domain containing 1	36.00 61.20
	111084 111132	H44186 AB037807	Hs.15456 Hs.83293	hypothetical protein	24.60
75	111229	AW389845	Hs.110855	ESTs	27.20
	111337	AA837396	Hs.263925	US1-interacting protein NUDE1, rat homo	48.00
	111987	NM_015310	Hs.6763 Hs.22116	KIAA0942 protein CDC14 (cell division cycle 14, S. cerevi	37.80 26.80
	112046 112268	AA383343 W39609	Hs.22003	solute carrier family 6 (neurotransmitte	63.80
80	112685	R87650	Hs.33439	ESTs, Weakly similar to ALU1_HUMAN ALU	26.40
·	112871	AL110216	Hs.12285	ESTs, Weakly similar to 155214 salivary	47.64
	112897	AW206453	Hs.3782	ESTs hypothetical emissis FL 110201	22.00 65.00
	112973 112992	AB033023 AL157425	Hs.318127 Hs.133315	hypothetical protein FLJ10201 Homo sapiens mRNA; cDNA DKFZp761J1324 (f	42.00
85	113073	N39342	Hs.103042	microtubule-associated protein 18	55.40

	W	O 02/0864	143		
	113494	T91451	Hs.86538	ESTs	22.80
	113560	T91015	Hs.268626	ESTs	22.80
	113849	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	51.80 28.20
5	113950 114339	Al267652 AA782B45	Hs.30504 Hs.22790	Homo sapiens mRNA; cDNA DKFZp434E082 (fr ESTs	20.20
3	114365	H42169	Hs.18653	hypothetical protein FLJ14627	21.00
	114455	H37903	Hs.271616	ESTs, Wealdy similar to ALU8_HUMAN ALU S	25.80
	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	23.60 27.20
10	114824 114837	AA960961 BE244930	Hs.305953 Hs.166895	zinc finger protein 83 (HPF1) ESTs	30.20
10	114974	AW966931	Hs.179662	nucleosome assembly protein 1-like 1	20.80
	115075	AA814043	Hs.88045	ESTs	30.60 28.86
	115084	BE383668	Hs.42484 Hs.122579	hypothetical protein FLJ10618 hypothetical protein FLJ10461	38.00
15	115291 115313	BE545072 AA808001	Hs.184411	albumin	22.60
	115697	D31382	Hs.63325	transmembrane protease, serine 4	173.60
	115909	AW872527	Hs.59761	ESTs, Wealthy similar to DAP1_HUMAN DEATH ESTs	27.77 20.80
	116090 116107	AL133916	Hs.61232 Hs.172572	hypothetical protein FLJ20093	164.20
20	116399	AA889120	Hs.110637	homeo box A10	38.00
	117099	H93699	11- 000000	gb:yv16a11.s1 Soares fetal liver spleen	21.60 49.40
	117881 118091	AF161470 AW005054	Hs.260622 Hs.47883	butyrate-induced transcript 1 ESTs, Weakly similar to KCC1_HUMAN CALCI	22.40
	118138	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	22.00
25	118720	N73515		gb:za49d07.s1 Soares fetal liver spleen	20.00 19.40
	118873 119126	AI824009 R45175	Hs.44577 Hs.117183	ESTs ESTs	111.20
	119717	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	33.00
•	119940	AL050097	Hs.272531	DKFZP586B0319 protein	31.00 20.20
30	120266 120515	AI807264 AA258356	Hs.205442	ESTs, Weakly similar to T34036 hypotheti gb:zr59c10.s1 Soares_NhHMPu_S1 Homo sapi	25.00
	120859	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	95.40
	120983	AA398209	Hs.97587	EST	105.20 38.80
35	121054 121369	AW976570 AW450737	Hs.97387 Hs.128791	ESTs CGI-09 protein	41.60
55	122335	AA443258	Hs.241551	chloride channel, calcium activated, fam	30.80
	122612	AA974832	Hs.128708	ESTs	19.60 33.20
	123130 123440	AA487200 A1733692	Hs.112488	gb:ab19f02.s1 Stratagene lung (937210) H ESTs	23.17
40	123596	AA421130	Hs.112640	EST	23.00
	123619	AA602964	11- 070016	gb:no97c02s1 NCI_CGAP_Pr2 Homo sapiens	28.80 77.60
	124006 124169	Al147155 BE079334	Hs.270016 Hs.271630	ESTs . ESTs	22.20
	124281	Al333756	Hs.111801	arsenate resistance protein ARS2	42.20
45	124472	N52517	Hs.102670	EST ESTs	32.60 21.80
	124617 124631	AW628168 NM_014053	Hs.152684 Hs.270594	FLVCR protein	30.40
	124839	R55784	Hs.140942	ESTs	21.20 42.80
50	125186 125321	AA610620 T86652	Hs.181244 Hs.178294	major histocompatibility complex, class ESTs	27.00
50	125535	NM_013243	Hs.22215	secretogranin III	23.80
	125646	AA628962	Hs.75209	protein kinase (cAMP-dependent, catalyti	23.20 21.20
	125684 125724	AW589427 AL360190	Hs.158849 Hs.295978	Homo sapiens cDNA: FLJ21663 fis, clone C Homo sapiens mRNA full length insert cDN	48.80
55	125847	AW161885	Hs.249034	ESTs	31.00
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	21.20 49.80
	126077 126299	M78772 AW979155	Hs.210836 Hs.298275	ESTs amino acid transporter 2	21.80
	126395	A1468004	Hs.278956	hypothetical protein FLJ12929	71.00
60	126433	AA325606	U- 220CA	gb:EST28707 Cerebellum II Homo sapiens c	23.20 23.80
	126509 126538	R47400 AB030656	Hs.23850 Hs.17377	ESTs coronin, actin-binding protein, 1C	23.10
	126666	AA648886	Hs.151999	ESTs	36.00
65	126812	AB037860 AW450979	Hs.173933	nuclear factor I/A gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	20.80 46.29
05	126872 127046	AA321948	Hs.293968	ESTs	22.80
	127431	AW771958	Hs.175437	ESTs, Moderately similar to PC4259 femi	30.00
	127489	AA550250	Hs.272076 Hs.164018	ESTs ESTs	20.80 25.20
70	127521 127742	AW297206 AW293496	Hs.180138	ESTs	28.00
	127925	AA805151	Hs.3628	mitogen-activated protein kinase kinase	21.20
	127930 127968	AA809672 AA830201	Hs.123304 Hs.124347	ESTs ESTs	20.54 28.20
	127987	AI022103	Hs.124511	ESTs	19.60
75	128116	H07103	Hs.286014	Homo sapiens, clone IMAGE:3867243, mRNA	20.40
	128609 128777	NM_003616 AI878918	Hs.102456 Hs.10526	survival of motor neuron protein interac cysteine and glycine-rich protein 2	34.40 53.80
	128949	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	23.00
00	129168	Al132988	Hs.109052	chromosome 14 open reading frame 2	37.60
80	129404 129527	A1267700 AA769221	Hs.317584 Hs.270847	ESTs delta-tubulin	28.60 40.80
	129527	AA026815	Hs.11463	UMP-CMP kinase	31.20
	129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	29.60 72.20
85	129785 129970	H19006 AV655806	Hs,184780 Hs,296198	ESTs chromosome 12 open reading frame 4	22,20
93	.203.0				

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0149	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	29.50	

	130149	AW067805	Hs.172665	methylenetetrahydrofolata dehydrogenasa	29.50
	130199	Z48579	Hs.172028	a disintegrin and metalloproteinase doma	27.60
	130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	28.36
_	130466	W19744	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	20.20
5	130482	AW409701	Hs.1578	bacutoviral IAP repeat-containing 5 (sur	22.40
	130617	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	19.60
	130703	R77776	Hs.18103	ESTs ·	19.40
	130732	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	21.40
	130867	NM_001072	Hs.284239	UDP glycosyltransferase 1 family, polype	110.00
10	131028	Al879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	25.20
	131086	AL035461	Hs.2281	chromogranin B (secretogranin 1)	40.60
	131284	NM_001429	Hs.25272	E1A binding protein p300	24.60
	131775	AB014548	Hs.31921	KLAA0648 protein	21.00
	131860	BE383676	Hs.334	Rho guanine nucleotide exchange factor (33.40
15	131945	NM 002916	Hs.35120	replication factor C (activator 1) 4 (37	60.80
	132040	NM 001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	20.40
	132084	NM_002267	Hs.3886	karyopherin alpha 3 (importin alpha 4)	29.40
	132389	AA310393	Hs.190044	ESTs	32.40
	132437	AA152106	Hs.4859	cyclin L ania-6a	27.40
20	132550	AW969253	Hs.170195	bone morphogenetic protein 7 (osteogenic	75.60
	132617	AF037335	Hs.5338	carbonic anhydrase XII	31.36
	132632	AU076916	Hs.5398	guanine monphosphate synthetase	32.40
	132672	W27721	Hs.54697	Cdc42 guanine exchange factor (GEF) 9	23.40
	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	61.20
25	132771	Y10275	Hs.56407	phosphoserine phosphatase	22.33
	133070	U92649	Hs.64311	a disintegrin and metalloproteinase doma	23.50
	133153	AF070592	Hs.66170	HSKM-B protein	30.00
	133181	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	23.80
	133282	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	51.60
30	133350	AJ499220	Hs.71573	hypothetical protein FLJ10074	33.00
	133592	AV652066	Hs.75113	general transcription factor IIIA	82.00
	133658	AA319146	Hs.75426	secretogranin II (chromogranin C)	
	133865	AB011155	Hs.170290	discs, large (Drosophila) homolog 5	69.33
	134032	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	33.20
35	134125	NM_014781	Hs.50421	KIAA0203 gene product	31.60
	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	30.60
	134321	BE538082	Hs.8172	ESTs, Moderately similar to A45010 X-lin	23.40
	134367	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	49.20
40	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	20.20
40	134753	NM_006482	Hs.173135	dual-specificity tyrosine-(Y)-phosphoryl	20.80
	135002	AA448542	Hs.251677	G antigen 7B	37.60
	135029	H58818	Hs.187579	hydroxysterold (17-beta) dehydrogenase	53.40
	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	31.60
15	135345	X53655	Hs.99171	neurotrophin 3	28.80
45					

TABLE 48 shows the accession numbers for those primekeys tacking uniquenelD's for Table 4A. For each probeset we have listed the gene cluster number from which the digonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (Double Twist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number CAT number: Gene cluster number
Accession: Genbank accession numbers

55

	Pkey	CAT number	Accessions
60	123619 126433 126872	127143_1 A 142696_1 A	NA602964 AA609200 NA325605 AA099517 N89423 NW4S0979 AA136653 AA136655 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 NB01367 BE011368 BE011368 BE011215 BE011215 BE011365
65	106851 118720 120515 117099 101447 123130	322947_1 A genbank_N73515 genbank_AA25835	N458623 AA639708 AA485409 R22065 AA485570 N73515 56 AA258356 193699 H97976 H80036 #21305

PCT/US02/12476

Table SA shows 680 genes up-regulated in squamous cell carcinoma or adenocarcinoma lung tumors relative to normal lung and chronically diseased lung. These genes were selected from \$9880 probesets on the Eos/Affymetrix Hu/03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5	Pkey: ExAccr:	Unique Eos probesel identifier number Exemplar Accession number, Genbank accession number
	Unigene!D:	Unigene number
	Unigene Title: R1:	Unigene gene fille 70th percentile of Al for squamous cell carcinoma and adenocarcinoma lung tumor samples divided by the 90th percentile of Al for normal and chronically
10	R2:	diseased lung samples. 80th percentile of Al adenocarcinoma lung tumor samples divided by the 90th percentile of Al for normal and chronically diseased lung samples. 80th percentile of Al squarmous cell carcinoma lung tumor samples divided by the 90th percentile of Al for normal and chronically diseased lung samples.
	R3:	
15	R4: R5:	80th percentile of Al adenocarchiona uniq unnot samples minuted by the outspace-time samples minus the 15th percentile of Al for all normal lung, chronically 70th percentile of Al for squamous cell carchiona and adenocarchiona lung timor samples minus the 15th percentile of Al for all diseased lung and timor samples divided by 90th percentile of Al for normal and chronically diseased lung samples minus the 15th percentile of Al for all normal lung, chronically diseased lung and timor samples

		1001110	iang, Gradinasi,	<u></u>					•
20	Pkey	ЕхАссп	UnigenelD	Unigene Title	R1	R2	R3	R4	R5
20	400000			AFFX control: GAPDH					6.76
	100035 100036			AFFX control: GAPDH					5.77
	100037	•		AFFX controt: GAPDH					5.75
	100071	A28102		Human GABAa receptor alpha-3 subunit		8.00			5.71
25	100114	X02308	Hs.82962	thymidylate synthetase	204				3.71
	100154	H60720	Hs.81892	KIAA0101 gene product	3.84 3.33				
	100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3	3.33				4.52
	100188	AW247090	Hs.57101	minichromosome maintenance deficient (S.					5.49
20	100202	BE294407	Hs.99910	phosphotructokinase, platelet					5.67
30	100216	AA489908	Hs.1390	proteasome (prosome, macropain) subunit, E2F transcription factor 3	2.55				
	100269	NM_001949	Hs.1189 Hs.1600	chaperonin containing TCP1, subunit 5 (e					5.66
	100287	AU076657	Hs.182429	protein disulfide isomerase related prot					3.81
	100297 100330	AU077258 AW410976	Hs.77152	minichromosome maintenance deficient (S.					4.50
35	100335	AW247529	Hs.6793	platelet-activating factor acetylhydrola	5.07				4.00
55	100360	W70171	Hs.75939	undine monophosphate kinase					4.82
	100372	NM_014791	Hs.184339	KIAA0175 gene product				45.05	3.79
	100474	NM 000699	Hs.300280	amylase, alpha 2A; pancreatic				15.65	5.49
	100486	T19006	Hs.10842	RAN, member RAS oncogene family					4.17
40	100491	D56165	Hs.275163	non-metastatic cells 2, protein (NM23B)		7.20			4.11
	100516	D90278	Hs.11	carcinoembryonic antigen-related cell ad		1.20		14.20	
	100522	X51501	Hs.99949	protectin-induced protein	3.10				
	100559	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	J. 10			9.30	
15	100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid mitogen-activated protein kinase kinase				20.60	
45	100629	AA015693	Hs.21291 Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	3.85				
	100661 100677	BE623001 AA353686	Hs.57813	zinc ribbon domain containing, 1		8.60			
	100696	D14887	Hs.121686	general transcription factor IIA, 1 (37k				10.00	
	100709	N26539	Hs.100469	myeloid/lymphoid or mixed-lineage teukem			24.80		
50	100761	BE208491	Hs.295112	KIAA0618 gene product		7.60			7.99
• •	100830	AC004770	Hs.4756	flap structure-specific endonuclease 1		10.20			1.55
	100867	U14622		gb:Human transketolase-like protein gene		8.00			
	100902	M16029	Hs.287270	ret proto-oncogene (multiple endocrine n		0.00			5.16
55	100906	AU076916	Hs.5398	guanine monphosphate synthetase keratin 14 (epidermolysis bullosa simple	2.57				
55	100960	J00124	Hs.117729	gb:Human proliferating cell nuclear anti					4.69
	101045 101061	J05614 NM_000175	Hs.180532	glucose phosphate isomerase					4.19
	101071		Hs.84244	polassium voltage-gated channel, Shab-re		12.91			
	101124	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	3.12				
60	101175	U82671	Hs.36980	melanoma antigen, family A, 2	3.50				5.69
00	101181	BE262621	Hs.73798	macrophage migration inhibitory factor (3.09
	101204	L24203	Hs.82237	ataxia-telangiectasia group D-associated	4.08		6.40		
	101210	L29301	Hs.2353	opioid receptor, mu 1	2.53		0.40		
15	101216	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	230				7.90
65	101228	AA333387	Hs.82916	chaperonin containing TCP1, subunit 6A (4.45
	101233		Hs.878 Hs.182505	sorbitol dehydrogenase POU domain, class 3, transcription facto	8.50				
	101273 101342		Hs.182018	interleukin-1 receptor-associated kinase					4.17
	101342		Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N				21.89	
70	101369	NM_000892	Hs.1901	kallikrein B, plasma (Fletcher factor) 1				12.80	
,,	101396		Hs.78996	proliferating cell nuclear antigen	3.24				7.00
	101431		Hs.1076	small proline-rich protein 1B (comitin)					7.90
	101448	NM_000424	Hs.195850	keralin 5 (epidermolysis bullosa simplex	8.31			38.80	
	101462		Hs.73853	bone morphogenetic protein 2				30.00	4.01
75	101466		Hs.170197	glutamic-oxaloacetic transaminase 2, mit				12.00	
	101484		Hs.20315	interferon-induced protein with tetratri	10.50				
	101502		U- 75000	gb:Human parathyroid hormone-related pro asparagine synthetase	10.00				4.46
	101505		Hs.75692	aconilase 1, soluble	4.02				
80	101526		Hs.154721 Hs.99853	fibrillarin					4.65
ov.	101535 101577		Hs.1041	v-ros avian UR2 sarcoma virus oncogene h				9.09	
	101649		Hs.1690	heparin-binding growth factor binding pr	54.00				
	101663			H2B histone family, member Q	5.59				
	101664		Hs.121017	H2A histone family, member A	7.00	7.00			
85	101669		Hs.80409	growth arrest and DNA-damage-inducible,		7.60			

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	101695	1469136	Hs.135626	chymase 1, mast cell	4.79				
	101724	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	15.21				
	101748 101759	NM_001944 M80244	Hs.1925 Hs.184601	desmoglein 3 (pemphigus vulgaris antigen solute carrier family 7 (casonic antino	55.50				4.10
5	101771	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant				18.57	
•	101804	M85699	Hs.169840	TTK protein kinase	4.50				
	101809	M86849	Hs.323733	gap junction protein, beta 2, 26kO (conn	140.00 2.56				
	101833 101842		Hs.117938 Hs.75182	collagen, type XVII, alpha 1 mannose receptor, C type 1	230			12.80	
10	101851		Hs.82045	middine (neurite growth-promoting factor					5.88
- •	102002		Hs.81469	nucleotide binding protein 1 (E.cofi Min		7.80			
	102039	AL134223	Hs.306098	aldo-keto reductase family 1, member C1			7.40		4.35
	102072 102083		Hs.78743 Hs.75117	zinc finger protein 131 (clone pHZ-10) interleukin enhancer binding factor 2, 4			7.40		5.12
15	102111	L36196	Hs.81884	sulfotransferase family, cytosolic, 2A,				12.00	
	102123	NM_001809	Hs.1594	centromere protein A (17kD)	6.20				
	102154	U17760	Hs.75517	laminin, beta 3 (nicein (125kO), kalinin	2.62 5.85				
	102193 102217	AL036335 AA829978	Hs.313 Hs.301613	secreted phosphoprotein 1 (osteopontin, JTV1 gene	400				6.18
20	102224		Hs.148495	proteasome (prosome, macropain) 26S subu					4.49
	102234	AW163390	Hs.278554	heterochromatin-like protein 1	4.50				5.80
	102251 102305	NM_004398 AL043202	Hs.41706 Hs.90073	DEAD/H (Asp-Gtu-Ala-Asp/His) box polypep chromosome segregation 1 (yeast homolog)	4.50				5.15
	102333	BE298063	Hs.77254	chromobox homolog 1 (Drosophila HP1 beta					4.17
25	102340	U37055	Hs.278657	macrophage stimulating 1 (hepatocyte gro				9.33	
	102348	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	8.87 15.91				
	102368 102394	U39817 NM_003816	Hs.36820 Hs.2442	Bloom syndrome a disintegrin and metalloproteinase doma	13.51		19.20		
	102404	NM_005429	Hs.79141	vascular endothelial growth factor C				14.00	
30	102537	U57094	Hs.50477	RAB27A, member RAS oncogene family				12.00	4.57
	102581	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2					4.57 3.98
	102605 102610	AJ435128 U65011	Hs.181369 Hs.30743	ubiquitin fusion degradation 1-like preferentially expressed antigen in mela	77.50				4.50
	102623		Hs.37110	melanoma antigen, family A, 9	12.50				
35	102642	AA205847	Hs.23016	G protein-coupled receptor		40.00	22.00		
	102654	AV649989	Hs.24385	Human hbc647 mRNA sequence CUG triplet repeat, RNA-binding protein		12.00		12.80	
	102659 102669	BE245169 U71207	Hs.211610 Hs.29279	eyes absent (Drosophila) homolog 2	6.50			12.00	
40	102672	U72056	Hs.29287	retinoblastoma-binding protein 8	8.50				224
40	102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C					9.24 5.54
	102696 102768	BE540274 U82321	Hs.239	forkhead box M1 gb:Horno sapiens clone 14.98 mRNA sequenc		6.60			5.57
	102781	BE258778	Hs.108809	chaperonin containing TCP1, subunit 7 (e					3.78
4.5	102784	U85658	Hs.61796	transcription factor AP-2 gamma (activat			44.40		4.26
45	102824 102829	U90916	Hs.82845 Hs.80962	Homo sapiens cDNA: FLJ21930 fis, clone H neurotensin	8.00		14.40		
	102888	NM_006183 Al346201	Hs.76118	ubiquifin carboxyl-terminal esterase L1					5.50
	102892	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin			6.70		
50	102913		Hs.80342	keratin 15	4.64 2.93				
20	102935 102951	BE561850 X15218	Hs.80506 Hs.2969	smail nuclear ribonucteoprotein polypept v-ski avian sarcoma viral oncogene homol	2.50			11.40	
	102983	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)					7.26
	103023	AW500470	Hs.117950	multifunctional polypeptide similar to S	3.01				
55	103035 103038	M13509 AA926960	Hs.83169 Hs.334883	matrix metalloprotelnase 1 (interstitlal CDC28 protein kinase 1	27.90				8.79
55	103060	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin					4.27
	103099	Al693251	Hs.8248	NADH dehydrogenase (ubiquinone) Fe-S pro		9.80			
	103119	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta glutathione peroxidase 2 (gastrointestin	4.05 3.07				
60	103168 103185	X53463 NM_006825	Hs.2704 Hs.74368	transmembrane protein (63kD), endoplasmi	0.01				5.62
•	103192	M22440	Hs.170009	transforming growth factor, alpha		7.40	•		
	103223	BE275607	Hs.1708	chaperonin containing TCP1, subunit 3 (g			100.00		4.70
	103242 103316	X76342 X83301	Hs.389 Hs.324728	atcohol dehydrogenase 7 (class IV), mu o SMA5			100.00	9.80	
65	103375		Hs.54416	sine oculis homeobox (Drosophila) homolo	9.71				
	103376	AL036166	Hs.323378	coated vesicle membrane protein	14.00			44.00	
	103385	NM_007069	Hs.37189	similar to rat HREV107	2.93			11.00	
	103391 103404	X94453 BE394784	Hs.114366 Hs.78596	pyrroline-5-carboxylate synthetase (glut proteasome (prosome, macropain) subunit,	2.50				5.15
70	103430		Hs.20716	translocase of inner mitochondrial membr					3.98
	103446		Hs.79971	sal (Drosophila)-like 2		13.00		21.40	
	103476 103477	Y07701 AJ011812	Hs.293007 Hs.119018	aminopeptidase puromycin sensitive transcription factor NRF		13.00	6.40		
	103478		Hs.38991	S100 calcium-binding protein A2	5.02				
75	103515	Y10275	Hs.56407	phosphoserine phosphatase	10.50				
	103558		Hs.2785	keratin 17	6.41				3.84
	103580 103587	AA328046 BE270266	Hs.46405 Hs.82128	polymerase (RNA) II (DNA directed) polyp 5T4 oncoletal trophoblast glycoprotein	78.50				VIOT.
	103594		Hs.816	SRY (sex determining region Y)-box 2	6.51				
80	103636	NM_006235	Hs.2407	POU domain, class 2, associating factor	3.50				4.48
	103768 103841	AF086009 AA314821	Hs.38178	gb:Homo sapiens full length insert cDNA hypothetical protein FLJ23468		8.00			7.70
	103847		Hs.102237	tubby super-family protein		10.40			
0.5	103913	AW967500	Hs.133543	ESTs			c cc	15.60	
85	104094	AA418187	Hs.330515	ESTs			6.60		

	***	A A 2 (0.00 C	142						PCT/US02/12476
	104150	O 02/086 Al122044	Hs.331633	hypothetical protein DKFZp566N034				26.00	PC 1/USU2/124/0
	104257	BE560621	Hs.9222	estrogen receptor binding site associate		6.80			
	104261	AW248364	Hs.5409	RNA polymerase I subunit		c 00			3.98
5	104331 104415	AB040450 BE410992	Hs.279862 Hs.258730	odk inhibitor p21 binding protein heme-regulated initiation factor 2-alpha		6.80 10.29			
_	104558	R56678	Hs.88959	hypothetical protein MGC4816	4.21				
	104590	AW373062	Hs.83623	nuclear receptor subfamily 1, group 1, m				15.79	
	104658 104660	AA360954 BE298665	Hs.27268 Hs.14846	Homo sapiens cDNA: FLJ21933 fis, clone H Homo sapiens mRNA; cDNA DKFZp564D016 (fr	6.40			17.40	
10	104589	AA420450	Hs.292911	ESTs, Highty similar to S60712 band-6-pr					6.55
	104754	Al206234	Hs.155924	cAMP responsive element modulator				10.00	4.47
	104758 104971	BE560269 BE311926	Hs.7010 Hs.15830	NPD002 protein hypothetical protein FLJ 12691	2.87				4.47
	105011	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	3.83				
15	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	2.86	44.00			
	105026 105076	AA809485 Al598252	Hs.124219 Hs.37810	hypothetical protein FLJ12934 hypothetical protein MGC14833		11.00			5.01
	105132	AA148164	Hs.247280	HBV associated factor					3.99
20	105143	AL358836	Hs.24808	ESTs, Weakly similar to I38022 hypotheti			11.00		
20	105158	AW976357	Hs.234545 Hs.25740	hypothetical protein NUF2R ERO1 (S. cerevisiae)-like	4.32	16.00			
	105175 105200	AA305384 AA328102	Hs.24641	cytoskeleton associated protein 2	3.00				
	105264	AA227934		gb:zr57e08.s1 Soares_NhHMPu_S1 Homo sapi				10.00	
25	105298	BE387790	Hs.26369	hypothetical protein FLJ20287	3.69			9.20	
25	105409 105460	AW505076 AW296078	Hs.301855 Hs.271721	DiGeorge syndrome critical region gene 8 Homo sagiens, clone IMAGE:4179986, mRNA,			7.80	3.20	
	105667	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	4.12				
	105743	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	3.82		47.00		
30	105782 105848	H09748 AW954064	Hs.57987 Hs.24951	B-cell CLL/lymphorna 118 (zinc finger pro ESTs			27.00 7.60		
50	105891	U55984	Hs.289088	heat shock 90kD protein 1, alpha					4.14
	106019	AF221993	Hs.46743	McKusick-Kaufman syndrome			16.80		
	106069 106073	BE566623 AL157441	Hs.29899 Hs.17834	ESTs, Wealdy similar to G02075 transcrip downstream neighbor of SON	9.50		23.40		
35	106126	AA576953	Hs.22972	hypothetical protein FLJ13352	6.00				
	106159	AK001301	Hs.3487	hypothetical protein FLJ 10439					3.95
	106220 106260	D61329 Al097144	Hs.32196 Hs.5250	mitochondrial ribosomal protein L36 ESTs, Weakly similar to ALU1_HUMAN ALU S			13.20		6.04
	106300	Y10043	Hs.19114	high-mobility group (nonhistone chromoso			10.20		5.02
40	106307	AA436174	Hs.37751	ESTs, Weakly similar to putative p150 [6.60			
	106318	AA025610	Hs.9605	cleavage and polyadenylation specific fa					5.04 7.25
	106341 105440	AF191020 AA449563	Hs.5243 Hs.151393	hypothetical protein, estradiol-induced glutamate-cysteine ligase, catalytic sub			13.80		1.23
45	106481	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	4.75				
45	106586	AA243837	Hs.57787	ESTS Hamp conjuga mPNA: aDNA DVEZGEARAZE for				10.84 45.60	
	106605 106654	AW772298 AW075485	Hs.21103 Hs.286049	Homo sapiens mRNA; cDNA DKFZp564B076 (fr phosphoserine aminotransferase	28.00			40.00	
	106785	Y15227	Hs.20149	deleted in lymphocytic leukernia, 1	3.00				
50	106813 106895	C05766 AK001826	Hs.181022 Hs.25245	CGI-07 protein			11.40 6.00		•
50	106913	Al219346	Hs.86178	hypothetical protein FLJ11269 M-phase phosphoprotein 9		6.56	0.00		
	106919		Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU S					4.27
	107054	A1076459 BE614410	Hs.15978	KIAA1272 protein	471			34.80	
55	107059 107098	Al823593	Hs.23044 Hs.27688	RADS1 (S. cerevisiae) homolog (E coli Re ESTs	4.71			24.80	
	107104	AU076640	Hs.15243	nucleolar protein 1 (120kD)					7.05
	107129	AC004770	Hs.4756	flap structure-specific endoruclease 1	2.60	40.00	•		
	107198 107203	AV657225 D20426	Hs.9846 Hs.41639	KIAA1040 protein programmed cell death 2		19.20 7.60			
60		AL080235	Hs.35861	DKFZP586E1621 protein	9.50				
	107284	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	2.71		0.74		
	107318 107516	174445 X57152	Hs.5957 Hs.99853	Homo sapiens clone 24416 mRNA sequence fibrillarin			8.71		4.33
	107529	BE515065	Hs.296585	rurdeolar protein (KKE/D repeat)					4.00
65	107728	AA019551	Hs.294151	Homo sapiens, clone IMAGE:3603836, mRNA,		10.80			
	107851 107901	AA022953 L42612	Hs.61172 Hs.335952	EST keratin 6B	3.40		8.00		
	107922	BE153855	Hs.61460	lg superfamily receptor LNIR	2.88			•	
70	107932		Hs.18878	hypothetical protein FLJ21620	7.50				
70	108015 108056	AW298357 AA043675	Hs.49927 Hs.62633	protein kinase NYD-SP15 ESTs				23.40 12.80	
	-108075	AI867370	Hs.139709	hypothetical protein FLJ12572				12.80	
	108187	BE245374	Hs.27842	hypothetical protein FLJ11210		7.00			
75	108296 108305	N31256 AA071391	Hs.161623	ESTs gb:zm61e06.r1 Stratagene fibroblast (937		6.60		11.80	
		AA075211		gb:zm86a08.r1 Stratagene ovarian cancer				11.80	
	108480	AL133092	Hs.68055	hypothetical protein DKFZp43410428				20.80	
	108554	AA084948 AA086005		gbzn 13b09.s 1 Stratagene hNT neuron (937		6.40		25.40	
80		AA088326	Hs.120905	gbzl84c04.s1 Stratagene colon (937204) Homo sapiens cDNA FLJ11448 fis, clone HE		9.60		25.40	
	108597	AK000292	Hs.278732	hypothetical protein FLJ20285				14.60	
		AB029000	Hs.70823	KIAA1077 protein	3.00			10.00	
	108699 108700	AA121514 AA121518	Hs.70832 Hs.193540	ESTs ESTs, Moderately similar to 2109260A B c			11.00	10.00	•
85		AU076442	Hs.117938	collagen, typa XVII, alpha 1	11.21				

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	108810	AW295647	Hs.71331	hypothetical protein MGCS350	8.50				
	108816	AA130884	Hs.270501	ESTs, Moderately similar to ALU2_HUMAN		7.40			
	108857	AK001458	Hs.62180	anžin (Drosophila Scraps homolog), act	4.00 6.09				
5	108860 108937	AA133334 AL050107	Hs.129911 Hs.24341	ESTs transcriptional co-activator with PDZ-bi	3.00				
,	109010	NIM_007240	Hs.44229	dual specificity phosphatase 12	2.69				
	109121	BE389387	Hs.49767	NADH dahydrogenase (ubiquinone) Fe-S pro					4.53
	109165	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	10.58				
10	109227	AA766998	Hs.85874	Human DNA sequence from clone RP11-16L21 trinucleofide repeat containing 9		9.00 51.40			
10	109415 109418	U80736 A1866946	Hs.110826 Hs.161707	ESTs		31.40		11.00	
	109454	AA232255	Hs.295232	ESTs, Moderately similar to A46010 X-B			17.60		
	109502	AW967069	Hs.211556	hypothetical protein MGC5487		10.07	9.49		
15	109543	AA564994	Hs.222851	ESTs ·		12.67		10.40	
15	109648 109680	H17800 AB037734	Hs.7154 Hs.4993	ESTs KIAA1313 protein			33.20	10.40	
	109700	F09609	113.4350	gb:HSC33H092 normalized infant brain cDN				16.00	
	109704	AI743880	Hs.12876	ESTs			11.00	40.00	
20	109792	R49625	LI- 00000	gbryg51f03.s1 Soares infant brain 1NIB H	4.00			12.60	
20	109981 109998	BE546208 AL042201	Hs.26090 Hs.21273	hypothetical protein FLJ20272 transcription factor NYD-sp10	4.00	7.80			
	110039	H11938	Hs.21907	histone acetyltransferase		7.00			
	110156	AA581322	Hs.4213	hypothetical protein MGC16207					4.24
25	110500	AA907723	Hs.36962	ESTs	4.50	8.60			
25	110551	AW450381 AA379597	Hs.14529 Hs.5199	ESTs HSPC150 protein similar to ubiquitin-con	3.06	0.00			
	110561 110854	BE612992	Hs.27931	hypothetical protein FLJ10507 similar to	0.05	6.80			
	110886	AW274992 ·	Hs.72249	three-PDZ containing protein similar to			8.80		
20	110916	BE178102	Hs.24349	ESTs		6.80		40.00	
30	111003	N52980	Hs.83765	dihydrofolate reductase	2.54			16.80	
	111337 111434	AAB37396 R01608	Hs.263925 Hs.142736	US1-interacting protein NUDE1, rat homo ESTs	2.04			9.80	
	111439	A1476429	Hs.19238	ESTs				10.40	
0.5	111540	U82670	Hs.9786	zinc finger protein 275			15.40		
35	111597	R11499	Hs.189716	ESTs		6.80		9.20	
	111895 111929	T80581 AF027208	Hs.12723 Hs.112360	Homo sapiens clone 25153 mRNA sequence prominin (mouse)-lika 1		6.00		14.67	
	112054	R43590	113.112000	gb:yc85g02.s1 Soares infant brain 1NIB H		10.80			
40	112210	R49645	Hs.7004	ESTs				10.20	
40	112244	AB029000	Hs.70823	KIAA1077 protein	2.99	e en			
	112382 112392	R59904 R60763	Hs.193274	gb:yh07g12.s1 Soares infant brain 1NIB H ESTs, Moderately similar to 157588 HSrel		6.60	7.10		
	112442	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	3.00				
	112539	R70318	Hs.339730	ESTs				37.20	
45	112772	AI992283	Hs.35437	ESTs, Moderately similar to I38026 MLN 6				14.60	. 4 03
	112869	BE261750 R71449	Hs.4747 Hs.268760	dyskeratosis congenita 1, dyskerin ESTs	2.73				4.83
	112935 112970	AA694010	Hs.6932	Homo saptens clone 23809 mRNA sequence	2.10			12.00	
	112973	AB033023	Hs.318127	hypothetical protein FLJ10201	11.50				
50	112992	AL157425	Hs.133315	Homo saplens mRNA; cDNA DKFZp761J1324 (f	45.00		10.89		
	113053	W15573	Hs.5027 Hs.103042	ESTs, Weakly similar to A47582 B-cell gr microtubule-associated protein 1B	15.00		15.31		
	113073 113078	N39342 T40444	Hs.118354	CAT56 protein		7.00	10.01		
	113238	R45467	Hs.189813	ESTs				41.20	·
55	113591	T91881	Hs.200597	KIAA0563 gene product				9.40	
	113702	T97307 Al369275	Lin 242010	gb:ye53h05.s1 Soares fetal liver spleen	25.00			13.91	
	113844 113984	R96696	Hs.243010 Hs.35598	Homo saptens cDNA FLJ14445 fis, clone HE ESTs		7.80		10.51	
	114073	R44953	Hs.22908	Homo sapiens mRNA; cDNA DKFZp434J1027 (f		7.20			
60	114162	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	3.42				
	114208	AL049466	Hs.7859	ESTs			6.74	33.20	
	114251 114285	H15261 R44338	Hs.21948 Hs.22974	ESTS ESTS				13.20	
	114313	H18456	Hs.27946	ESTs				10.00	
65	114339	AA782845	Hs.22790	ESTs		7.80			***
	114407	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp43480425 (f				9.80	4.14
	114560 114699	AI452469 AA127386	Hs.165221	ESTs ob:zn90d09.r1 Stratagene lung carcinoma		7,60		3.00	
	114767	A1859865	Hs.154443	minichromosome maintenance deficient (S	3.21	.,55			
70	114793	AA158245		gb:zo76c03.s1 Stratagene pancreas (93720			6.00		
	114833	Al417215	Hs.87159	hypothetical protein FLJ12577				11.40	4.24
	115047 115060	BE270930 AF052693	Hs.82916 Hs.198249	chaperonin containing TCP1, subunit 6A (gap junction protein, beta 5 (connexin 3					4.31 4.03
	115097	AA256213	Hs.72010	ESTs				35.40	
75	115113	AA256460		gb:zr81a04.s1 Soares_NhHMPu_S1 Homo sapi				15.20	
	115123	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m				40.40	4.19
	115134 115291	AW968073 BE545072	Hs.194331 Hs.122579	ESTs, Highly similar to A55713 inositol hypothetical protein FLJ10461	25.00			12.40	
	115347	AA356792	Hs.334824	hypothetical protein FLJ14825	20.00	7.00			
80	115414	AA662240	Hs.283099	AF15q14 protein	3.25	. ,			
	115522	BE614387	Hs.333893	o-Myc target JPO1	3.68				
	115536 115566	AK001468 Al142336	Hs.62180 Hs.43977	anilin (Drosophila Scraps homolog), act Human DNA sequence from clone RP11-196N1	10.50			24.40	
	115645	Al207410	Hs.69280	Homo saniens, clone IMAGE:3636299, mRNA,	4.17			L-1. 10	
85	115648	AW016811	Hs.234478	Homo sapiens cDNA: FLJ22648 fis, clone H			6.00		

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	115652	BE093589	Hs.38178	hypothetical protein FLJ23463	3.81				
	115697 115793	D31382 AA424883	Hs.63325 Hs.70333	transmembrane protease, serine 4 hypothetical protein MGC10753	62.14			11.80	
_	115816		Hs.287588	Homo sapiens cDNA FLJ13675 fis, clone PL				9.71	
5		AA291377	Hs.50831	ESTS	2.53		27.40		
	115906 115909	A1767756 AW872527	Hs.82302 Hs.59761	Homo sapiens cDNA FLJ14914 fis, clone NT ESTs, Weakly similar to DAP1_HUMAN DEATH	11.82				
	115965	AA001732	Hs.173233	hypothetical protein FLJ10970				34.29	0.02
10	115978	AL035864	Hs.69517 Hs.268115	cDNA for differentially expressed CO16 g ESTs, Wealdy similar to T08599 probable	3.00				8.23
10	115985 116090	AA447709 AJ591147	Hs.61232	ESTs	5.17				
	116096	AA682382	Hs.59982	ESTs		10.60	8.20		
	116127 116157	AF126743 BE439838	Hs.279884 Hs.44298	DNAJ domain-containing mitochondrial ribosomal protein S17		10.00			5.82
15	116190	Al949095	Hs.67776	ESTs, Wealdy similar to T22341 hypotheti					4.08
	116278	NM_003686	Hs.47504	exonuclease 1 desmocollin 3	9.50 3.67				
	116335 116496	AK001100 AW450694	Hs.41690 Hs.21433	hypothetical protein DKFZp547J036	0.0.	7.00			
20	116503	AI925316	Hs.212617	ESTs			22.00	12.60	
20	116674 116929	AI768015 AA586922	Hs.92127 Hs.80475	ESTs polymerase (RNA) II (DNA directed) polyp		7.60	32.00		
	116973	AI702054	Hs.166982	phosphatidylinositol glycan, class F		9.80			•
	116993	AI417023	Hs.40478	ESTs gb:ys85f05.s1 Soares retina N2b4HR Homo				10.20 15.20	
25	117079 117317	H92325 Al263517	Hs.43322	ESTs				13.40	
	117326	N23629	Hs.241420	Homo sapiens mRNA for KIAA1756 protein,				20.60	
	117396 117412	W20128 N32536	Hs.296039 Hs.42645	ESTs ESTs				10.60 16.00	
	117519	N32528	Hs.146286	kinesin family member 13A				9.11	
30	117693	AW179019	Hs.112110	mitochondrial ribosomal protein L42				19.60	4.01
	117721 117881	N46100 AF161470	Hs.93939 Hs.260622	EST butyrate-induced transcript 1	2.71			13.00	
	117903	AA768283	Hs.47111	ESTs				17.80	4 17
35	117992		Hs.172089	Homo sapiens mRNA; cDNA DKFZp586I2022 (f ESTs				10.60	4.17
23	118013 118017	A1674126 A1813444	Hs.94031 Hs.42197	ESTS			8.82	,,,,,	
	118186	N22886	Hs.42380	ESTs		7.00		13.80	
	118325 118367	A1868065 N64269	Hs.166184 Hs.48946	intersectin 2 EST			6.14	13.00	
40	118368	N64339	Hs.48956	gap junction protein, beta 6 (connexin 3	3.14				
	118472	AL157545	Hs.42179	bromodomain and PHD finger containing, 3			12.40	12.20	
	118709 119025	AA232970 BE003760	Hs.293774 Hs.55209	ESTs Homo sapiens mRNA; cDNA DKFZp434K0514 (f	4.50			12.20	•
45	119027	AF086161	Hs.114611	hypothetical protein FLJ11808	3.22	0.00			
45	119052 119164	R10889 AF221993	Hs.46743	gb:yf38d02.s1 Soares fetal liver spleen McKusick-Kaufman syndrome		9.60	6.60		
	119186	A1979147	Hs.101265	hypothetical protein FLJ22593				10.80	
	119243	T12603	Un 2020E0	gb:CHR90123 Chromosome 9 exon II Homo sa ESTs, Moderately similar to B34087 hypot				9.44 11.80	
50	119490 119499	AA195276 AI918906	Hs.263858 Hs.55080	ESTs, widderately similar to Bordon hypot			14.80	11.00	
	119599	W45552		gb:zc26d03.s1 Soares_senescent_fibroblas	47.00	12.60			
	119780 119845	NM_016625 W79123	Hs.191381 Hs.58561	hypothetical protein G protein-coupled receptor 87	17.00 13.50				
	119941	AA699485	Hs.58896	ESTs		8.00			
55	119994	AA642402	Hs.59142 Hs.170218	ESTs KIAA0251 protein	7.73		39.60		•
	120102 120104	W67353 AK000123	Hs.180479	hypothetical protein FLJ20116	2.91				•
	120294	AK000059	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par	0.72		8.20		
60	120486 120599	AW368377 AA804448	Hs.137569 Hs.104463	tumor prolein 63 kDa with strong homolog ESTs	8.73	7.00			
00	120699	A1683243	Hs.97258	ESTs, Moderately similar to S29539 ribos				10.00	
	120715	AA292700	Un 00070	gb:zs59a06.s1 NCI_CGAP_GCB1 Homo sapiens staufen (Drosophila, RNA-binding protein		9.40		13.80	
	120821 120859	Y19062 AA826434	Hs.96870 Hs.1619	achaele-scute complex (Drosophila) homol		9.00		10.00	
65	120880	AA360240	Hs.97019	EST		15.60	22.66		
	120983 121034	AA398209 AL389951	. Hs.97587 Hs.271623	EST nucleoparin 50kD			27.66 20.80		
	121121	AA399371	Hs.189095	similar to SALL1 (sal (Drosophila)-like		22.80			
70	121313	AA402713	Hs.97872	ESTs CGI-09 protein	25.71			10.00	
70	121369 121376	AW450737 AA448103	Hs.128791 Hs.187958	solute carrier family 6 (neurotransmitte	20.71				5.42
	121476	AA412311	Hs.97903	ESTs		8.30			
	121509 121553	AA868939 AA412488	Hs.97888 Hs.48820	ESTs TATA box binding protein (TBP)-associat	18.50	8.59			
75	121753	AK000552	Hs.323518	WD repeat domain 5	7.00			40.15	
	121838	AA425880	Hs.98441* Hs.280858	ESTs ESTs, Highly similar to A35661 DNA excis	6.00			10.40	
	121857 121991	BE387162 AA430058	Hs.280656 Hs.98649	EST S, Highly similar to A33001 DNA excis	0.00			12.20	
00	122089	AW016543	Hs.98682	hypothetical protein FKSG32			8.60 6.14		
80	122105 122163	AW241685 AA435702	Hs.98699 Hs.98829	ESTs EST			0.14	10.40	
	122318	AA429743		gb:zv60b05.r1 Soares_testis_NHT Homo sap				18.20	
	122335	AA443258 AA443311	Hs.241551 Hs.98998	chloride channel, calcium activated, fam ESTs	13.50 4.80				
85	122338 122414		Hs.99087	ESTs, Wealdy similar to S47073 finger pr		8.00			

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		AF053305	Hs.98558	budding uninhibited by benzimidazoles 1			8.80		
		AA449352	Hs.99217	ESTs				9.40	
		AJ220089	Hs.99439	ESTs		9.20		40.40	
_		A1580056	Hs.98992	ESTs		6.60		10.40	
5		AW268962	Hs.111335	ESTs integrin, beta 8		0.00	12.60		
		AV/369771 AK001035	Hs.52620 Hs.130881	B-cell C11/lymphoma 11A (zinc finger pro					5.35
		AA488587	Hs.284235	ESTs, Weakly similar to 138022 hypotheti			6.06		
		AA495369		gbczv37d10.s1 Soares ovary tumor NbHOT H			12.40		
10	123329	Z47542	Hs.179312	small nuclear RNA activating complex, po		12.00	11.60		
		AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein hypothetical protein		12.00	13.00		
		AL035414 AW015887	Hs.21068 Hs.112574	ESTs		12.20			
	123514		Hs.98806	hypothetical protein			7.80		
15	123616		Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L				10.60	
	123673		Hs.158549	ESTs, Weakly similar to T2D3_HUMAN TRANS	23.00	7.00			
	123727	A1083986	Hs.282977	hypothetical protein FLJ13490 gbcae52f01.s1 Stratagene lung carcinoma		7.00	9.80		
	123731	AA609839 AA227714	Hs.179703	KIAA0129 gene product	3.50		*		
20	123732		Hs.112953	EST				12.80	
	124006		Hs.270016	ESTs	97.00				
	124059	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	3.02		27.80		
	124069		Hs.7327 Hs.248549	claudin 1 ESTs, Moderately similar to S65657 alpha			21.20	35.80	
25	124191	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma		7.20			
20	124297		Hs.102301	Homo sapiens mRNA; cDNA DKFZp586J0323 [f				11.00	
	124305	AW963221		gb:EST375294 MAGE resequences, MAGH Homo				16.00	6.08
	124676			phosphoglycerate mutase 1 (brain) RalGEF-like protein 3, mouse homolog				21.00	4.50
30	124874	BE550182 AK000483	Hs.127826 Hs.93872	KIAA1682 protein		9.40			•
50	124969		Hs.100256	ESTs				10.80	
	125000		Hs.110640	ESTs		7.00		9.80	
	125201		Hs.103158	ESTs, Weakly similar to T33296 hypotheti		7.60 6.59			
35	125266		Hs.186809 Hs.102720	ESTs, Highly similar to LCT2_HUMAN LEUKO ESTs		0.55		9.57	
33	125299 125356		Hs.133554	ESTs, Weakly similar to Z195_HUMAN ZINC				14.00	
	125370		Hs.134158	Homo sapiens, Similar to KIAA0092 gene p			8.20		
	125418	AA777690	Hs.188501	ESTs		24.40		13.20	
40	125433		Hs.54320	hypothetical protein DKFZp762D096		21.40 6.96			
40	125437 125446		Hs.140197 Hs.166982	ESTs phosphalidylinositol glycan, class F		8.80			
	125711		Hs.5672	hypothetical protein AF140225				11.20	
	125756		Hs.289721	growth arrest specific transcript 5				15.60	4.31
15	125757		Hs.166835	ESTs, Highly similar to 1814460A p53-ass	3.20			15.60	
45	125769 125839	BE270266 AW836261	Hs.82128 Hs.337717	5T4 oncofetal trophoblast glycoprotein ESTs	0.20	8.20			
	125850		Hs.99804	ESTs	2.65				•
	125875	H14480		gb:ym18b09.r1 Soares infant brain 1NIB H		7.40			4.23
50	125924		Hs.82109	syndecan 1 ESTs, Highly similar to unnamed protein					3.98
50	125972 126034		Hs.35406	gh:yr39b04.r1 Soares fetal liver spleen				10.60	
	126327		Hs.44648	ESTs		11.60			
	126345	N49713		gb:yv23f06.s1 Soares fetal liver spleen		6.67		10.60	
55	126435		Hs.285847	CGI-19 protein solute carrier family 7 (cationic arrino				10.00	4.38
23	126487 126521		Hs.184601 Hs.203933	ESTs		6.60			
	126522		12.200000	gb:zc76d03.s1 Pancreatic Islet Homo sapi				14.80	*
	126543	AL035864	Hs.69517	cDNA for differentially expressed CO16 g					4.01
CO	126567	AA058394	Hs.57887	ESTs, Weakly similar to KIAA0758 protein			7.80	11.60	
60	126605	AA676910	Hs.20887	gb:zj65h07.s1 Soares_fetal_liver_spleen_ hypothetical protein FLJ10392				14.60	
	126627 126628	AA497044 N49776	Hs.170994	hypothetical protein MGC10946	8.00				
	126737	AW976516	Hs.283707	Homo sapiens cDNA: FLJ21354 fis, clone C	2.92				
	126795	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cer	7.50	11.60			
65	126802		Hs.97056	hypothetical protein FLJ21634 sorting nexin 6	3.50	11.00			
	126892 126928		Hs.284291 Hs.137401	ESTs	0.00			22.83	
	126979		110.101 101	gb:zq89h10.r1 Stratagene hNT neuron (937				11.80	
	126986	Al279892	Hs.46801	sorting nexin 14				11.60	
70	126992		•	gb:wf30e03.x1 Soares_NFL_T_GBC_S1 Homo s				20.80 27.50	
	127066 127099			gb:yg42c07.r1 Soares infant brain 1NIB H gb:EST54026 Fetal heart II Homo sapiens				21.60	
	127033		Hs.293585	ESTs				11.20	
	127209		Hs.81964	SEC24 (S. cerevisiae) related gene famil	3,10				
75	127221	BE062109	Hs.241551	chloride channel, calcium activated, fam	2.76			16.80	
	127225		Hs.120879	ESTs Homo sapiens cDNA FLJ11458 fis, clone HE	14.00			10.60	
	127313 127444		Hs.47546 Hs.7560	Homo sapiens cuna FLJ 1 1456 its, croite HE Homo sapiens mRNA for KIAA1729 protein,	14.00			13.60	
	127500		Hs.162115	ESTs		11.20			
80	127524	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	. ~		7.80		
	127540		Hs.105362	Homo saplens, clone MGC:18257, mRNA, com	3.53			13.80	
	127599 127609		Hs.150399 Hs.530	ESTs collagen, type IV, alpha 3 (Goodpasture				28.00	
	127662		Hs.8294	KIAA0196 gene product				19.80	
85	127668		Hs.139993	ESTs				11.20	

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		A1239495	Hs.120189	ESTs				14.18	
		AA741368	Hs.291434	ESTs	4.50			24.60	
	127817 127959	AA836641 Al302471	Hs.163085 Hs.124292	ESTs Homo sapiens cDNA: FLJ23123 fis, clone L				9.20	
5	127950	Al613226	Hs.41569	phosphatidic acid phosphatase type 2A				16.83	
	127969	F06498	Hs.93748	Homo sapiens cDNA FLJ14676 fis, clone NT		13.60			
	128015 128027	Z21169 AI433721	Hs.334659 Hs.164153	hypothetical protein MGC14139 ESTs		7.00		37.40	
	128077	AI310330	Hs.128720	ESTs				9.60	
10	128166	NM_006147	Hs.11801	interfaron regulatory factor 6				9.24	
	128226	AI284940	Hs.289082	GM2 ganglioside activator protein	19.00			10.40	
	128305 128341	A1954968 AA191420	Hs.279009 Hs.185030	matrix Gla protein ESTs		9.00		10.10	
	128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul					4.30
15	128539	R46163	Hs.258618	ESTs		12.60			4.56
	128568 128572	H12912 AA933022	Hs.274691 Hs.256583	adenylate kinase 3 interleukin enhancer binding factor 3, 9				10.00	4.30
	128777	Al878918	Hs.10526	cysteine and glycine-rich protein 2			16.80		
•	128781	N71826	Hs.105465	small nuclear ribonucleoprotein polypept		0.40			4.48
20	128796	AJ000152	Hs.105924 Hs.166468	defensin, beta 2 programmed cell death 5		8.12			4.62
	128920 128924	AA622037 BE279383	Hs.26557	plakophilin 3					4.04
	128971	H05132	Hs.107510	ESTs		12.60			
0.5	129008	AL079648	Hs.301088	ESTs		8.80			6.05
25	129041 129075	BE382756 BE250162	Hs.169902 Hs.83765	solute carrier family 2 (facilitated glu dihydrofolate reductase	2.59				6.65
	129105	Al769160	Hs. 108681	Homo sapiens brain tumor associated prot			6.67		
	129189	AB023179	Hs.9059	KIAA0962 protein		8.00			
20	129229	AF013758	Hs.109643	polyadenylate binding protein-interactin	4.00				4.06
30	129241	AI878857	Hs.109706 Hs.110165	hematological and neurological expressed ribosomal protein L26 homolog	2.55				4.00
	129300 129404	W94197 Al267700	Hs.317584	ESTs	18.00				
	129457	X61959	Hs.207776	aspartylglucosaminidase	6.50				
2.5	129466	L42583	Hs.334309	keratin 6A	12.94			11.00	
35	129494	AI148976	Hs.112062 Hs.115947	ESTs keratin 16 (focal non-epidermolytic palm				11.00	4.46
	129605 129641	AF061812 Al911527	Hs.11805	ESTs				12.00	
	129665	AW163331	Hs.118778	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic					4.70
40	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA					4.02 5.71
40	129720 129748	AA156214 M16707	Hs.12152 Hs.123053	APMCF1 protein H4 histone, family 2	3.50				
	129890	Al868872	Hs.282804	hypothetical protein FLJ22704					4.21
	129896	BE295568	Hs.13225	UDP-Gat:betaGlcNAc beta 1,4- galactosylt	2.56				4.02
45	129945	BE514376	Hs.165998	PAI-1 mRNA-binding protein nucleotar phosphoprotein Nopp34			7.00		4.03
43	130010 130026	AA301116 T40480	Hs.142838 Hs.332112	EST To a serior of the serior		6.40			
	130080	X14850	Hs.147097	H2A histone family, member X					4.65
	130149	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	2.74		7.40		
50	130285 130441	AA063546 U63630	Hs.75981 Hs.155637	ubiquilin specific protease 14 (tRNA-gua protein kinase, DNA-activated, catalytic			1.40		3.91
30	130482	AW409701	Hs.1578	bacutoviral IAP repeat-containing 5 (sur	4.87				
	130500	AB007913	Hs.158291	KIAA0444 protein			40.40	9.60	
	130524	U89995	Hs.159234 Hs.211584	forkhead box E1 (thyroid transcription f neurofilament, light polypeptide (68kD)			13.40 8.20		
55	130541 130553	X05608 AF062649	Hs.252587	pituitary tumor-transforming 1			O.L.		6.06
-	130567	AA383092	Hs.1608	replication protein A3 (14kD)			7.00		
	130577	M69241	Hs.162	insulin-like growth factor binding prote	3.04				
	130627 130648	BE003054 A!458165	Hs.1695 Hs.17296	matrix metalloproteinase 12 (macrophage hypothetical protein MGC2376	3.87			16.20	
60	130697	L29472	Hs.1802	major histocompatibility complex, class				17.80	
-	130744	H59696	Hs.18747	POP7 (processing of precursor, S. cerevi					5.28
	130800	Al187292	Hs.19574	hypothetical protein MGC5469 UDP glycosyltransferase 1 family, polype	16.84				4.43
	130867 130869	NM_001072 J03626	Hs.284239 Hs.2057	uridine monophosphate synthetase (orotat	10.04				4.92
65	130925	ÅF093419	Hs.169378	multiple PDZ domain protein				9.60	
	130994	W17044	Hs.327337	ESTs	40.04	12.40			
	131028	Al879165	Hs.2227 Hs.288650	CCAAT/enhancer binding protein (C/EBP), aquaporin 4	10.21			9.80	
	131031 131041	NM_001650 T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,				9.60	•
70	131058	W28545	Hs.101514	hypothetical protein FLJ10342				17.00	
	131090	Al143139	Hs.2288	visinin-like 1	2.74		8.80		
	131112 131148	H15302 AW953575	Hs.168950 Hs.303125	Homo saplens mRNA; cDNA DKFZp566A1046 (f p53-induced protein PIGPC1	3.12		0.00		
	131185	BE280074	Hs.23960	cyclin B1	3.07				
75	131200	BE540516	Hs.293732	hypothetical protein MGC3195	3.07				
	131219	W25005 AW339037	Hs.24395 Hs.24908	small inducible cytokine subfamily B (Cy ESTs	2.87			14,67	
	131257 131375	AW293165	Hs.143134	ESTs			19.20		
00	131460	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	3.50				
80	131476	AI521663	Hs.334644	hypothetical protein FLJ 14668	15.00		7 00		
	131510 131646	BE245374 BE302464	Hs.27842 Hs.30057	hypothetical protein FLJ 11210 MRS2 (S. cerevisiae)-like, magnesium hom			7.80 7.00		
	131786	BE000971	Hs.306083	Novel human gene mapping to chomosome 22	2.65				
0.5	131839	AB014533	Hs.33010	KIAA0633 protein				35.20	A 11
85	131843	AA192315	Hs.184062	putative RabS-interacting protein					4.11

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	131877 131885	J04088 8E502341	Hs.156346 Hs.3402	topoisomerase (DNA) (I alpha (170kD) ESTs	19.00 6.48				
	131921	AA456093	Hs.34720	ESTs	50.00		8.40		
5	131945 131958	NM_002916 NM_014062	Hs.35120 Hs.3568	replication factor C (activator 1) 4 (37 ART-4 protein	56.00				3.82
,	131965	W79283	Hs.35962	ESTs	3.03				
	132000	AW247017	Hs.36978	melanoma antigen, family A, 3		9.80			
	132040	NM_001196 AW190902	Hs.315689 Hs.40098	Homo sapiens cDNA: FLJ22373 fis, clone H cysteine knot superfamily 1, BMP antagon	3.30 21.00				
10	132109 132114	NM_006152	Hs.40202	lymphoid-restricted membrane protein	21.00	8.40			
	132162	AA315805	Hs.94560	desmoglein 2					12.25
	132164	AI752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio	2.70				
	132180 132181	NM_004460 AVV961231	Hs.418 Hs.16773	fibroblast activation protein, alpha Homo sapiens clone TCCCIA00427 mRNA sequ	2.71 3.83				
15	132182	NM_014210	Hs.70499	ecotropic viral integration site 2A	440			13.20	
	132231	AA662910	Hs.42635	hypothetical protein DKFZp434K2435	9.50				
	132277	AK001745	Hs.184628	hypothetical protein FLJ10833	4.50			9.20	
	132328 132394	NM_014787 AKD01680	Hs.44896 Hs.30488	OnaJ (Hsp40) homolog, subfamily 8, membe DKFZP434F091 protein				19.60	
20	132424	AA417878	Hs.48401	ESTs, Moderately similar to ALU8_HUMAN A			8.60		
	132528	T78736	Hs.50758	SMC4 (structural maintenance of chromoso	4.00		27.40		
	132543 132544	BE568452 L19778	Hs.5101 Hs.51011	protein regulator of cytokinesis 1 H2A histone family, member P	4.38	7.00			
	132550	AW969253	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.64				
25	132552	BE621985	Hs.296922	thiopurine S-methyltransferase				15.83	
	132581	AK000631	Hs.52256	hypothelical protein FLJ20624 carbonic anhydrase XII	4.95		6.60		
	132617 132638	AF037335 AI796870	Hs.5338 Hs.54277	DNA segment on chromosome X (unique) 992	4.50	8.20			
	132653	Z15008	Hs.54451	taminin, gamma 2 (nicein (100kD), kalini	4.38				
30	132669	W38586	Hs.293981	guanine nuclectide binding protein (G pr	4.00				4.36
	132710 132771	W74001 Y10275	Hs.55279 Hs.56407	serine (or cysteine) proteinase inhibito phosphoserine phosphatase	4.60 3.71				
	132799	W73311	Hs.169407	SAC2 (suppressor of actin mutations 2,				9.48	
25	132833	U78525	Hs.57783	eukaryotic translation initiation factor				40.00	5.83
35	132892 132906	AW834050 BE613337	Hs.9973 Hs.234896	tensin geminin	3.09			12.00	
	132959	AW014195	Hs.61472	ESTs, Weakly similar to YAE6_YEAST HYPOT	•••				3.87
	132962	AA576635	Hs.6153	CGI-48 protein	3.50				
40	132990 132994	X77343 AA112748	Hs.334334 Hs.279905	transcription factor AP-2 alpha (activat clone HQ0310 PRO0310p1	6.18 3.19				
40	133000	AL042444	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	2.96				
	133050	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	2.55				
	133083 133086	BE244588 L17131	Hs.6456 Hs.139800	chaperonin containing TCP1, subunit 2 (b high-mobility group (nonhistone chromoso					4.00 8.96
45	133134	AF198620	Hs.65648	RNA binding motif protein 8A					4.28
	133155	M58583	Hs.662	cerebellin 1 precursor				10.80	
	133181 133204	X91662 BE267696	Hs.66744 Hs.254105	twist (Drosophila) homolog (acrocephalos enolase 1, (alpha)	3.00				4.63
	133412		Hs.73112	guanine nucleotide binding protein (G pr		12.50			1.00
50	133421	AF134160	Hs.7327	claudin 1	2.85				4.00
	133451 133453	AW970026 Al659306	Hs.73818 Hs.73826	ubiquinol-cytochrome c reductase hinge p protein tyrosine phosphatase, non-recept		6.80			4.66
	133504	NM_004415	Hs.74316	desmoplakin (DPI, DPII)	6.14	5.55			
55	133506	BE562958	Hs.74346	hypothetical protein MGC14353				47.00	4.55
55	133615 133627	M62843 NM_002047	Hs.75236 Hs.75280	ELAV (embryonic lethal, abnormal vision, glycyl-IRNA synthetase				17.80	4.85
	133649	U25849	Hs.75393	acid phosphatase 1, soluble					6.34
	133669	NM_006925	Hs.166975	splicing factor, arginine/serine-rich 5				14.00	
60	133749 133776	L20852 BE268649	Hs.10018 Hs.177766	solute carrier family 20 (phosphate tran ADP-ribosyltransferase (NAD+; poly (ADP-			6.11		4.91
•	133865	AB011155	Hs.170290	discs, large (Drosophila) homolog 5	3.07				
	133946	AJ001258	Hs.173878	NIPSNAP, C. elegans, homolog 1				42.00	4.60
	133973 134047	N55540 BE262529	Hs.78026 Hs.78771	ESTs, Weakly similar to similar to ankyr phosphoglycerate kinase 1				13.00	3.85
65	134098	BE513171	Hs.79086	mitochondrial ribosomal protein L3	2.56				
	134107	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte			8.20		
	134112 134158	AW449809 U15174	Hs.79150 Hs.79428	chaperonin containing TCP1, subunit 4 (d BCL2/adenovirus E1B 19kD-interacting pro	31.00				4.08
	134160	T98152	Hs.79432	fibrillin 2 (congenital contractural ara	51.00		24.60		
70	134168	AA398908	Hs.181634	Homo sapiens cDNA: FLJ23602 fis, clone L					6.71 .
	134185 134201	AA285136 L35035	Hs.301914 Hs.79886	neuronal specific transcription factor D ribose 5-phosphate isomerase A (ribose 5		8.40		14.74	
	134272		Hs.278614	protease, serine, 15	4.50	0.10			
75	134276	BE083936	Hs.80976	antigen identified by monoclonal antibod		9.00		40.40	
13	134353 134357	AL138201 AA339449	Hs.82120 Hs.82285	nuclear receptor subfamily 4, group A, m phosphoribosylglycinamide formyltransfer	2.80			16.40	
	134380	AU077143	Hs.179565	minichromosome maintenance deficient (S.	4.68				
	134423	H53497	Hs.83006	CGI-139 protein					3.84
80	134469 134470	AA279661 X54942	Hs.83753 Hs.83758	small nuclear ribonucleoprotein polypept CDC28 protein kinase 2					5.81 4.21
55	134498	AW246273	Hs.84131	threonyl-IRNA synthetase					7.30
	134502	BE148534	Hs.84168	UV-B repressed sequence, HUR 7		13.60			
	134510 134548	NM_002757 N95406	Hs.250870 Hs.333495	mitogen-activated protein kinase kinase Deleted in split-hand/split-foot 1 regio				9.70	4.63
85	134654	AK001741	Hs.8739	hypothetical protein FLJ 10879	6.00				

	W	O 02/086-	143		PCT/US				
	134724	AF045239	Hs.321576	ring finger protein 22				12.00	
	134743	AA044163	Hs.89463	potassium large conductance calcium-acti	4.00				
	134781	AA374372	Hs.89626	parathyroid hormone-like hormone			25.20		
_	134806	AD001528	Hs.89718	spermine synthase					4.58
5	134853	BE268326	Hs.90280	5-aminoimidazole 4-carboxamide ribonucle					4.79
	134859	D26488	Hs.90315	KIAA0007 protein			6.20		
	134891	R51083	Hs.90787	ESTs			7.40		
	134950	BE246400	Hs.285176	acetyl-Coenzyme A transporter	4.00				
4.0	134993	BE409809	Hs.301005	purine-rich element binding protein B					4.48
10	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	9.50				
	135080	AI761180	Hs.94211	rod1 (required for cell differentiation,	5.00				
	135103	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)		11.00			
	135145	AW014729	Hs.95262	nuclear factor related to kappa 8 blndin					4.01
	135184	U13222	Hs.96028	forkhead box D1			7.00		
15	135242	AJ583187	Hs.9700	cyclin E1	13.50				
	135286	AW023482	Hs.97849	ESTs	6.46				
	135289	AW372569	Hs.9788	hypothetical protein MGC10924 similar to		8.80			
	135355	AK001652	Hs.99423	ATP-dependent RNA helicase	10.00				
20	135371	NM_006025	Hs.997	protease, serine, 22	8.00			44.00	
20	135393	L11244	Hs.99886	complement component 4-binding protein,				14.60	

TABLE 58 shows the accession numbers for those primekeys lacking unigenelD's for Table 5A. For each probeset we have listed the gene cluster number from which the dignancieotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (Double Twist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the 25

Unique Eos probeset identifier number CAT number: Gene cluster number 30 Genbank accession numbers Accession: CAT number Accessions Pkey H92325 T97125 117079 1621717_1 35 242183_1 AW963221 AA344870 AA344871 H93331 124305 101502 18202_-6 M26958 109792 754958_1 R49625 F10674 126034 1598157_1 H60340 N91637 U82321 H66077 44641_1 102768 40 126345 1653833_1 N49713 N49819 W03810 R25066 R20144 R20145 Z43845 127066 1703458_1 AA347668 AW956810 Z44271 F07065 F07064 R13506 244301_1 1774795_1 127099 119243 T12603 T12604 1566433_1 1538292_1 125875 H144R0 N98295 45 R43590 F10439 112054 AA210954 AA211007 Al809521 H12174 Z42556 126979 171411_1 126992 880655 1 AA429743 AA442754 292419_1 122318 AA127386 R15644 AA127404 AA158245 AA158235 114699 135322_1 50 150742 1 114793 108305 111550_1 AA071391 AA069892 AA069891 108393 100867 113411_1 AA075211 AA075245 AA075126 AA074946 tigr_HT4586 U genbank_AA609839 U14622 AA609839 123731 55 genbank_F09609 F09609 genbank_AA292700 109700 AA292700 120715 genbank_T97307 T97307 113702 115113 genbank_AA256460 AA256460 J05614 entrez J05614 101045 60 108554 genbank_AA084948 AA084948 genbank_AA086005 149538_1 R 416020_1 W 108573 05 AA086005 R10889 R10888 119052 W31912 Al167491 126522 AA676910 AA778853 AA778865 W86800 W42667 AJ580740 AJ690440 AJ561350 AW467906 AW151450 AJ825927 AL041716 AJ885600 AJ742213 AW248624 AJ955498 AA033947 126605 439280 1 65 103768 46922 1 VM4267 ALSBU740 NBS9440 ALSB 150 AWM52950 AWM51850 AWES297 ALBAT17 B ABD52778 AIB28008 API55518 AAB45559 API62595
AAB45559 ALBAZ711 NBSB35 C00054 AA193557 AW083868 AW163216 AA191955 AA522778 AIB28008 API55518 AA843508 API625195
AA176265 AW167963 AA992115 W93647 AW103572 AIB62994 AI342059 AA911719 AA176155 AA024712 AA069988 AA205591 AI591107
A1199673 AIB11766 AI275832 AI422233 A1191852 AI095682 AI580124 AI683612 AA582453 AA927559 AA486415 T32414 AI084978 H44849
H44848 H20477 T91695 W47039 AA070055 AA024795 AA328855 AA379248 AA3789330 AA385580 W25590 W03568 AA448359 AA093881
AW352477 AA089997 AI350265 W33475 N99688 AA932257 AW351469 H68550 AA663402 AA069771 AW087986 AI858420 AA600214
AI970774 AIB57712 AI683081 AI885584 AW131150 AI567881 AW002714 AW189973 AW075495 AW168303 AA953714 AW516881 AI357375 70 A1566663 AW512676 A1570580 A1023690 AA448216 A1079853 A1422707 AA779516 AW026972 AW130082 AW162307 AW438646 AA709332 AW192394 A1167350 A1217879 A1129152 AA719509 A1350480 AA663418 A1003634 AW118546 AA180261 AA442833 A1268625 AA888881 A1038759 AA846723 A1248770 AA993694 A1280335 A1885107 AW518649 AA641563 AA595835 AA582521 A1276744 AA436478 A1017360 75 AI620763 AI859887 N73926 AI076327 A1741615 A1160617 AW172819 AI492005 AA677429 AA996334 AI693771 AI950039 AI245629 AI288515 AI866186 T93293 AA173262 AA599779 AI680092 AW439316 AI084555 AI272672 AI583507 AW473219 AA738132 AW473283 AI367492 AA995410 AI689624 AA206353 AI033095 AI040382 AA873630 AI221074 AI934840 AI418680 AA844306 R94503 AA773520 AA843169 AA219425 AA623658 AIB11719 AW411275 AI5999B1 W37997 AI591178 AI684051 AA983238 AA669347 AA976239 AA704570 AI628339 AI884391 AI241580 AI003539 AW176687 AA009650 N34566 AI333493 AI186070 AA070827 AA411683 AI280884 AA872023 AA207255 AA021576 N71953 AI885888 AW076039 T15777 AI537673 AW248048 H09554 W93480 W47001 AW079114 AA063160 AA757453 R60788 80 ARBS9431 H20478 AA218882 AA757465 AA100995 AI864135 AIS34209 AA070503 H47008 AA21846 W61039 W93907 AW385050 W37967 W78028 AA189007 AAA78136 R93650 AA442312 T30287 AA847628 AA180262 AA009649 C03892 AW149464 AA310963 AA219639 AA069747 R29207 AA094784 AA293615 AA447848 AI984167 N90393 C05097 N56499 AW292351 AW149464 AA310963 AA219639 AA069747 R29207 AA094784 AA293615 AA447848 AI984167 N90393 C05097 N56499 AW292351 AW149681 AW1473258 AA629322 AI004409 AW105577 AI954937 AI811070 AA902422 AW514437 AAS36460 AA916877 AW517122 AA974657 AA975649 AW517130 AW517129 F31737 W07688 AA193645 AA378994 AA489273 F32267 W39303 AA021181 N86810 AA406524 AA062553 AA436801 H08985 H15979 N40310

AA436789 AA232172 AW360778 W25632 R60282 AA436530 AA378894 AA187461 AU940635 AA604210 AA089514 AA360421 N88243 N84281 AA209340 N56174 N83374 AA191088 AW247691 AA249013 AA093111 AA972536 AW298594 AA375893 T12139 W28186 AW243849 AZ68629 AA843996 W15260 A1188266 AW243849 R15836

genbank_W45552 W45552 119599 5 112382 genbank_R59904_R59904 AA227934 genbank_AA227934 AA227934 entrez_A28102 A28102 714071_1 AA496369 AA496646 105264 100071 123315

Table 6A shows 99 genes up-regulated nonsmokers with lung cancer relative to smokers with lung cancer. These genes were selected from \$9680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number Unigene number 15 Pkey:

10

Pkey:
Exacers:
Exemplar Accession number, Genbank accessor number.
UnigenelD:
Unigene Title:
Unigene enumber
Unigene pene title
average of Al for samples from non-smokers with adenocarcinoma divided by the 90th percentile of Al for samples from smokers with adenocarcinoma average of Al for samples from non-smokers with squamous cell carcinoma divided by the 90th percentile of Al for samples from smokers with squamous cell carcinoma divided by the 90th percentile of Al for samples from smokers with squamous cell carcinoma divided by the 90th percentile of Al for samples from smokers with squamous cell carcinoma divided by the 90th percentile of Al for samples from smokers with squamous cell carcinoma divided by the 90th percentile of Al for samples from smokers with squamous cell carcinoma divided by the 90th percentile of Al for samples from smokers with squamous cell carcinoma divided by the 90th percentile of Al for samples from smokers with squamous cell carcinoma divided by the 90th percentile of Al for samples from smokers with squamous cell carcinoma divided by the 90th percentile of Al for samples from smokers with squamous cell carcinoma divided by the 90th percentile of Al for samples from smokers with squamous cell carcinoma divided by the 90th percentile of Al for samples from smokers with squamous cell carcinoma divided by the 90th percentile of Al for samples from smokers with squamous cell carcinoma divided by the 90th percentile of Al for samples from smokers with squamous cell carcinoma divided by the 90th percentile of Al for samples from smokers with squamous cell carcinoma divided by the 90th percentile of Al for samples from smokers with squamous cell carcinoma divided by the 90th percentile of Al for samples from smokers with squamous cell carcinoma divided by the 90th percentile of Al for samples from smokers with squamous cell carcinoma divided by the 90th percentile of Al for samples from smokers with squamous cell carcinoma divided by the 90th percentile of Al for samples from smokers w 20

	Pkey	ExAcon	UnigenelD	Unigene Title	R1	R2
25	100071	BE379727	Hs.83213	fathy acid blinding protein 4, adipocyte		3.64
25	100971	L17330	Hs.280	pre-T/NK cell associated protein	15.00	
	101174 101296	Y12490	Hs.85092	thyroid hormone receptor interactor 11		2.46
	101304	AA001021	Hs.6685	thyroid hormone receptor interactor 8		12.00
	101806	AA586894	Hs.112408	S100 catcium-binding protein A7 (psorias		2.68
30	101972	S82472	113.112400	qb:beta -pol=DNA polymerase beta (exon a		211
30	102274	U30930	Hs.158540	UDP gtycosyltransferase 8 (UDP-galactose	7.50	
	102394	NM_003816		a disintegrin and metalloproteinase doma	7.50	
	102832	U92015	163.2.412	qb:Human clone 143789 defective mariner	13.50	
	103010	X52509	Hs.161640	tyrosine aminotransferase	9.50	
35	103439	X98266	113.101010	gb:H.sapiens mRNA for ligase like protei	•	2.50
33	103439	L02911	Hs.150402	activin A receptor, type I	9.00	
	103353	A1076795	Hs.45033	lacrimal proline rich protein		3.94
	104239	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	13.50	
	104590	AW373062	Hs.83623	nuclear receptor subfamily 1, group I, m		12.66
40	1049907	AA055829	Hs.196701	ESTs, Weakly similar to ALU1_HUMAN ALU	16.50	
70	106131	BE514788	Hs.296244	SNARE protein		2.17
	106672	H47233	Hs.30643	ESTs	7.00	
	106872	T56887	Hs.18282	KIAA1134 protein	11.50	
	106960	AA156238	Hs.32501	ESTs		2.38
45	106971	Z43846	Hs.194478	Homo sapiens mRNA; cDNA DKFZp43401572 (f	9.50	
77	107982	AA035375	Hs.57887	ESTs, Weakly similar to KIAA0758 protei		2.95
	108562	AA100796	10.0100	gb:zm26c06.s1 Stratagene pancreas (93720	16.50	
	108599	AB018549	Hs.69328	MD-2 protein	13.00	
	108663	BE219231	Hs.292653	ESTs, Weakly similar to T26845 hypotheti		2.40
50	109247	AA314907	Hs.85950	ESTs	7.00	
50	109630	R44607	Hs.22672	ESTs		5.00
	110193	A1004874	Hs.310764	Homo sapiens mRNA; cDNA DKFZp434M082 (fr	12,50	
	110234	H24458	Hs.32085	EST	16.50	
	110644	R94207	Hs.268989	ESTs, Highly similar to type II CALM/AF1	8.00	
55	110886	AW274992	Hs.72249	three-PDZ containing protein similar to	17.00	
55	111057	T79639	Hs.14629	ESTs	16.50	
	111950	AF071594	Hs.110457	Wolf-Hirschhorn syndrome candidate 1	11.00	
	112291	R53972	Hs.26026	ESTs		3.00
	112956	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)		2.79
60	113009	T23699	Hs.7246	ESTs		4.50
•	113060	BE564162	Hs.250820	hypothetical protein FLJ14827	9.79	
	113073	N39342	Hs.103042	microtubule-associated protein 1B	32.50	
	113074	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t		3.82
	113121	T48011	Hs.8764	EST		2.21
65	113125	AA968672	Hs.8929	hypothetical protein FLJ11362	19.50	
	113757	AA703095	Hs.18631	ESTs		2.65
	113848	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	6.00	
	113884	AJ333076	Hs.28529	chromosome 12 open reading frame 2		6.00
	113936	W17056	Hs.83623	nuclear receptor subfamily 1, group I, m		4.63
70	114875	AA235609	Hs.236443	Homo sapiens mRNA; cDNA DKFZp564N1063 (7.00
	114987	AA251016	Hs.87808	EST		6.00
	115460	AW958439	Hs.38613	ESTs		2.27
	115722	W91892	Hs.59609	ESTs		9.00
	116261	AA481788	Hs.190150	ESTs	9.50	
75	116830	H61037	Hs.70404	ESTs, Weakly similar to ALU2_HUMAN ALU	8.50	
	116970	AB023179	Hs.9059	KIAA0962 protein	7.50	2.68
	117178	H98675	Hs.269034	ESTs	7.50	2.00
	117757	AF088019	Hs.46732	EST	7.50	
00	118283	AA287747	Hs.173012	ESTs, Weakly similar to A46010 X-linked	16.50	2.50
80	118384	AF217525	Hs.49002	Down syndrome cell adhesion molecule		
	118657	Al822106	Hs.49902	ESTs		2.39
	120328	AA923278	Hs.290905	ESTs. Weakly similar to protease [H.sapi	7.00	3.50
	120404	AB023230	Hs.96427	KIAA1013 protein	7.00	
0.5	120524	AA261852	Hs.192905	ESTs	6.00	
85	120688	AW207555	Hs.97093	Homo sapiens cDNA: FLJ23004 fis, clone L	17.92	
					•	

	W	O 02/0864	143				PCT/US02/12476
	121558	AA412497		gb:zt95g12.s1 Soares_testis_NHT Homo sap		295	
	121676	H56037	Hs.108145	ESTs	10.03		
	121936	AJ024600	Hs.98612	ESTs	15.00		
	121938	AA428659	Hs.98610	ESTs	14.00		
5	122177	AA435789	Hs.98833	EST	8.93		
•	123442	AA299652	Hs.111495	Homo sapiens cDNA FLJ11643 fis, clone HE	13.04		
	123551	AA608837		ob:af03h12.s1 Soares_testis_NHT Homo sap	11.50		
	123756	AA609971	Hs.112795	EST	11.00		
	123861	AA620840		qb:af89g01.s1 Soares_testis_NHT Homo sap		2.50	
10	124371	N24924	Hs.188601	ESTs	6.50		
10	127477	BE328720	Hs.280651	ESTs		4.33	
	127591	Al190540	Hs.131092	ESTs		3.02	
	128252	AA455924	Hs.192228	ESTs	7.00		
	128426	Al265784	Hs.145197	ESTs		2.08	
15	128925	R67419	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT		2.11	
LJ	128945	A1990506	Hs.8077	Homo saciens mRNA; cDNA DKFZp547E184 (fr	10.00		
	129105	A1769160	Hs.108681	Homo sapiens brain tumor associated prot	15.50		
	129235	AW977238	Hs.126084	KIAA1055 protein	*****	4.25	
		AB020684	Hs.11217	KIAA0877 protein	6.50		
20	129506		Hs.1154	oviductal glycoprolein 1, 120kD (mucin 9	•	10.00	
20	129595 130160	U09550 AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	20.00		
			Hs.239106	solute carrier family 3 (cystine, dibasi	11.50		
	130340	D82326 AB023194	Hs.300855	KIAA0977 protein	17.50		
	131220 131430	ABU23194 AI879148	Hs.26770	fatty acid binding protein 7, brain	6.10		
25		NM 006152		lymphoid-restricted membrane protein	4.0	6.15	
25	132114 132458	AA935315	Hs.48965	Homo sapiens cONA: FLJ21693 fis, clone C		5.58	
		NM_006927		sialyltransferase 4B (beta-galactosidase	7.50		
	132647	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	1.00	2.53	
	132655	AI077500	Hs.54900	serologically defined colon cancer antig		2.50	
30	132682		Hs.55950	ESTs. Weakly similar to KIAA1330 protein		2.83	
30	132747	AA345241	Hs.92186	Leman coiled-coil protein		3.82	
	132812	R50333 AF085983	Hs.293676	ESTs		5.00	
	133337		Hs.771	phosphorylase, glycogen; liver (Hers dis		3.00	
	133876	AL134906	Hs.79226	fasciculation and elongation protein zet		2.06	
35	134119	AW157837	Hs.239720	CCR4-NOT transcription complex, subunit	•	2.27	
22	134464	AA302983	Hs.85112	insulin-like growth factor 1 (somatomedi		11.50	
	134542	M14156		G antigen 7B	87.00	,,,,,,	
	135002	AA448542	Hs.251677	Homo sapiens cDNA FLJ14903 fis, clone PL	07.50	6.50	
	135305	AA203555	Hs.98288	Homo Sapiens CORA PLU (4500 ils, Giore PL		0.00	
40							
40	*****		anian numbam	for those primekeys lacking unigenelD's for Table 6A. F	or each nonheset we t	ave listed the ge	ne cluster number from which the
	olicomiclo	ofides were de-	signed Gene	clusters were compiled using seguences derived from Ge	inbank ESIS and mikin	las, inese sequ	euces mete chrateren basen ou sedaen
	similarity (ising Clustering	and Alignmen	it Tools (DoubleTwist, Oakland California). The Genbank	accession numbers for	r sequences con	nprising each cluster are listed in the
	"Accession		-	·			
45							

 Pkey:
 Unique Eos probeset identifier number

 CAT number:
 Gene cluster number

 Accession:
 Genbank accession numbers

 Pkey
 CAT number
 Accessions

 108562
 36375_1
 AA100796 AF020589 AA074629 AA075946 AA100849 AA085347 AA126309 AA079311 AA079323 AA085274

 103439
 35330_1
 X98266 N41124

 123551
 genbank_AA608837
 AA608837

 123861
 genbank_AA620840
 AA620840

 102832
 entrez_U92015
 U92015

 101972
 entrez_S82472
 S82472

 121558
 genbank_AA412497
 AA412497

50

55

WO 02/086443

Table 7A shows 98 genes down-regulated in non-smokers with lung cancer relative to smokers with lung cancer. These genes were selected from \$9530 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

	the relati	ve level of mRN	A expression.			
5	Pkey:	I trione i	ins nroheset in	lentitier number		
3	ExAccn:			umber, Genbank accession number		
	Unigene					
	Unigene	Title: Unigene				
10	R1:	90th pen	centile of Al for	r samples from smokers with adenocarcinoma divide	d by the average	of Al for samples from non-smokers with adenocarcinoma.
10	R2:			r samples from smokers with squamous cell carbinon	na divided by the	average of Al for samples from non-smokers with squamous cell
		carcinon	id.			
	Pkey	ExAcon	UnigenelD	Unigene Tille	R1	R2
1.5						40449
15	100187	D17793	Hs.78183	atrio-keto reductase family 1, member C3 neuroblastoma (nerve tissue) protein		164.10 77.40
	100380 100576	D82343 X00356	Hs.18551 Hs.37058	calcitorin/calcitonin-related polypeptid	102.40	77.40
	100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	463.80	
	101046	K01160		(NONE)	672.00	•
20	101056	AW970254	Hs.889	Charot-Leyden crystal protein	66.00	
	101175	U82671	Hs.36980	melanoma antigen, family A, 2	62.80	77.20
	101497 101663	W05150 NM_003528	Hs.37034 Hs.2178	homeo bax A5 H2B histone family, member Q	78.00	•
	101663	NM_000715	Hs.1012	complement component 4-binding protein,	186.20	
25	101745	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci	80.08	
	101941	S77583		gb:HERVK10/HUMMTV reverse transcriptase	99.20	
	102125	NM_006456	Hs.288215	sialytransferase		103.10
	102242	U27185	Hs.82547	retinoic acid receptor responder (tazaro	67.00	
30	102340 102369	U37055 U39840	Hs.278557 Hs.299867	macrophage stimulating 1 (hepatocyte gro hepatocyte nuclear factor 3, alpha	71.60	69.70
50	102355	NM_001394	Hs.2359	dual specificity phosphatase 4	153.00	00.70
	102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2		65.70
	102796	AL079646	Hs.107019	symplekin; Hunlingtin interacting protei		58.80
2.5	102829	NM_006183	Hs.80962	neurotensin		268.80
35	103207	X72790		gb:Human endogenous retrovirus mRNA for	70.00	212.10
	103242 103260	X76342 X78416	Hs.389 Hs.3155	alcohol dehydrogenase 7 (class IV), mu o casein, alpha		212.10 130.70
	103260	X89211	113.3133	gb:H.sapiens DNA for endogenous retrovir	64.60	100.10
	104212	AB002298	Hs.173035	KIAA0300 protein	66.80	
40	104252	AF002246	Hs.210863	cell adhesion molecule with homology to	63.80	
	104258	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	94.40	
	105024	AA126311	Hs.9879	ESTs	68.20	74.60
	106260	A1097144	Hs.5250 Hs.151393	ESTs, Weakly similar to ALU1_HUMAN ALU S glutamate-cystelne ligase, catalytic sub		74.60 71.10
45	106440 106566	AA449563 BE298210	115.131333	gb:601118016F1 NIH_MGC_17 Homo sapiens c	73.20	71.10
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp5648076 (fr	83.80	
	106614	AA648459	Hs.335951	hypothetical protein AF301222		62.30
	106654	AW075485	Hs.286049	phosphoserine aminotransferase		202.40
50	105999	H93281	Hs.10710	hypothetical protein FLJ20417		89.60
50	108700 108810	AA121518 AW295647	Hs.193540 Hs.71331	ESTs, Moderately similar to 2109260A 8 c hypothetical protein MGC5350		66.40 95.50
	108857	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act		63.40
	109597	AA989362	Hs.293780	ESTs	85.00	
	109691	T65568	Hs.12860	ESTs		58.70
55	109704		Hs.12876	ESTs	70.40	60.60
	110942 111722		Hs.28419 Hs.23596	ESTS EST	76.40 74.60	
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-li	64.80	
	112992		Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	555	76.70
60	113073	N39342	Hs.103042	microtubule-associated protein 18		120.20
	114251	H15261	Hs.21948	ESTs	127.20	•
	115230	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	174.00	04.00
	115291 115815	BE545072 AW905328	Hs.122579 Hs.180842	hypothetical protein FLJ10461 ribosomal protein L13	66.40	91.00
65	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	00.40	226.60
00	115965		Hs.173233	hypothetical protein FLJ10970	82.80	
	116107	AL133916	Hs.172572	hypothetical protein FLJ20093		361.60
	116552		Hs.164649	hypothetical protein DKFZp434H247	69.00	
70	116571	D45652		gb:HUMGS02848 Human adult lung 3' direct	64.20	63.50
70	118466 120484	N66741 AA253170	Hs.96473	gb:yz33g08.s1 Morton Fetal Cochlea Homo EST	81.60	00.00
	120983		Hs.97587	EST	01.00	81.10
	121034		Hs.271623	nucleoporin 50kD		66.20
25	121423		Hs.290585	ESTs	64.40	
75	122553		Hs.190121	ESTS	400.00	60.40
	122946 123130	A1718702 AA487200	Hs.308026	major histocompatibility complex, class gb:ab19f02.s1 Stratagene lung (937210) H	188.60	80.20
		N52517	Hs.102670	EST	71.00	60.20
	124526		Hs.293185	ESTs, Weakly similar to JC7328 amino aci	· 1.00	104.90
80	125489		Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A		72.00
	125731	R61771	Hs.26912	ESTs		69.90
	125747	NM_002884	Hs.865	RAP1A, member of RAS oncogene family	69.00	62.40
	126020 126547	H79863 U47732	Hs.114243 Hs.84072	ESTs transmembrane 4 superfamily member 3		62.80
85	126956		Hs.182575	solute carrier family 15 (H+/peptide tra		60.10

	W	O 02/086	443				PCT/US02/12470
	127472	AA761378	Hs.192013	ESTs	70.20		
	127610	AA960867	Hs.150271	ESTs, Highly similar to unnamed protein	64.00		
	127742	AW293496	Hs.180138	ESTs	85.20		
	127987	AM022103	Hs.124511	ESTs	96.60		
5	128233	AW889132	Hs.11916	ribokinase		78.90	
	128420	AA650274	Hs.41295	fibronectin laucine rich transmembrane p		105.90	
	128766	AW160432	Hs.296460	craniofacial development protein 1	66.80		
	129014	AW935187	Hs.170162	KIAA1357 protein		58.53	
	129215	AB040930	Hs.126085	KIAA1497 protein	64.20		
0	130090	H97878	Hs.132390	zinc finger protein 36 (KOX 18)	63.80		
•	130385	AW067800	Hs.155223	stanniocatcin 2		139.60	
	130732	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)		64.60	
	131025	AB040900	Hs.6189	KIAA1457 protein	64.40		
	131241	BE501914	Hs.24654	Homo saciens cDNA FLJ11640 fis, clone HE	76.20		
5	131775	AB014548	Hs.31921	KIAA0648 protein	97.80		
_	132240	AB018324	Hs.42676	KIAA0781 protein		71.00	
	132856	NM_001448	Hs.58367	glypican 4		88.40	
	132977	AA093322	Hs.301404	RNA binding motif protein 3	133.20		
	133749	L20852	Hs.10018	solute carrier family 20 (phosphate tran		59.30	
0	133818	Al110684	Hs.7645	fibrinogen, B beta polypeptide	341.00		
•	134264	AF149297	Hs.8087	NAG-5 protein		64.30	
	134265	M83772	Hs.80876	flavin containing monooxygenase 3		232.53	
	134346	X84002	Hs.82037	TATA box binding protein (TBP)-associate	66.00		
	134395	AA456539	Hs.8262	lysosomal-associated membrane protein 2		75.80	
5	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su		108.30	
,	135056	N75765	Hs.93765	linoma HMGIC fusion partner	71.40		
	135309	AL564123	Hs.42500	ADP-ribosylation factor-like 5	70.40		
	:33303	74507120	13.72000	LIEU JIMON JANON HANDI BAD O			

TABLE 7B shows the accession numbers for those primekeys lacking unigenelD's for Table 7A. For each probeset we have listed the gene cluster number from which the ofigonucteotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number CAT number: Gene cluster number Accession: Genbank accession numbers

CAT number Accessions Pkey 30635_4 X72790
120358_1 BE298210 AI672315 AW086489 BE298417 AA455921 AA902537 BE327124 R14963 AA085210 AW274273 AI333584 AI369742 AI039658
AI885095 AI476470 AI287650 AI885299 AI985381 AW592624 AW340136 AI266556 AA456390 AI310815 AA484951
genbank_N66741 N66741 N66741
entrez_K01160 K01160
entrez_S77583 S77583
entrez_X89211 X89211
genbank_AA487200 AA487200 106566 118466

Table 8A shows 1720 genes either up or down-regulated in lung tumors or chronically diseased lung relative to a broad collection of over 40 distinct normal body lissues. Chronically diseased lung samples represent chronic non-matignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 39494 probesets on the EostAffymetrix Hu02 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5

Pitey: Unique Eos probeset identifier number
EXACOT: Exemptar Accession number, Genbank accession number
Unigeneiti: Unique en number
Unique Title: Unique gene title
R1: 70th percentile of Al for lung tumors divided by 90th percentile of Al for normal lung
R2: 70th percentile of Al for chronically diseased lung divided by 90th percentile of Al for normal lung 10

	142	rous per	CELLING OF AT ICE	curous and discovery mild divided by sout belowing	OI AL IOI IAAI	ildi wiig
	Pkey	ExAcon	UnigenelD	Unigene Title	R1	R2
15	300097	AI916973	Hs.213603	ESTs	5.46	4.69
	300117	AW189787	Hs.147474	ESTs	0.58	0.56
	300197	AI686661	Hs.218286	ESTs	4.26	5.44
	300201	Al308300		gb:ta90c06.x1 NCI_CGAP_Bm20 Homo sapien	0.62	0.83
20	300225	Al989963	Hs.197505	ESTs	1.68	1.75
20	300247	AW274682		ESTs	1.08	2.28
	300256	Al469095	Hs.298241	Transmembrane protease, serine 3	0.86	1.00
	300337 300362	Al707881 Z42308	Hs.202090	ESTs gb:HSC0FB121 normalized infant brain cDN	5.80 4.18	9.09 12.78
	300374	Al859947	Hs.314158	ESTs	2.99	4.38
25	300387	AW270150		ESTs	1.50	2.53
	300440	Al421541	Hs.146164	ESTs	3.98	5.25
	300441	R10367	Hs.307921	EST, Weakly similar to Z232_HUMAN ZINC F	3.18	6.80
	300449	Al362967	Hs.132221	hypothetical protein FLJ12401	0.43	0.62
20	300469	AW135830	Hs.233955	hypothetical protein FLJ20401	0.16	0.83
30	300552 300627	X85711 W27363	Hs.21838	hypothetical protein FLJ11191	4.10 4.60	9.75 12.60
	300627	AW118822	Hs.128757	gb:ab37d01.r1 Stratagene HeLa cell s3 93 ESTs	2.91	5.85
	300716	AI216113	Hs.126280	hypothetical protein FLJ23393	1.00	0.92
	300738	Al623332	Hs.130541	KIAA1542 protein	1.82	1.71
35	300777	AA235361	Hs.96840	KIAA1527 protein	4.48	8.22
	300790	AI492471	Hs.188270	ESTs	1.29	1.18
	300832	A1688147	Hs.220615	ESTs, Weakly similar to T03829 transcrip	5.51	8.56
	300836	Z44942	Hs.22958	calcium channel alpha2-delta3 subunit	4.90	6.34
40	300838 300878	AI582897 AW449802	Hs.192570 Hs.285901	hypothetical protein FLJ22028 Homo sapiens cDNA FLJ20428 fis, clone KA	1.70 4.56	2.81 7.91
40	300897	A1890356	Hs.127804	ESTs, Weakly similar to T17233 hypotheti	2.23	1.58
	300926	AA504860	113.12.7004	gb:ab03a10.s1 Stratagene fetal retina 93	2.13	3.50
	300960	AI041019	Hs.152454	ESTs	2.74	4.46
4.5	300961	AW204069	Hs.312716	ESTs, Weakly similar to unnamed protein	1.00	1.00
45	300962	AA593373	Hs.293744	ESTs	1.46	1.51
	300967	AA565209	Hs.269439	ESTs	0.39	1.30
	300987 300988	AW450840 AI927208	Hs.148590 Hs.208952	ESTs, Weakly similar to AF208846 1 BM-00 ESTs	1.49 0.16	1.08 0.37
	301050	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen i	3.23	1.94
50	301098	AA677570	Hs.185918	ESTs	6.76	14.28
	301157	AA729905	Hs.231916	ESTs	3.16	8.85
	301162	Al142118	Hs.129004	ESTs	1.68	7.18
	301170	AA737594	Hs.247606	ESTs	4.40	6.42
55	301192	AI808751	Hs.121188	ESTs	6.38	11.59
55	301193 301267	AA758115 AW297762	Hs.128350 Hs.255690	ESTs, Wealdy similar to JC5423 2-hydroxy ESTs	4.35 1.56	7.78 1.61
	301281	AA843986	Hs.190586	ESTs	2.19	1.78
	301341	Al819198	Hs.208229	ESTs	0.76	0.76
	301382	AA912839	Hs.163369	ESTs	1.00	1.81
60	301407	AW450466	Hs.126830	ESTs	1.48	1.51
	301452	AA975688	Hs.159955	ESTs	0.51	1.46
	301483	AW272467	Hs.254655	Untilled	2.40	5.02
	301494 301521	Al678034 Al733621	Hs.131099 Hs.133011	ESTs zinc finger protein 117 (HPF9)	2.79 0.67	3.41 0.67
65	301531	AI077462	Hs.134084	ESTs	2.52	3.76
	301580	AI878959	Hs.73737	splicing factor, arginine/serine-rich 1	7.41	11.92
	301676	Z43570	Hs.27453	ESTs, Moderately similar to G01251 Rar p	8.31	10.70
•	301690	F05865	Hs.108323	ubiquitin-conjugating enzyme E2E 2 (homo	2.70	4.22
70	301718	F07744	Hs.7987	DKFZP434F162 protein	4.20	8.78
70	301799 301804	AA384252 AA581004	Hs.286132	D15F37 (pseudogene)	5.93	7.04
	301822	X17033	Hs.62180 Hs.271986	anillin (Drosophita Scraps homolog), act	1.70 1.58	0.76 1.36
	301846	R20002	Hs.6823	integrin, alpha 2 (CD49B, alpha 2 subuni hypothetical protein FLJ10430	1.00	1.00
	301868	171508	Hs.13861	ESTs. Weakly similar to pH sensitive max	2.88	5.49
75	301882	T78054		gb:yc97g09.r1 Soares infant brain 1NIB H	2.28	3.80
	301905	AI991127	Hs.117202	ESTs	1.00	1.00
	301948	AA344647	Hs.116724	aldo-keto reductase family 1, member B11	5.28	2.28
	301960 302011	AW070252 T91418	Hs.27973 Hs.125156	KIAA0874 protein	5.3B	6.48
80	302016	N40834	Hs.23495	transcriptional adaptor 2 (ADA2, yeast, hypothetical protein FLJ11252	3.03 1.00	3.42 1.25
	302041	NM_001501		gonadotropin-releasing hormone 2	0.71	0.99
	302072	AJ238381	Hs.132576	paired box gene 9	1.60	1.71
	302094	A1286176	Hs.6786	ESTs	0.52	1.20
85	302095	AW044300	Hs.137506	Homo sapiens BAC clone RP11-120J2 from 7	2.75	4.93
65	302148	AW269618	Hs.23244	ESTs	3.04	3.87

	W	O 02/08	5443			
	302155	A1088485	Hs.144759	ESTs	0.45	1.15
	302201	AJ006276	Hs. 159003	transient receptor potential channel 6	0.33	0.84
	302202	AF097159	Hs.159140	UDP-GatbelaGlcNAc beta 1,4- galactosylt	0.52	0.54
_	302206	Al937193	Hs.41143	phosphoinositide-specific phospholipase	2.76	3.65
5	302209	AF047445	Hs.159297	killer cell lectin-like receptor subfami	1.00	1.00
	302235	AL049987	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	1.68	1.50
	302290	AL117607	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564ND763 (f	1.00	2.11
	302328	AA354849	Hs.23240	Homo sapiens cDNA FLJ13496 fis, clone PL	9.38	13.08
10	302346	AL039101	Hs.194625	dynein, cytoplasmic, light intermediate	3.27	7.24
10	302360	AJ010901	Hs.198267	much 4, tracheobronchial	2.54	1.88
	302384	Y08982	Hs.202676	synaptonemal complex protein 2	1.00	0.91
	302406	U86751	Hs.211956	CD3-epsilon-associated protein; antisens	263	2.67
	302409	AF155156	Hs.218028	adaptor-related protein complex 4, epsil	5.82	9.34
15	302423	AB028977	Hs.225974	KIAA1054 protein	3.66 2.44	3.18 6.77
15	302432	AL080068	Hs.272534	Homo septens mRNA; cDNA DKFZp564J062 (fr	0.44	0.84
	302435	AF092047	Hs.227277	sine oculis homeobox (Orosophila) homolo	4.18	5.64
	302437	AB024730 AA356923	Hs.227473 Hs.240770	UDP-N-acetylglucosamine:a-1,3-D-mannosid	1.85	0.92
	302455 302472	AA317451	Hs.6335	nuclear cap binding protein subunit 2, 2 SWI/SNF related, matrix associated, acti	2.04	2.13
20	302472	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSm8	1.44	1.89
20	302489	T80660	Hs.230424	Homo sapiens cDNA FLJ 13540 fis, clone PL	0.51	1.10
	302490	AA885502	Hs.187032	ESTs	2.64	4.87
	302562	AJ005585	Hs.48956	gap junction protein, beta 6 (connexin 3	5.34	2.68
	302566	AA085996	Hs.248572	hypothetical protein FLJ22965	1.00	1.21
25	302630	AB029488	Hs.272100	SMS3 protein	0.52	1.24
	302634	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	1,00	1.00
	302638	AA463798	Hs.102696	MCT-1 protein	1.58	1.02
	302647	X57723	Hs. 198273	NADH dehydrogenase (ubiquinone) 1 beta s	2.72	6.85
	302655	AJ227892	Hs.146274	ESTs	1.00	4.32
30	302656	AW293005	Hs.70704	Homo sapiens, clone IMAGE:2823731, mRNA,	2,97	0.93
-	302668	AA580691	Hs.180789	S164 protein	0.80	0.95
	302679	H65022		gb:yu66g11.r1 Weizmann Olfactory Epithel	1.68	5.04
	302680	AW192334	Hs.38218	ESTs	2.70	7.98
	302697	AJ001408		gb:Homo saplens mRNA for immunoglobutin	4.25	8.13
35	302705	U09060		gb:Human Immunoglobulin heavy chain, V-r	3.91	8.68
	302711	L08442		gb:Human autonomously replicating sequen	2.20	2.73
	302719	W69724	Hs.288959	hypothetical protein FLJ20920	0.54	1.02
	302742	L12069		gb:Homo sapiens (clone WR4.10VH) anti-th	4.28	11.57
40	302755	AW384815	Hs.149208	KIAA1555 protein	1.57	2.38
40	302771	H98476	Hs.42522	ESTs Substitution of the Control of	2.94	4.68
	302789	AJ245067	070000	gb:Homo sapiens mRNA for immunoglobulin	3.49	6.31
	302795	AJ245313	Hs.272838	hypothetical protein FLJ10494	0.80	2.74
	302802	Y08250	11- 202004	gb:H.sapiens mRNA for variable region of	1.13	0.77
45	302803	AA442824	Hs.293961	ESTs, Moderately similar to putative DNA	3.14 3.04	10.68 8.24
43	302812	N31301	Hs.152664	hypothetical protein FLJ20051	1.80	1.92
	302847 302885	X98940 AL137763	Hs.132127	gb:H.sapiens rearranged ig heavy chain (1.00	1.00
	302943	AL137763 Al581344	Hs.127812	hypothetical protein LOC57822 ESTs, Weakly similar to T17330 hypotheti	0.53	0.67
	302977	AW263124	Hs.315111	hypothetical protein FLJ12894	2.45	2.62
50	303006	AF078950	Hs.24139	Homo sapiens cDNA: FLJ23137 fis, done L	4.88	8.61
•	303011	AF090405	110.21100	gb:Homo saciens clone 2A1 scFV anitbody	1.41	1.86
	303013	F07898	Hs.288968	RAB22A, member RAS oncogene family	1.51	1.19
	303061	AF151882	Hs.27693	peptidylprolyl isomerase (cyclophilin)-l	0.72	0.76
	303077	AF163305		gb:H.sapiens T-cell receptor mRNA	1.17	3.90
55	303090	AA443259	Hs.146286	kinesin family member 13A	4.08	6.46
	303091	AF192913	Hs.130683	zinc finger protein 180 (HHZ168)	2.50	4.37
	303094	AF195513	Hs.278953	Pur-gamma	5.38	8.38
	303095	AF202051	Hs.134079	NM23-H8	3.26	4.08
	303131	AW081061	Hs.103180	DC2 protein	2.02	1.83
60	303195	AA082211	Hs.233936	myosin, light polypeptide, regulatory, n	1.32	3.95
	303196	AA082298	Hs.59710	ESTs	0.77	0.53
	303216	AA581439	Hs.152328	ESTs	0.24	0.63
	303222	AA333538	Hs.204501	hypothetical protein FLJ10534	3.56	6.22
65	303234	AA132255	Hs.143951	ESTs	2.28	3.17
65	303251	AW340037	Hs.115897	protocadherin 12	0.38	1.02
	303295	AA205625	Hs.208067	ESTs	2.30	1.00
	303297	T80072	Hs.13423	Homo sapiens clone 24468 mRNA sequence	1.86	4.48
	303316	AF033122	Hs.14125	p53 regulated PA26 nuclear protein	0.10	0.80
70	303467 303506	AA398801 AA340605	Hs.323397 Hs.105887	ESTs Woodly similar to Hamalan of sat 7	4.54 0.09	9.65 0.04
, ,	303552	AA359799	Hs.224662	ESTs, Weakly similar to Homolog of rat Z ESTs, Weakly similar to unnamed protein	1.00	1.72
	303598	AA382814	113.224002	gb:EST96097 Testis I Homo sapiens cDNA 5	4.96	9.14
	303637	AF056083	Hs.24879	phosphatidic acid phosphatase type 2C	2.06	2.02
_	303655	AA504702	Hs.258802	ATPase, (Na+)/K+ transporting, beta 4 po	1.00	1.24
75	303756	AI738488	Hs.115838	ESTs	1.08	1.43
-	303856	AA968589	Hs.180532	glucose phosphate isomerase	1.76	1.31
	303893	N88597	Hs.113503	karyopherin (importin) beta 3	2.30	2.57
	303907	AW467774	Hs.171880	polymerase (RNA) II (DNA directed) polyp	3.10	5.79
	303946	AW474196	Hs.306637	Homo saplens cDNA FLJ12363 fis, clone MA	5.06	11.86
80	303978	AW513315		gb:xo43c12.x1 NCI_CGAP_Ut1 Homo sapiens	5.14	7.31
	303981	AW513804	Hs.278834	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.83	4.06
	303990	AW515465		gb:xu71a11.x1 NCI_CGAP_Kid8 Homo sapiens	1.15	2.35
	303998	AW516449		gb:xt68f05.x1 NCI_CGAP_Ut2 Homo sapiens	2.20	9.35
0.5	303999	AW516611		gb:xp70b11.x1 NCI_CGAP_Ov39 Homo sapiens	4.85	6.28
85	304006	AW517947		gbbd56h02.x1 NCI_CGAP_Ut2 Homo sapiens	3.21	4.07

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	304003	AW518198	Hs.3297	ribosomal protein S27a	6.50	11.08
	304009	AW518206	Hs.181165	eukaryolic translation elongation factor	1.88	3.27
	304024	T03036		gb:FB21B7 Fetal brain, Stratagene Homo s	2.15	3.55
_	304026	T03160		gbtFB26F2 Fetal brain, Stratagene Homo s	5.88	11.80
5	304028	T03266	Hs.244621	gb:FB7C1 Fetal brain, Stratagene Homo sa ribosomal protein S14	5.59 6.55	13.46 14.43
	304036 304046	T16855 T54803	FIS.244021	obyb42d06.s1 Stratagene fetal spleen (9	6.18	12.19
	304061	T61521		gbryb73g01.s1 Stratagene ovary (937217)	2.64	8.23
	304063	T62536		gbryc04c12.s1 Stratagene lung (937210) H	0.53	1.61
10	304097	R25376	Hs.177592	ribosomal protein, large, P1	6.49	11.67
	304114	R78946		ghryi87g02.s1 Soares placenta Nb2HP Homo	2.90	4.18
	304122	H28966		gbrym31a06.s1 Soares infant brain 1NIB H	1.00 0.79	2.76 1.18
	304155 304203	H68696 N56929		gb:yr78b06.s1 Soares fetal liver spieen gb:yy82d08.s1 Soares_multiple_sclerosis_	4.28	11.34
15	304203	W81608		gb:zd88h06.s1 Soares_felal_heart_NbHH19W	6.47	11.03
13	304267	AA064862	Hs.73742	ribosomal protein, large, PO	1.34	1.16
	304270	AA069711	Hs.297753	vimentin	3.40	5.40
	304287	AA079286	Hs.78466	proteasome (prosome, macropain) 26S sub	2.93	4.42
20	304348	AA179868	11 400470	gb:zp38g12.s1 Stratagene muscle 937209 H	3.98 3.32	10.96 5.99
20	304415	AA290747	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase gb:EST54044 Fetal heart II Homo sapiens	1.00	1.00
	304430 304456	AA347682 AA411240		gb:zv26g05.s1 Soares_NhHMPu_S1 Homo sapi	1.42	3.33
	304521	AA464716		gbzx82c11.s1 Soares ovary tumor NbHOT H	2.18	1.15
	304526	AA476427		gb:zx02c05.s1 Soares_total_fatus_Nb2HF8_	5.38	14.11
25	304542	AA482602	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.16	8.23
	304546	AA486074	Hs.297681	serine (or cysteine) proteinase inhibito	0.55	1.20
	304607	AA513322	11-444004	gb:nh85e08.s1 NCI_CGAP_Br1.1 Homo sapien	1.95 2.10	2.10 2.83
	304640	AA524440 AA527489	Hs.111334 Hs.3463	ferritin, light polypeptide ribosomal protein S23	3.33	12.62
30	304650 304735	AA576453	ns.5400	gb:nm75h11.s1 NCI_CGAP_Co9 Homo sapiens	1.33	0.88
50	304760	AA580401		gb:nn13g09.s1 NCI_CGAP_Co12 Homo sapiens	3.68	8.14
	304849	AA588157	Hs.13801	KIAA1685 protein	2.77	3,70
	304917	AA602685	Hs.284136	PRO2047 protein	7.16	11.01
25	304921	AA603092	Hs.297753	vimentin	2.47	4.24 11.66
35	304966	AA613893 AA618044	Hs.282435	ESTs immunoglobulin heavy constant gamma 3 (G	6.78 0.90	1.23
	304987 305016	AA626876	Hs.300697	cb:zu89h06.s1 Soares_testis_NHT Homo sap	6.46	10.17
	305034	AA630128		gb:ab99c04.s1 Stratagene lung (937210) H	1.00	1.00
	305072	AA641012		gb:nr72a12.s1 NCI_OGAP_Pr24 Homo sapiens	5.68	11.59
40	305111	AA644187	Hs.303405	ESTs	1.48	1.37
	305148	AA654070		gb:nt01g08.s1 NCI_CGAP_Lym3 Homo sapiens	1.76	4.61
	305159	AA659166	Hs.275668	EST, Weakly similar to EF1D_HUMAN ELONG	1.00 5.31	2.15 8.14
	305190 305232	AA665955 AA670052	Hs.169476	gb:ag57d12.s1 Gessler Wilms tumor Homo s glyceraldehyde-3-phosphate dehydrogenase	0.78	1.18
45	305235	AA670480	133.103410	gb:ag37e01.s1 Jia bone marrow stroma Hom	3.11	8.66
	305245	AA676695	Hs.81328	nuclear factor of kappa light polypeptid	4.38	7.53
	305312	AA700201		gb:zj44f07.s1 Soares_fetal_liver_spleen_	2.13	2.66
	305322	AA701597	Hs.163019	EST	1.20	1.40 0.68
50	305394	AA720942	Hs.300697	immunoglobulin heavy constant gamma 3 (G gb:ai10/08.s1 Soares_parathyroid_tumor_N	1.16 5.86	9.87
50	305413 305447	AA724659 AA737856		gb:nx10c08.s1 NCI_CGAP_GC3 Homo sapiens	2.21	2.86
	305476	AA745664	Hs.287445	hypothetical protein FLJ11726	3.36	6.54
	305483	AA748030	Hs.303512	EST	1.00	2.02
	305528	AA769156		gb:nz12e05.s1 NCL_CGAP_GCB1 Homo sapiens	6.44	9.10
55	305612	AA782347	Hs.272572	hemoglobin, alpha 2	0.19	0.79
	305614 305616	AA782866	Un 275055	gb:aj09h02.s1 Soares_parathyroid_tumor_N	1.00 7.57	1.00 10.20
	305637	AA782884 AA806124	Hs.275865	ribosomal protein S18 gb:oe29a12.s1 NCI_CGAP_Pr25 Homo sapiens	4.78	12.42
	305639	AA806138		gb:oe29c12.s1 NCI_CGAP_Pr25 Homo sapiens	0.89	0.70
60	305650	AAB07709		gb:nw31e04.s1 NCI_CGAP_GC80 Homo sapiens4	.49	8.71
	305690	AA813477		gb:ai67a05.s1 Soares_testis_NHT Homo sap	4.91	9.40
	305726	AA828156	Hs.73742	ribosomal protein, large, PO	0.19	0.81
	305728	AA828209 AA835353		gb:of34a02.s1 NCI_CGAP_Kid6 Homo sapiens	5.12 1.66	9.29 4.11
65	305759 305792	AA845256		gb:ak72b06.s1 Barstead spleen HPLRB2 Hom gb:ak84a08.s1 Barstead spleen HPLRB2 Hom	2.34	4.25
05	305864	AA864374	Hs.73742	ribosomal protein, large, PO	0.30	1.40
	305901	AA872968	1,0,1,0,1	gb:oh63h08.s1 NCI_CGAP_Kid5 Homo sapiens	2.10	5.21
	305910	AA875981		gb:nx21h02.s1 NCI_CGAP_GC3 Homo sapiens	0.32	1.01
70	306015	AA897116		gb:am08b07.s1 Soares_NFL_T_GBC_S1 Homo s1		1.12
70	306017	AA897221	Hs.109058	ribosomal protein S6 kinase, 90kD, polyp	5.21	7.90
	306020	AA897630 AA906316	Hs.130027	EST gb:ok03g03.s1 Soares_NFL_T_GBC_S1 Homo s	1.96 7.38	6.59 20.69
	306063 306065	AA906725		gb:ok78g02.s1 NCI_CGAP_GC4 Homo sapiens	7.19	13.48
	306104	AA910956		gb:ok85h11.s1 NCI_CGAP_Kid3 Homo sapiens	6.50	9.13
.75	306109	AA911861		gb:og21a07.s1 NCI_CGAP_PNS1 Homo sapiens	4.21	5.25
	306148	AA917409	Hs.288036	tRNA isopentenylpyrophosphate transferas	2.20	270
	306242	AA932805		gb:oo60g04.s1 NCL CGAP_Lu5 Homo sapiens	2.84	5.35
	306288 306325	AA936900 AA953072	Nº SINERE	gb:oi53h05.s1 NCI_CGAP_HN3 Homo sapiens	1.60 1.65	1.12 2.26
80	306353	AA961382	Hs.210546 Hs.275865	interleukin 21 receptor ribosomal protein S18	3.78	6.32
-	306375	AA968650	Hs.276018	EST, Moderately similar to JC4662 ribos	4.30	5.74
	306396	AA970223		gb:op09d05.s1 NCI_CGAP_Kid6 Homo sapiens	0.95	2.45
	306428	AA975110	Hs.191228	hypothetical protein FLJ20284	3.19	4.10
85	306442	AA976899		gb:oq35e09.s1 NCI_CGAP_GC4 Homo sapiens	4.67 3.92	7.44 6.27
0J	306446	AA977348		gb:oq72e12.s1 NCI_CGAP_Kid6 Homo saplens	3.92	6.27

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	306458	AA978186		gb:op33c06.s1 Soares_NFL_T_GBC_S1 Homo s	3.35	5.77
	306467	AA983508	Hs.163593	ribosomal protein L18a	3.72	5.37
	306510	AA988546		gb:or84d07.s1 NCI_CGAP_Lu5 Horno saptens	1.00	1.00
	306555	AA994304	Hs.276083	EST, Wealthy similar to RL23_HUMAN 60S R	6.61	10.91
5	306557	AA994530		gb:ou57e08.s1 NCI_CGAP_Br2 Homo sapiens	16.20	31.83
-	306572	AA995685		gb:os25c12.s1 NOI_CGAP_Kid5 Homo sapiens	2.51	6.52
	306582	AA996248		gb:os18c10.s1 NCI_CGAP_Kid5 Homo sapiens	1.42	3.13
	306598	Al000320	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.91	8.68
	306605	Al000497	Hs.119500	ribosomal protein, large P2	1.96	8.60
10	306656	At004024		about 1607 x1 Soares_NFL_T_GBC_S1 Homo s	0.11	0.45
	306676	AI005603	Hs.284136	PRO2047 protein	9.56	17.28
	305686	AI015615		gb:ov29f10.x1 Soares_testis_NHT Homo sap	1.86	3.60
	306702	AI022565	Hs.307670	EST	1.47	1.19
	306728	AI027359	Hs.272572	hemoglobin, alpha 2	1.28	2.83
15	306751	At032589	100010012	gbzw70h12s1 Soares_fetal_fiver_spleen_	3.91	5.21
13	305757	A1038963	Hs.249118	ESTs	3.33	6.06
	306892	A1092465	155,245110	gb:qa75h12x1 Soares_fetal_heart_NbHH19W	3.77	7.46
	306897	A1093967		gb:qa33c06.s1 Soares_NhHMPu_S1 Homo sapi	2.12	2.85
	306956	Al125111		gb:am66f03.s1 Barstead spleen HPLRB2 Hom	6.10	10.52
20	306958	Al125152		gb:am55e09.x1 Johnston frontal cortex Ho	1.72	1.56
20	307035	A1142774	Hs.119122	ribosomal protein L13a	2.00	4.70
	307041	Al144243	113.113122	gb:qb85b12.x1 Soares_fetal_heart_NbHH19W	9.12	12.56
		AI167439		gb:ox70h06.s1 Soares_NhHMPu_S1 Homo sapi	4.88	8.52
	307091			gb:pc99g06.x1 Soares_pregnant_uterus_NbH	3.55	6.44
25	307181	Al189251	Hs.111334	ferrifin, light polypeptide	2.46	4.65
23	307297	AI205798			5.64	10.13
	307317	Al208303	Hs.147333	EST CDC8 colfoca	3.18	5.15
	307327	AI214142	Hs.246381	CD68 antigen	2.02	3.73
	307382	Al223158	Hs.147885	ESTs	0.72	0.48
20	307410	A1241715	Hs.77039	ribosomal protein S3A	2.38	3.51
30	307415	AI242118	11 470	gb:gh92b02.x1 Soares_NFL_T_GBC_S1 Homo s	2.60	5.44
	307423	Al243206	Hs.179573	collagen, type I, alpha 2	3.18	7.67
	307426	A1243364		gb:qh30g11x1 Soares_NFL_T_GBC_S1 Homo s		1.00
	307517	A1275055		gb:ql72d03.x1 Soares_NhHMPu_S1 Homo sapi	1.00	11.20
25	307551	Al281556		gb:qu52f11.x1 NCI_CGAP_Lym6 Homo sapiens	3.40	15.51
35	307561	AJ282207		gh:qp65a12.x1 Soares_fetal_lung_NbHL19W	4.74	
	307608	Al290295		gb:qm01f02.x1 Soares_NhHMPu_S1 Homo sapi	3.50	7.19
	307657	AJ306428	Hs.298262	ribosomal protein S19	1.76	2.44
	307691	Al318285		gb:tb17b01.x1 NCI_CGAP_Ov37 Homo sapiens	1.59	1.31
40	307701	Al318583	Hs.276672	EST, Weakly similar to RL6_HUMAN 60S RI	1.90	2.13
40	307718	AJ333406	Hs.83753	small nuclear ribonucleoprotein polypept	0.45	0.99
	307730	Al336092		gb:qt43b07.x1 Soares_fetal_lung_NbHL19W	1.51	0.99
	307760	AJ342387		gb:qt27f07.x1 Soares_pregnant_uterus_NbH	1.00	1.00
	307764	Al342731		gb:qo26a07.x1 NCI_CGAP_Lu5 Homo sapiens	4.52	12.58
4.5	307783	A1347274		gb:tc05d02_x1 NCI_CGAP_Co16 Homo sapiens	1,42	1.00
45	307796	A1350556		gb:qt18i09.x1 NCl_CGAP_GC4 Homo sapiens	6.57	9.61
	307807	Al351799		gb:q109d02.x1 NCI_CGAP_GC4 Homo sapiens	3.38	7.68
	307808	Al351826		gb:qt09g03.x1 NCI_CGAP_GC4 Homo sapiens	0.33	0.86
	307820	Al355761		gb:ql94a11.x1 NCI_CGAP_Co14 Homo sapiens	7.94	21.57
	307830	Al358722	Hs.276737	EST, Weakly similar to R5HU22 ribosomal	2.05	3.32
50	307852	Al365541		gb:qz08g05.x1 NCI_CGAP_CLL1 Homo sapiens	3.18	5.21
	307902	AI380462		gb:tg02h05.x1 NCI_CGAP_CLL1 Homo sapiens	3.13	4.99
	307997	AI434512	Hs.181165	eukaryotic translation elongation factor	1.00	3.01
	308002	AI435240	Hs.283442	ESTs	5.86	12.64
	308011	A1439473		gb:ti60a08.x1 NCI_CGAP_Lym12 Homo sapien	3.79	5.83
55	308023	A1452732	Hs.251577	hemoglobin, alpha 1	0.38	0.88
	308041	Al458824	Hs.169476	glyceraldehyde-3-phosphale dehydrogenase	4.36	6.06
	308059	AJ468938	Hs.276877	EST, Weakly similar to RL10_HUMAN 60S R	1.80	1.98
	308085	Al474135	Hs.181165	eukaryotic translation etongation factor	3.38	4.14
	308101	A1475950	Hs.181165	eukaryotic translation elongation factor	1.30	3.87
60	308106	A1476803		gb:tj77e12.x1 Soares_NSF_F8_9W_OT_PA_P_S2	38	8.72
	308122	A1480123	Hs.309411	EST	2.70	3.86
	308154	Al500600		gb:tn93d08.x1 NCI_CGAP_Ut2 Homo sapians	0.66	1.33
	308171	A1523632	Hs.298766	ESTs, Weakly similar to schlafen4 [M.mu	2.48	4.86
~-	308211	Al557029	Hs.278572	anaplastic lymphoma kinase (Ki-1)	2.43	2.14
65	308213	Al557041		gb:PT2.1_12_E04.r tumor2 Homo sapiens cD	3.34	3.79
	308216	Al557135		gb:PT2.1_13_H06.r tumor2 Homo sapiens cD	4.61	4.78
	308219	AL557246		gb:PT2.1_15_D07.r tumor2 Homo sapiens cD	4.87	7.94
	308271	AI567844	Hs.252259	ribosomal protein S3	2.40	6.35
	308319	AI583983	Hs.181165	eukaryotic translation elongation factor	2.45	3.33
70	308362	Al613519	Hs.105749	KIAA0553 protein	1.24	1.41
	308413	A1636253	Hs.196511	ESTs	3.16	4.82
	308450	AI650860	Hs.96840	KIAA1527 protein	1.79	2.68
	308464	A)672425	Hs.277117	EST, Moderately similar to 138055 myosi	4.87	8.27
	308588	AJ718299		gb:as51g12.x1 Barstead aorta HPLRB6 Homo	3.90	5.64
75	308599	AJ719893		gb:as47d07.x1 Barstead aorta HPLRB6 Homo	3.32	5.12
	308615	A1738593	Hs.101774	hypothetical protein FLJ23045	3.11	2.36
	308643	A1745040		gb:tr19a12.x1 NCI_CGAP_Ov23 Homo sapiens	3.98	3.69
	308673	AI760864		gb:wi09c10.x1 NCI_CGAP_CLL1 Homo sapiens	0.82	0.99
~~	308697	A1767143		gb:wi97a07.x1 NCI_CGAP_Kid12 Homo sapien	2.76	5.59
80	308762	Al807405	Hs.259408	ESTs .	3.17	6.30
	308778	AI811109		gb:tr04c11.x1 NCI_CGAP_Ov23 Homo sapiens	1.00	1.00
	308782	AI811767	Hs.2186	eukaryotic translation elongation factor	2.94	5.15
	308808	AI818289		gb:wk52c01.x1 NCI_OGAP_Pr22 Homo saplens	4.41	8.34
0.5	308823	Al824118	Hs.217493	annexin A2	1.85	1.92
85	308875	AI832332		gb:at48g03.xt 8arstead colon HPLR87 Homo	2.52	3.B0

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	308879	AI832763	Hs.75968	thymosin, beta 4, X chromosome	3.38	7.96
	308886	A1833240		ghtat76d10.x1 Barstead colon HPLRB7 Homo	3.06 2.45	2.65 3.44
	308898 308934	A1858845 A1865023	Hs.177	gb:w/32d10.x1 NCI_CGAP_Ut1 Homo sapiens phosphatidylinositol gtycan, class H	4.14	6.76
5	308966	A1870704		gb:wf47h01.x1 NOI_CGAP_Ut1 Homo saplens	1.00	1.00
	308979	AI873111		gb:wi52h05.x1 NCI_CGAP_Bm25 Homo sapien	7.15 0.61	11.10 0.59
	309045 309051	AJ910902 AJ911975		gb:tq39f01.x1 NCI_CGAP_Ut1 Homo sapiens gb:wd78d01.x1 NCI_CGAP_Lu24 Homo sapiens	1.78	4.42
	309069	AI917366	Hs.78202	SWI/SNF related, matrix associated, act	3.27	5.88
10	309083	Al922426	Hs.119598	ribosomal protein L3	2.39 5.54	3.34 17.78
	309105 309122	Al925503 Al928178	Hs.265884	gb:wo95a11.x1 NCI_CGAP_Kid11 Homo sapien	1.00	2,92
	309128	Al928816	Hs.180842	ribosomal protein L13	1.38	5.55
1.5	309164	Al937761		gb:wp84b09.x1 NCI_CGAP_Bm25 Homo sapien	2.43	3.11
15	309177	Al951118	U- 20042E	gbnex63g05.x1 NCI_CGAP_Br18 Homo sapiens ESTs	0.81 4.86	0.97 7.46
	309288 309299	Al991525 AW003478	Hs.299426	gh:wq66c06.x1 NCI_CGAP_GC6 Homo sapiens	4.36	9.43
	309303	AW004823		gb.ws93a08.x1 NCI_CGAP_Co3 Homo sepiens	2.88	7.54
20	309411	AW085201	Hs.244144	EST	4.30 2.49	7.14 3.11
20	309437 309459	AW090702 AW117645	Hs.278242 Hs.65114	tubulin, alpha, ubiquitous keratin 18	2.88	4.55
	309476	AW129368		gboxe14b05.x1 NCI_CGAP_Ut4 Homo sapiens	2.08	6.60
	309499	AW136325	Hs.279771	Homo sapiens clone PP1596 unknown mRNA	2.82 4.78	3.55 3.95
25	309529 309532	AW150807 AW151119	Hs.181357	taminin receptor 1 (67kD, ribosomal pro gbcxg33e10.x1 NCI_CGAP_Ut1 Homo sapiens	1.18	4.40
23	309626	AW192004	Hs.297681	serine (or cysteine) proteinase inhibit	4.46	12.06
	309641	AW194230	Hs.253100	EST, Moderately similar to GHHU Ig gamm	1.47	1.39
	309675	AW205681	Hs.253506	EST, Moderately similar to ATPN_HUMAN A laminin receptor 1 (67kD, ribosomal prol	5.68 1.00	15.20 1.00
30	309693 309695	AW237221 AW238011	Hs.181357 Hs.295605	mannosidase, alpha, class 2A, member 2	5.45	9.61
50	309700	AW241170	Hs.179661	tubulin, beta polypeptide	1.41	1.25
	309747	AW264889		gb:xq35h02.x1 NCI_CGAP_Lu28 Homo sapiens	5.00 5.76	8.35 11.90
	309769 309782	AW272346 AW275156	Hs.156110	gbcs13c10.x1 NCI_CGAP_Kid11 Homo sapien immunoglobulin kappa constant	0.42	0.69
35	309783	AW275401	Hs.254798	EST	1.00	4.11
	309799	AW276964		gb:xp58h01.x1 NC1_CGAP_Ov39 Homo sapiens	1.68	1.44
	309866	AW299916 AW339071	Hs.300697	gb:xs44c01.x1 NCI_CGAP_Kid11 Homo sapien immunoglobulin heavy constant gamma 3 (G	3.02 1.05	5.04 1.18
	309903 309923	AW340684	16,00001	gb:hd05g08.x1 Soares_NFL_T_GBC_S1 Homo s	2.30	3.67
40	309928	AW341418		gb:hd08c03.x1 Soares_NFL_T_GBC_S1 Homo s	7.41	13.71
	309931	AW341683		gb:hd13d01.x1 Soares_NFL_T_GBC_S1 Homo s gb:hb73f10.x1 NCL_CGAP_Ut2 Homo sapiens	1.20 4.90	12.70 18.29
	309933 309964	AW341936 AW449111	Hs.257111	hypothetical prolein MGC3265	1.99	3.07
	310002	A1439096	Hs.323079	Homo sapiens mRNA; cDNA DKFZp564P116 (fr	0.20	0.47
45	310096	AW136822	Hs.172824	ESTs, Weakly similar to 848013 proline-r	1.51 0.31	1.22 0.76
	310098 310109	AI685841 AI203094	Hs.161354 Hs.148633	ESTs ESTs	2.06	5.83
	310112	AW197233	Hs.147253	ESTs	2.92	3.55
50	310115	AI611317	Hs.223796	ESTs	1.25	0.84 2.71
50	310121 310146	AW195642 Al206614	Hs.148901 Hs.197422	ESTs ESTs	1.00 9.50	15.31
	310193	Al627653	Hs.147562	ESTs	2.85	4.18
	310255	AW450439	Hs.153378	ESTs	4.26	10.63
55	310261 310264	Al240483 · Al915771	Hs.201217. Hs.74170	ESTs metallothionein 1E (functional)	3.28 0.26	4.40 0.86
55	310204	AJ242102	Hs.213636	ESTs	5.43	8.19
	310282	AI243332	Hs.156055	ESTs	3.15	8.06
	310290	AW013815	Hs.149103 Hs.145402	ESTs	2.19 1.17	3.12 1.91
60	310333 310346	Al253200 Al261340	Hs.145402	ESTs ESTs	4.81	9.95
•	310385	AI263392	Hs.156151	ESTs	5.96	7.79
	310443	AW119018	Hs.164231	ESTs	2.90	4.63
	310444 310446	AW196632 AJ275715	Hs.252956 Hs.145926	ESTs ESTs	0.85 2.18	1.01 3.85
65	310468	AI984074	Hs.196398	ESTs	3.39	5.19
	310477	Al948801	Hs.171073	ESTs	1.00	1.00
	310512 310514	AW275603 AIS81145	Hs.200712 Hs.160724	ESTs ESTs	3.87 3.30	8.12 7.33
	310524	AW082270	Hs.12496	ESTs, Highly similar to AC004836 1 simil	0.72	1.44
70	310547	Al302654	Hs.208024	ESTS	3.26	3.46
	310584 310608	AI653007	Hs.156304	ESTs ESTs	2.39 5.60	4.08 6.49
	310624	Al962234 Al341594	Hs.198102	gb:Human endogenous retrovirus H proteas	4.91	9.09
75	310636	AI814373	Hs.164175	ESTs	1.85	1.71
75	310648	A1347863	Hs.156672	ESTs Homo sapiens mRNA full length insert cON	0.17 5.40	0.69 13.22
	310694 310695	A1654370 A1472124	Hs.157752 Hs.157757	ESTs	4.82	6.27
	310714	AJ418446	Hs.157882	ESTs	1.76	3.51
90	310722	A1989803	Hs.157289	ESTs	1.14 8.46	6.85 13.01
80	310756 310764	Al916560 Al376769	Hs.158707 Hs.167172	ESTs ESTs	4.76	7.37
	310848	AI459554	Hs.161286	ESTs	2.84	1.96
	310851	AW291714	Hs.221703	ESTs	1.00	2.32
85	310854 310858	AI421677 AI871000	Hs.161332 Hs.161330	ESTs ESTs	6.37 6.07	7.94 9.84
55	310000	WALL 1990	15.101330	-013		

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	310864	A1924558	Hs.151399	ESTs	0.87	0.78
	310875 310896	T47764	Hs.132917 Hs.270982	ESTs ESTs, Moderately similar to ALU7_HUMAN A	1.00 7.07	3.63 16.68
	310922	AW157731 AW195634	Hs.170401	ESTs	1.00	1.00
5	310955	A1560210	Hs.263912	ESTs	10.08	17.66
	310957	AV/190974	Hs.196918	ESTs	2.18	3.18
	311000	A1521830	Hs.171050 Hs.241097	ESTs ESTs	3.06 1.23	6.64 3.77
	311012 311034	AW298070 A1564023	Hs.311389	ESTs, Moderately similar to PT0375 natur	2.44	2.09
10	311074	AW290922	Hs.199848	ESTs	6.04	14.19
	311134	A1990849	Hs_198971	ESTs	3.54	6.96
	311174	AW450552	Hs.205457	periaxin ESTs	0.65 2.46	0.95 2.78
	311187 311220	A1638374 A1656040	Hs.224189 Hs.196532	ESTS	1.10	2.52
15	311230	AI989808	Hs.197663	ESTs	1.41	1.75
	311236	A1653378	Hs.197674	ESTs	2.18	211
	311242 311258	AW016812 Al671221	Hs.200266 Hs.199887	ESTs ESTs	0.63 1.00	5.11 1.41
	311277	AW072813	Hs.270868	ESTs, Moderately similar to ALU4_HUMAN A	2.56	1.94
20	311294	AA826425	Hs.291829	ESTs	1.04	2.69
	311308	F12664	Hs.49000	ESTs	1.96 4.77	6.70 9.38
	311351 311390	A1682303 AW392997	Hs.201274 Hs.202280	ESTs ESTs	2.80	6.06
	311405	AW290961	Hs.201815	ESTs	3.80	11.66
25	311409	A1698839		gb:wd31f02_x1 Soares_NFL_T_G8C_S1 Homo s	3.84	6.94
	311420	AI936291	Hs.209867	ESTS	5.30 4.39	12.56 6.09
	311443 311457	AI791521 AI934909	Hs.192206 Hs.175377	ESTs ESTs	1.00	1.04
	311479	AI933672	Hs.211399	ESTs	2.76	5.61
30	311488	R57390	Hs.301064	arfaptin 1	2.50	5.73
	311495	AW300077	Hs.221358 Hs.210303	ESTs . ESTs	3.63 2.00	6.09 2.87
	311511 311534	AW444568 AW130351	Hs.243549	ESTS	0.31	1.33
	311537	AI805121	Hs.211828	ESTs	3.69	5.85
35	311543	AI681360	Hs.201259	ESTs	1	- 1.34 6.12
	311551 311557	AW449774 Al819230	Hs.296380 Hs.211238	POM (POM121 rat homolog) and ZP3 fusion interleukin-1 homolog 1	3.31 1.00	1.00
	311558	Z44432	Hs.63128	KIAA1292 protein	2.25	3.41
.40	311559	AW008271	Hs.265848	similar to rat myomegalin	2.68	5.90
40	311563	Al922143	Hs.211334	ESTS	2.39 2.47	3.32 3.85
	311586 311616	A1827834 AW450675	Hs.211227 Hs.212709	ESTs .	1.00	1.00
	311621	Al924307	Hs.213464	ESTs	4.16	6.74
45	311635	AI928456	Hs.213081	ESTs	2.17 2.60	3.76 3.12
43	311668 311672	AW193674 R11807	Hs.240044 Hs.20914	ESTs hypothetical protein FLJ23056	2.79	5.18
	311683	AW183738	Hs.232644	ESTs	0.19	0.96
	311700	R49601	Hs.171495	relinoic acid receptor, beta ESTs, Weakly similar to CIKG_HUMAN VOLTA	6.28 5.00	8.83 8.17
50	311714 311735	AW131785 AW294416	Hs.246831 Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	0.96	0.72
•	311743	T99079	Hs.191194	ESTs	1.00	1.95
	311783	AI682478	Hs.13528	hypothetical protein FLJ14054	0.16	0.77
	311785 311799	AI056769 AA780791	Hs.133512 Hs.14014	ESTs ESTs, Weakly similar to KIAA0973 protein	1.34 8.52	3.97 13.32
55	311819	AW265275	Hs.254325	ESTs	3.58	3.91
	311823	A1089422	Hs.131297	ESTs	1.40	1.72
	311877	AA349893	Hs.85339	G protein-coupled receptor 39	0.95 0.88	0.91 0.87
	311886 311896	AA522738 AW206447	Hs.132554	ESTs gb:UI-H-BI1-afg-g-02-0-UI.s1 NCI_CGAP_Su	1.66	1.13
60	311910	N28365	Hs.22579	Homo sapiens clone CDABP0036 mRNA sequen	1.66	2.30
	311923	T60843	Hs.189679	ESTs	0.42	2.63
	311933	Al597963	Hs.118726 Hs.124733	ESTs ESTs	1.88 2.02	3.02 2.33
	311959 311960	T67262 AW440133	Hs.189690	ESTs	3.87	6.62
65	311967	Al382726	Hs.182434	ESTs	5.80	8.14
	311975	AA804374	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	0.98	3.26
	312005 312028	178450 178886	Hs.13941 Hs.284450	ESTs ESTs	0.12 3.78	1.39 4.92
	312026	Al580018	Hs.268591	ESTs	4.11	7.32
70	312056	T83748	Hs.268594	ESTs	2.36	3.08
	312064	AA676713	Hs.191155	ESTS	3.34 1.60	5.28 1.15
	312088 312093	AW303760 T91809	Hs.13685 Hs.121296	ESTs ESTs	0.68	0.85
	312094	Z78390		gb:HSZ78390 Human fetal brain S. Meier-E	3.05	4.48
75	312097	AI352096	Hs.112180	zinc finger protein 148 (pHZ-52)	4.52	9.70
	312118 312128	T85332 A1052609	Hs.178294 Hs.17631	ESTs Homo sapiens cDNA FLJ20118 fis, clone CO	2.40 2.39	2.60 3.53
	312147	T89855	Hs.17651	ESTs	0.67	1.03
00	312175	AA953383	Hs.127554	ESTs	5.85	10.60
80	312179	AI052572	Hs.269864	ESTs	2.41 0.24	3.32 0.89
	312201 312207	Al928365 H90213	Hs.91 139 Hs.191330	solute carrier family 1 (neuronal/epithe ESTs	2.20	4.55
	312220	N74613		gb:za55a07.s1 Soares fetal liver spleen	4.28	11.13
95	312252	Al128388	Hs.143655	ESTs	1.64	1.57
85	312304	AA491949	Hs.269392	ESTs	0.12	2.47

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	312318	AV/235092	Hs.143981	ESTs	3.46	5.69
	312319	AA216698	Hs.180780	TERA protein	5.78	4.46
	312321	R66210	Hs.186937	ESTs	0.44	1.74
5	312331	AA825512	Hs.289101	glucose regulated protein, 58kD	3.73 3.07	5.96 0.95
,	312339 312363	AA524394 Al675558	Hs.165544 Hs.181867	ESTs ESTs	10.08	16.73
	312375	A1375096	Hs.172405	cell division cycle 27	2.78	3.71
	312376	R52089	Hs.172717	ESTs	1.00	1.00
	312389	AI863140	•	gbtz43h12.x1 NCI_CGAP_Bm52 Homo sapien	2.37	3.98
10	312437	AA995028		gb:RC4-BT0629-120200-011-b10 BT0629 Homo	4.06	5.41
	312440	AI051133	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	1.00	1.00
	312451	R59989	Hs.176539	ESTs	4.96 1.11	10.04 1.00
	312458	A1167637 A1168177	Hs.145924 Hs.143653	ESTs ESTs	5.89	8.24
15	312507 312520	AI742591	Hs.205392	ESTs	3.30	8.92
13	312548	A1566228	Hs.159426	hypothetical protein PRO2121	1.38	1.65
	312564	H21520	Hs.35088	ESTs	0.40	0.77
	312583	Al193122	Hs.124141	ESTs	0.13	0.94
20	312599	AI865073	Hs.125720	ESTs	3.75 6.78	5.29 12.93
20	312602	AA046451	Hs.165200 Hs.193007	ESTs ESTs	0.38	1.13
	312645 312666	H52121 AI240582	Hs.214578	ESTs	0.98	2.03
	312689	AW450461	Hs.203965	ESTs	0.21	0.61
	312817	H75459	Hs.233425	ESTs	1.51	0.85
25	312846	AW152104	Hs.200879	ESTs	8.93	13.78
	312873	AI690071	Hs.283552	ESTs, Wealdy similar to unnamed protein	4.20 2.57	6.23 3.15
	312893 312902	Al016204 AW292797	Hs.172922 Hs.130316	ESTs ESTs, Wealdy similar to T2D3_HUMAN TRANS	1.19	0.71
	312925	N90868	Hs.271695	ESTs	2.50	4.25
30	312936	AI681581	Hs. 121525	ESTs	1.00	1.17
	312975	AI640506	Hs.293119	ESTs, Wealty similar to ALU7_HUMAN ALU S	2.30	4.80
	312978	N24887	Hs.292500	ESTs	0.80	1.05
	312980	AA497043	Hs.115685	ESTs	3.12 2.03	3.60 2.13
35	312984	N25871	Hs.177337	ESTs ESTs	5.52	8.42
33	313000 313029	Al147412 AA731520	Hs.146657 Hs.170504	ESTs .	0.96	1.39
	313039	Al419290	Hs.149990	ESTs, Weakly similar to unnamed protein	6.48	13.20
	313049	AW293055	Hs.119357	ESTs	6.44	10.73
40	313056	Al651930	Hs.135684	ESTs	1.51	2.04
40	313058	D81015	Hs.125382	ESTs	0.25 8.56	1.50 11.60
	313070	AI422023	Hs.161338 Hs.204339	ESTs ESTs	3.72	4.56
	313097 313130	Al676164 AW449171	Hs.168677	ESTs	3.28	5.06
	313136	N59284	Hs.288010	ESTs	0.49	1.36
45	313153	AI240838	Hs.132750	ESTs	5.36	5.52
	313210	N74077	Hs.197043	ESTs	0.30	0.66
	313236	AW238169	Hs.83513	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.16	8.76 3.87
	313239	W19632 N93466	Hs.124170 Hs.121764	ESTs ESTs, Wealdy similar to testicular teldi	1.00 0.74	2.06
50	313265 313267	AI770008	Hs.129583	ESTs	0.23	1.30
J 0	313275	AI027604	Hs.159650	ESTs	6.68	9.57
	313290	AI753247	Hs.29643	Homo sapiens cDNA FLJ 13103 fis, clone NT	1.34	1.07
	313292	AJ362991	Hs.202121	ESTs, Weakly similar to env protein (H.s	2.00	4.32
55	313325	AJ420611	Hs.127832	ESTs	1.20 4.02	2.27 5.33
75	313357 313393	AW074848 AJ674685	Hs.201501 Hs.200141	ESTs ESTs	1.36	2.84
	313399	AW376889	Hs.194097	ESTs	2.58	5.26
	313414	Al241540	Hs.132933	ESTs	6.57	15.07
	313417	AA741151	Hs.137323	ESTs	0.63	3.01
60	313457	AA576052	Hs.193223	Homo sapiens cDNA FLJ11646 fis, clone HE	2.78	4.70
	313499	AI261390	Hs.146085	KIAA1345 protein	0.91 3.41	2.37 7.08
	313516 313556	AA029058 AA628517	Hs.135145 Hs.118502	ESTs ESTs	0.23	0.70
	313569	Al273419	Hs.135146	hypothetical protein FLJ13984	1.88	1.00
65	313570	AA041455	Hs.209312	ESTs	0.73	2,27
	313638	AI753075	Hs.104627	Homo sapiens cDNA FLJ10158 fis, clone HE	1.00	1.72
	313662	AA740151	Hs.130425	ESTs	0.20	1.42
	313671	W49823	Hs.104613	RP42 homolog	1.00 3.46	1.00 5.80
70	313672 313690	AW468891 AI493591	Hs.122948 Hs.78146	ESTs platelet/endothelial cell adhesion motec	0.51	0.97
, 0	313711	AA398070	Hs.133471	ESTs	0.18	1.01
	313723	AA070412		gb:zm68c10.s1 Stratagene neuroepithelium	1.08	1.03
	313726	AJ744687	Hs.257806	ESTs	213	2.99
75	313774	AW136836	Hs.144583	ESTs	1.38	1.19
75	313784	AA910514	Hs.134905 Hs.177043	ESTs ESTs	3.88 0.22	5.78 2.06
	313790 313832	AW078569 AW271022	Hs.177043 Hs.133294	ESTS	1.15	0.91
	313834	AW418779	Hs.114889	ESTs	0.68	3.14
~~	313835	Al538438	Hs.159087	ESTs	5.74	8.88
80	313852	H18633	Hs.123641	protein tyrosine phosphatase, receptor t	0.16	1.14
	313854	AW470806	Hs.275002	ESTs	2.09	4.06
	313865 313871	AA731470 AW471088	Hs.163839 Hs.145950	ESTs ESTs	3.41 5.28	4.09 6.83
	313883	A1949384	110.140000	gb:nu76d01.s1 NCI_CGAP_Alv1 Homo sapiens	2.90	10.91
85	313915	AI969390	Hs.163443	Homo sapiens cONA FLJ11576 fis, clone HE	1.00	1.00

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	313926	AW473830	Hs.171442	ESTS	3.40	4.11
	313948	AW452823	Hs.135268 Hs.13957	ESTs ESTs	5.77 0.46	9.15 0.75
	313978 313983	A1870175 A1829133	Hs.226780	ESTs	4.10	6.40
5	314035	AA164199	Hs.270152	ESTs	5.83	7.90
	314037	AW300048	Hs.275272	ESTs	1.00 7.60	3.79 11.33
	314040 314067	AA166970 AW293533	Hs.118748 Hs.51743	ESTs KIAA1340 protein	1.85	1.21
	314103	AI028477	Hs.132775	ESTs	2.90	5.29
10	314107	AAS06113	Hs.189025	ESTs	2.00	1.66
	314113 314124	AA218986	Hs.118854 Hs.9460	ESTs Homo sapiens mRNA; cDNA DKFZp547C244 (fr	0.91 2.53	4.17 3.32
	314126	AW118745 AA226431	H2.5400	gbmc18b12.s1 NCI_CGAP_Pr1 Homo sapiens	3.13	5.08
	314128	AA935633	Hs.194628	ESTs	2.90	6.35
15	314151	AA236163	Hs.202430	ESTs	4.15	6.45
	314184 314192	AW081795 AW290975	Hs.233465 Hs.118923	ESTs ESTs	3.44 1.00	4.65 1.23
	314244	AL036450	Hs.103238	ESTs	2.88	3.67
20	314253	AA278679	Hs.189510	ESTs	4.98	7.16
20	314262	AW086215	Hs.246096	ESTs	0.38 3.34	1.94 5.66
	314320 314332	AA811598 AL037551	Hs.275809 Hs.95612	ESTs .	2.85	2.09
	314335	AA287443	Hs.142570	Homo saplens clone 24629 mRNA sequence	4.35	4.78
25	314340	AW304350	Hs.130879	ESTs, Moderately similar to putative p15	0.77	0.86
25	314351 314376	AA292275 Al628633	Hs.193746 Hs.324679	ESTs ESTs	3.07 4.10	3.77 6.11
	314443	AA827125	Hs.192043	ESTs	6.20	13.67
	314458	AJ217440	Hs.143873	ESTs	0.58	2.49
20	314466	AA767818	Hs.122707	ESTs .	2.53	2.62
30	314478 314482	A1521173 AL043807	Hs.125507 Hs.134182	DEAD-box protein ESTs	3.94 1.30	5.65 1.44
	314506	AA833655	Hs.206868	Homo sapiens cDNA FLJ14056 fis, clone HE	3.28	3.47
	314519	R42554	Hs.210862	T-box, brain, 1	3.12	6.16
35	314529	AL046412	Hs.202151	ESTs	3.43 1.38	6.87 1.00
33	314546 314562	AW007211 Al564127	Hs.16131 Hs.143493	hypothetical protein FLJ 12876 ESTs	2.29	5.27
	314579	AW197442	Hs.116998	ESTs	3.87	5.75
	314580	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 pro	0.10	0.71 1.40
40	314585 314589	AA918474 AW384790	Hs.216363 Hs.153408	ESTs Homo sapiens cDNA FLJ10570 fis, clone NT	1.08 1.00	1.40
70	314592	AA435761	Hs.192148	ESTs	0.90	2.60
	314603	AA418024	Hs.270670	ESTs	4.56	6.29
	314604	AA946582	Hs.8700	deleted in liver cancer 1	3.42 2.97	3,92 4.55
45	314606 314648	AA418241 AA878419	Hs.188767	eSTs gb:EST391378 MAGE resequences, MAGP Homo:		1.36
	314699	AI038719	Hs.132801	ESTs	3.66	4.97
	314701	A1754634	Hs.131987	ESTs	0.03	0.90
	314710 314750	Al669131 Al095005	Hs.290989 Hs.135174	EST ESTs	3.40 2.80	7.52 6.54
50	314767	AW135412	Hs.164002	ESTs	3.20	4.26
• •	314801	AA481027	Hs.109045	hypothetical protein FLJ10498	1.00	1.00
	314817	Al694139	Hs.192855	ESTs	0.91	0.99
	314835 314852	AJ281370 AJ903735	Hs.76064	ribosomal protein L27a ab:MR-8T035-200199-031 BT035 Homo sapien	5.75 1.68	7.44 4.34
55	314853	AA729232	Hs.153279	ESTs	0.60	1.85
	314940	AW452768	Hs.162045	ESTs	10.10	16.20
	314941	AA515902	Hs.130650	ESTs	0.31 2.18	1.02 0.37
	314943 314955	Al476797 AA521382	Hs.184572 Hs.192534	cell division cycle 2, G1 to S and G2 to ESTs	2.59	3.90
60	314973	AW273128	Hs.300268	ESTs	1.05	1.25
	315004	AA527941	Hs.325351	EST	5.64	13.63
	315006 315033	A1538613 A1493046	Hs.298241 Hs.146133	Transmembrane protease, serine 3 ESTs	0.52 2.46	1.78 1.00
	315035	AI569476	Hs.177135	ESTs	0.34	1.33
65	315056	Al202703	Hs.152414	ESTs	2.10	2.64
	315069	AIB21517	Hs.105866	ESTS	1.00 1.78	1.30 1.00
	315071 315073	AA552690 AW452948	Hs.152423 Hs.257631	Homo sapiens cDNA: FLJ21274 fis, clone C ESTs	1.17	1.52
	315078	AA568548	Hs.190616	ESTs	3.00	3.79
70	315080	AA744550	Hs.136345	ESTs	1.00	1.00
	315120	AA564991 Al025842	Hs.269477 Hs.152530	ESTs ESTs	0.64 0.61	1.44 1.91
	315175 315193	AJ241331	Hs.131765	ESTs	1.06	0.97
75	315196	AA972756	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	0.48	1.96
75	315200	A1808235	Hs.307686	EST	3.76	9.40
	315254 315353	AI474433 AW452608	Hs.179556 Hs.279610	ESTs hypothelical protein FLJ10493	5.37 1.00	9.36 1.30
	315397	AA218940	Hs.137516	fidgelin-like 1	3.38	2.24
00	315403	AW362980	Hs.163924	ESTs	2.04	5.23
80	315431	AA622104	Hs.184838	ESTS	2.36	8.04
	315454 315455	A1239473 AW393391	Hs.156919	gb:qh36f02.x1 Soares_NFL_T_GBC_S1 Homo s ESTs	3.46 3.78	7.64 5.76
	315453	A1681671	Hs.312671	ESTs, Moderately similar to OVCA1	0.89	215
0.5	315483	AW512763	Hs.222024	transcription factor BMAL2	2.32	1.96
85	315526	Al193048	Hs.128685	ESTs	1.67	1.78

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	315530	AI200852	Hs.127780	ESTs	1.05	1.01
	315541	Al168233	Hs.123159	sperm associated antigen 4	0.85	0.56
	315552	AVV445034	Hs.256578	ESTs	1.00	2.22
_	315562	AA737415	Hs.152826	ESTs	2.66	2.48
5	315577	AW513545	Hs.17283	hypothetical protein FLJ10590	2.20	2.25
	315587	Al268399	Hs.140489	ESTs	1.00	1.04 1.05
	315589	AV072387	Hs.158258	Homo sapiens mRNA; cDNA DKFZp434B1272 (f	0.14 7.44	12.56
	315623 315634	AA364078 AA837085	Hs.258189 Hs.220585	ESTs ESTs	0.50	1.40
10	315668	AA912347	Hs.136585	ESTs	0.43	1.22
10	315677	Al932662	Hs.164073	ESTs	0.60	1.39
	315706	AW440742	Hs.155556	hypothetical protein FLJ20202	2.18	3.77
	315707	AJ418055	Hs.161160	ESTs	2.88	2.63
	315730	H25899	Hs.201591	ESTs	0.11	0.60
15	315745	Al821759	Hs.191856	ESTs	3.50	7.25
	315791	AA678177		gbzi15a05.s1 Soares_fatal_liver_spleen_	1.78	2.63
	315801	AA827752	Hs.266134	ESTs	4.31	6.23
	315820	Al652022	Hs.258785	ESTs	2.35	3.01
20	315878	AA683336	Hs.189046	ESTs	2.12	2.64
20	315905	AI821911	Hs.209452	ESTs	1.03 2.63	1.97 5.06
	315923	Al052789 AW276810	Hs.133263 Hs.254859	ESTs ESTs, Moderately similar to ALU5_HUMAN A	1.21	0.85
	315954 315978	AA830893	Hs.119769	ESTs	3.09	3.41
	316001	Al248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	2.20	6.82
25	316011	AW516953	Hs.201372	ESTs	0.35	1.63
	316012	AA764950	Hs.119898	ESTs	6.56	8.13
	316040	Al983409	Hs.189226	ESTs	5.69	10.69
	316048	Al720759	Hs.224971	ESTs	2.84	10.45
• •	316076	AW297895	Hs.116424	ESTs	0.30	1.05
30	316124	Al308862	Hs.167028	ESTs	1.00	1.43
	316151	Al806016	Hs.156520	ESTs	5.80	9.03
	316187	AW518299	Hs.192253	ESTs	1.20	3.96
	316204	AA731509	Hs.120257	ESTs	4.92 1.48	6.94 1.60
35	316232	AW297853	Hs.251203 Hs.292611	ESTs ESTs, Moderately similar to ALU1_HUMAN A	5.86	12.14
33	316275 316291	Al671041 AW375974	Hs. 156704	ESTs	2.73	2.69
	316303	AA740994	Hs.209609	ESTs	1.53	1.26
	316344	AA744518	Hs.120610	ESTs	3.66	8.34
	316346	Al028478	Hs.157447	ESTs	3.51	6.69
40	316365	Al627845	Hs.210776	ESTs	2.50	4.33
	316380	Al393378	Hs.164496	ESTs	1.16	2.16
	316470	AA809902	Hs.243813	ESTs	5.40	10.34
	316509	AA767310	Hs.291766	ESTs	2.46	2.89
45	316514	AA768037	Hs.291671	ESTs .	4.70	6.04
45	316519	A1929097	11- 400000	gb:od10c11.s1 NCI_CGAP_GCB1 Homo sapiens	4.41	9.70
	316609	AW292520	Hs.122082	ESTs ESTs	1.00 2.61	2.89 3.72
	316633 316700	A1125586 AW172316	Hs.127955 Hs.252961	ESTs, Weakty similar to ALU1_HUMAN ALU S	3.46	4.64
	316711	Ai743721	Hs.285316	ESTs, Moderately similar to ALU7_HUMAN A	4.45	6.95
50	316713	AI090671	Hs.134807	hypothetical protein FLJ12057	0.30	2.40
	316715	Al440266	Hs.170673	ESTs, Weakly similar to AF126780 1 retin	0.20	1.45
	316787	AW369770	Hs.130351	ESTs	4.05	5.53
	316809	AA825839	Hs.202238	ESTs	2.25	3.82
E E	316811	AA922060	Hs.132471	ESTs	1.00	1.32
55	316812	AW135045	Hs.232001	ESTs	3.28	4.70
	316818	AA827176	Hs.124316 Hs.124299	ESTs ESTs	0.67 3.53	1.81 6.00
	316824	AAB37416 Al380429	Hs.172445	ESTs	0.72	1.56
	316827 316891	AW298119	Hs.202536	ESTs	1.64	2.97
60	316951	AA134365	Hs.57548	ESTs ·	1.45	1.08
	316970	AA860172	Hs.132406	ESTs	1.00	1.53
	316971	AA860212	Hs.170991	ESTs	1.08	1.96
	316990	AA861611	Hs.130643	ESTs	5.44	10.04
	317001	AJ627917	Hs.233694	hypothetical protein FLJ11350	3.56	4.37
65	317008	AW051597	Hs.143707	ESTs	0.69	1.37
	317051	AA873253	Hs.126233	ESTs	6.18	12.72
	317128	AA971374	Hs.125674	ESTs	1.87	2.66
	317129	H12523	Hs.78521 Hs.125710	Homo sapiens cDNA: FLJ21193 fis, clone C ESTs	4.12 2.82	6.64 5.12
70	317137 317196	AW341567 Al348258	Hs.153412	ESTs	1.98	2.51
70	317212	AI866468	Hs.148294	ESTs	1.86	2.83
	317223	AW297920	Hs.130054	ESTs	0.83	1.57
	317224	D56760	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	2.74	0.86
	317266	AA906289	Hs.203614	ESTs	1.00	1.00
75	317282	AIB07444	Hs.176101	ESTs	2.60	4.21
	317285	AW370882	Hs.222080	ESTs	1.96	3.49
	317302	AA908709	Hs.135564	ESTs	7.16	8.32
	317304	AW449899	Hs.130184	ESTs ESTs	1.38	2.28
80	317320 317413	AA927151 AW341701	Hs.130452 Hs.126622	ESTs ESTs	3.58 2.08	8.13 4.92
00	317413	AA918420	Hs.145378	ESTs	3.06	4.79
	317452	AA972965	Hs.135568	ESTs	4.22	9.21
	317519	AI859695	Hs.126860	ESTs	1.88	4.15
	317521	AI824338	Hs.126891	ESTs	3.12	4.55
85	317529	AI916517	Hs.126865	ESTs	2.73	3.34

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	317570	Al733361	Hs.127122	ESTs	1.00	2.43
	317571	AA938663 AW206035	Hs.199828 Hs.192123	ESTs ESTs	5.20 0.33	11.95 1.56
	317598 317627	Al345110	Hs.132553	ESTs	1.50	1.39
5	317650	Al733310	Hs.127346	ESTs	0.48	1.46
	317659	AA961216	Hs.127785	ESTs	4.18 2.92	7.14 3.20
	317674 317686	AW294909 AA969051	Hs.132208 Hs.187319	ESTs ESTs	1.00	1.01
	317692	Al307659	Hs.174794	ESTs	5.33	9.59
10	317701	AI674774	Hs.128014	ESTs	1.00	1.00
	317711	AI733015	Hs.272189	ESTs ESTs	5.13 2.50	7.81 6.03
	317722 317755	A1733373 AA973667	Hs.128119 Hs.128320	ESTs	1.59	1.30
	317777	Al143525	Hs.47313	KIAA0258 gene product	1.00	2.48
15	317799	Al498273	Hs.128808	ESTs	1.78	211
	317803 317821	AA983251 Al368158	Hs.128899 Hs.70983	ESTs PTPL1-associated RhoGAP 1	0.80 0.17	1.06 0.68
	317848	AI820575	Hs.129086	Homo sapiens cDNA FLJ12007 fis, clone HE	5.30	8.16
••	317850	N29974	Hs.152982	hypothetical protein FLJ13117	1.30	2.28
20	317861	AW341054	Hs.129119	ESTs	2.18 4.48	5.93 8.20
	317865 317869	Al298794 AVV295184	Hs.129130 Hs.129142	ESTs deoxyribonuclease II beta	0.44	0.99
	317881	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	4.06	2.23
25	317890	Al915599	Hs.129225	ESTs	4.68	7.48
25	317899	A1952430	Hs.150614	ESTs, Weakly similar to ALU4_HUMAN ALU S ESTs, Weakly similar to T12545 hypotheti	3.14 0.28	3.37 1.66
	317986 318001	AJ005163 AW235697	Hs.201378 Hs.130980	ESTs. Weakly Surman to 112545 hypothesi	5.12	9.97
	318016	AI016694	Hs.256921	ESTs	1.86	4.50
••	318023	AW243058	Hs.131155	ESTs	2.92	5.22
30	318054	AW449270	Hs.232140	ESTs	3.92 1.21	6.37 1.27
	318068 318117	AJ024540 AJ208304	Hs.131574 Hs.250114	ESTs ESTs	0.86	1.17
	318187	A1792585	Hs.133272	ESTs, Weakly similar to ALUC_HUMAN !!!!	5.90	6.98
	318223	A1077540	Hs.134090	ESTs	1.05	0.90
35	318240	AJ085377	Hs.143610	ESTs	3.10 0.02	2,40 1.05
	318255 318266	AJ082692 AJ554341	Hs.134662 Hs.271443	ESTs ESTs	6.12	10.55
	318330	Al093840	Hs.143758	ESTs	4.98	7.90
	318369	Al493501	Hs.170974	ESTs	2.46	5.62
40	318428	AI949409	Hs.194591	ESTs	0.77	0.45 4.92
	318458	AI149783 AI151395	Hs.158438 Hs.144834	ESTs ESTs	3.54 4.56	5.62
	318467 318473	A1939339	Hs.146883	ESTs	2.08	4.05
	318476	Al693927	Hs.265165	ESTs	4.22	8.07
45	318487	A)167877	Hs.143716	ESTs	1.47	1.05
	318488 318491	AJ217431 - T26477	Hs.144709 Hs.22883	ESTs ESTs, Weakly similar to ALU8_HUMAN ALU S	1.40 1.84	4.14 1.90
	318499	T25451	163.22000	gb:PTHI188 HTCDL1 Homo sapiens cDNA 5/3	2.58	5.20
	318537	AA377908	Hs.13254	ESTs	3.26	4.18
50	318538	N28625	Hs.74034	Homo sapiens clone 24651 mRNA sequence	0.35 3.22	1.07 4.60
	318547 318552	R20578 R18364	Hs.90431 Hs.90363	ESTs ESTs	4.87	9.06
	318575	R55102	Hs.107761	ESTs, Weakly similar to unnamed protein	1.91	1.98
	318580	T34571	Hs.49007	poly(A) polymerase alpha	2.74	6.22
55	318587	AA779704	Hs.168830	Homo saptens cDNA FLJ12136 fis, clone MA	0.85	2.46
	318596 318622	AJ470235 T48325	Hs.172698 Hs.237658	EST apolipoprotein A-II	4.88 4.80	4.93 12.51
	318629	N25163	Hs.8861	ESTs	0.39	1.04
	318637	AA243539	Hs.9196	hypothetical protein	1.72	3.57
60	318648	T77141	Hs.184411	albumin	6.27 3.00	9.91
	318650 318671	AA393302 AA188823	Hs.176626 Hs.299254	hypothetical protein EDAG-1 Homo sapiens cDNA: FLJ23597 fis, clone L	3.96 1.53	8.84 0.81
	318679	T58115	Hs.10336	ESTs	1.00	2.19
	318711	Al936475	Hs.101282	Homo sapiens cDNA: FLJ21238 fis, clone C	3.05	3.18
65	318725	AI962487	Hs.242990	ESTs	1.08	2.46
	318728	Z30201 NM_002543	Hs.291289	ESTs, Weakly similar to ALU1_HUMAN ALU S oxidised low density lipoprotein (lectin	0.77 0.25	1.33 1.49
	318740 318776	R24963	Hs.23766	ESTs	1.00	3.01
	318784	H00148	Hs.5181	proliferation-associated 2G4, 38kD	2.70	3.86
70	318816	F07873	Hs.21273	ESTs	3.90	7.13
	318865 318879	H10818 R56332	Hs.18268	gb:ym04f10.r1 Soares infant brain 1NIB H adenylate kinase 5	2.25 1.78	3.56 5.00
	318881	Z43224	Hs.124952	ESTs	4.79	14.13
25	318894	F08138	Hs.7387	DKFZP564B116 protein	5.31	7.00
75	318901	AW368520	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	1.03	0.91
	318925 318936	Z43577 Al219221	Hs.21470 Hs.308298	ESTs ESTs	2.23 1.86	3.80 7.16
	318982	Z44140	Hs.269622	ESTS	5.84	9.79
00	318986	Z44186	Hs.169161	ESTs, Highly similar to MAON_HUMAN NADP-	1.00	1.00
80	319041	Z44720	Hs.98365	ESTs, Weakly similar to weak similarity	3.38	6.11
	319103	H05896	Hs.4993	KIAA1313 protein putative selenocysteine lyase	1.00 3.79	1.07 5.03
	319170 319198	R13678 F07953	Hs.285306 Hs.16085	putative G-protein coupled receptor	1.00	2.98
	319199	F07361	Hs.13306	ESTs	3.53	5.66
85	319242	F11472	Hs.12839	ESTs	5.87	7.26

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	319263	T65331	Hs.81360 .	Homo sapiens cDNA: FLJ21927 fis, clone H	1.81	1.57
	319267	F11802	Hs.6818	ESTs	1.10	4.72
	319270	R13474	Hs.290263	ESTs	4.80	10.40
5	319279 319282	T65094 AA461358	Hs.12677 Hs.12876	CGI-147 protein ESTs	1.50 1.00	2.11 1.00
,	319269	W07304	Hs.79059	transforming growth factor, beta recepto	0.18	0.68
	319291	W86578	Hs.285243	hypothetical protein FLJ22029	0.26	0.62
	319293	F12119	Hs.12583	ESTs	3.13	4.50
	319312	Z45481		gb:HSC2QE041 normalized infant brain cDN	1.10	1.00
10	319370	H54254	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	0.16	0.73
	319391	R06304	Hs.13911	ESTs	1.26	2.43
	319395	H67130	Hs.301743 Hs.191196	ESTs	0.70 2.45	0.76 3.59
	319398 319407	AA359754 R05329	HS. 191190	ESTs gb;ye91b04.r1 Soares fetal liver spleen	2.00	3.54
15	319425	T82930		gb:yd39:07.r1 Soares fetal liver spleen	4.28	8.81
	319433	R06050	Hs.191198	ESTs	6.15	14.13
	319437	AA282420	Hs.111991	ESTs, Wealthy shrillar to Y48A5A.1 [C.eleg	3.26	5.68
	319466	AI809937	Hs.116417	ESTs	1.76	5.65
20	319471	R06546	Hs.19717	ESTs	4.29	4.84
20	319480	R06933	Hs.184221	ESTS	1.00 2.81	1.00 4.88
	319484 319486	T91772 Al382429	Hs.250799	gb:yd52a10.s1 Soares felal liver spleen ESTs	2.08	2.82
	319508	T99898	Hs.270104	ESTs, Moderately similar to ALU8_HUMAN A	2.80	4.39
	319523	T69499	Hs.191184	ESTs	1.55	3.25
25	319545	R83716	Hs.14355	Homo saplens cDNA FLJ13207 fis, clone NT	1.65	1.19
	319545	R09692		gb:yf23b12.r1 Soares fetal liver splaen	5.11	8.54
	319552	AA096106	Hs.20403	ESTs	1.89	3.36
	319582	T82998	Hs.250154	hypothetical protein FU12973	3.48	4.82
30	319586	D78808 R11679	Hs.283683	chromosome 8 open reading frame 4 vimentin	0.26 1.68	0.82 3.41
50	319604 319609	AW247514	Hs.297753 Hs.12293	hypothetical protein FLJ21103	3.06	4.24
	319611	H14957	15.12.50	gb:ym19c10.r1 Soares infant brain 1NiB H	2.76	4.24
	319653	AA770183	Hs.173515	uncharacterized hypothalamus protein HTO	2.51	3.55
	319657	R19897	Hs.106604	ESTs	5.32	7.68
35	319658	R13432	Hs.167481	syntrophin, gamma 1	3.35	5.00
	319661	H08035	Hs.21398	ESTs, Moderately similar to A Chain A, H	5.18	12.55
	319662	H06382	Hs.21400	ESTs	1.58 1.00	1,56 1,22
	319708 319742	R15372 T77668	Hs.22664 Hs.21162	ESTs ESTs	2.48	3,13
40	319748	R18178	Hs.295866	Homo sapiens mRNA; cDNA DKFZp434N1923 (f	3.02	4.85
	319772	R76633	Hs.22646	ESTs	4.36	11.61
	319788	AA321932	Hs.117414	KIAA1320 protein	2.56	3.68
	319805	R92857	Hs.271350	likely ortholog of mouse polydom	4.63	6.56
45	319812	N74880	Hs.264330	N-acylsphingosine amidohydrolase (acid c	0.63	1.32
43	319834	AA071267 T78517	Hs.13941	gb:zm61g01_r1 Stratagene fibroblast (937 ESTs	0.30 3.99	0.94 6.44
	319878 319882	AA258981	Hs.291392	ESTs ·	5.09	7.36
	319912	T77559	Hs.94109	Homo sapiens cDNA FLJ13634 fis, clone PL	3.24	3.21
	319935	H79460	Hs.271722	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.40	9.42
50	319944	T79248	Hs.133510	ESTs	3.31	5.39
	319947	AA160967	Hs.14479	Homo sapiens cDNA FLJ14199 fis, clone NT	2.90	4.95
	319962	H06350	Hs.135056	Human ONA sequence from clone RP5-850E9	1.81	1.57
	320007 320018	AA336314 T83263		gb:EST40943 Endometrial tumor Homo sapie gb:yd40h09.r1 Soares fetal liver spleen	3.42 2.77	6.29 5.14
55	320030	H63789	Hs.296288	ESTs, Weakly similar to KIAA0638 protein	4.10	6.69
	320032	Al699772	Hs.292664	ESTs, Weakly similar to A46010 X-linked	3.27	3.27
	320040	AA233671	Hs.87164	hypothetical protein FLJ14001	1.81	1.64
	320047	T86564	Hs.302256	EST	3.38	7.36
<i>c</i> n	320063	AA074108	Hs. 120844	FOXJ2 forkhead factor	5.90	16.73
60	320096	H58138	Hs.117915	ESTs	2.08	4.47
	320099 320112	AW411307 T92107	Hs.114311 Hs.188489	CDC45 (cell division cycle 45, S.cerevis ESTs	1.00 2.27	1.00 2.06
	320140	H94179	Hs.119023	SMC2 (structural maintenance of chromoso	1.00	1.00
	320188	AW419200	Hs.172318	ESTs	1.26	1.00
65	320193	AA831259	Hs.17132	ESTs	2.58	6.23
	320195	R62203	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	2.85	4.53
	320199	R78659	Hs.29792	ESTs	0.40	0.94
	320203	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (f	0.84	1.18
70	320219 320220	AA327564 AF054910	Hs.127011 Hs.127111	tubulointerstitial nephritis antigen tektin 2 (testicular)	1.00 0.18	1.17 1.09
70	320225	AF058989	Hs.128231	G antigen, family B, 1 (prostate associa	5.26	13.75
	320231	H03139	Hs.24683	ESTs	1.59	1.93
	320260	NM_003608	Hs.131924	G protein-coupled receptor 65	1.38	4.56
75	320267	AL049337	Hs.132571	Homo sapiens mRNA; cDNA DKFZp564P016 (fr	1.00	1.92
75	320268	H06019	Hs.151293	Homo sapiens cDNA FLJ10664 fis, clone NT	5.58	5.70
	320322	AF077374	Hs.139322	small proline-rich protein 3 caveolin 2	1.41	1.01
	320325 320330	A1167978 AF026004	Hs.139851 Hs.141660	caveoun 2 chloride channel 2	0.05 2.17	0.67 1.26
	320339	H10807	Hs.281434	Homo sapiens cDNA FLJ14028 fis, clone HE	1.81	2.32
80	320388	H16055	-Hs.31286	ESTs	1.00	3.22
	320402	R22291	Hs.23368	Homo sapiens done FLC0578 PRO2852 mRNA,	1.41	1.36
	320413	AA203711	Hs.173269	ESTs	2.31	3.61
	320432	R62786	Hs.124136	ESTs	11.25	20.78
85	320436	AA253352	Hs.293663	ESTS	2.22 3.53	3.49 8.14
55	320438	W24548	Hs.5669	ESTs	••••	8.14

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	320448	AJ240233	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	1.42	3.46
	320451	R26944	Hs.180777	Homo sapiens mRNA; cDNA DKFZp564M0264 (f	0.87	0.81
	320484	AA094436	Hs.296267	folistatin-like 1 Homo saciens cDNA FLJ12028 fis, clone HE	0.65 3.44	1.18 7.15
5	320499 320514	R32555 AB007978	Hs.24321 Hs.158278	KIAA0509 protein	6.44	13.62
,	320521	N31464	Hs.24743	hypothetical protein FLJ20171	1.48	1.04
	320526	AW374205	Hs.111314	ESTs	3.66	7.87
	320527	R34672	Hs.324522	ESTs	3.16	5.63
10	320536	AA331732	Hs.137224	ESTs	2.83 1.28	5.83 1.00
10	320556	AF054177 AF056209	Hs.14570 Hs.159396	hypothetical protein FLJ22530 peptidylglycine alpha-amidating monooxyg	1.22	0.81
	320564 320587	Z44524	Hs.167456	Homo sapiens mRNA full length insert cDN	1.84	2.44
	320635	R54159	Hs.80506	small nuclear ribonucteoprotein polypept	1.00	6.25
	320539	AA243258	Hs.7395	hypothetical protein FLJ23182	2.60	2.30
15	320648	N48521	Hs.26549	Homo sapiens mRNA for KIAA1708 protein,	1.00 0.14	1.53 0.79
	320651	AA489268	Hs.111334 Hs.91251	ferritin, light polypeptide hypothetical protein FLJ11198	5.02	8.84
	320664 320676	A1904216 AA132650	Hs.300511	ESTs	3.63	5.37
	320683	R59291	Hs.26638	ESTs, Weakly similar to unnamed protein	0.37	1.31
20	320689	AA334609	Hs.171929	ESTs, Wealdy similar to A54849 collagen	1.27	1.02
	320696	AW135016	Hs.172780	ESTs	3.53	4.60 0.85
	320714	Al445591	11- 101105	gb:yq04a10.r1 Soares fetal liver spleen immunoglobulin lambda locus	1.06 1.35	1.49
	320727 320771	U96044 A1793266	Hs.181125 Hs.117176	poly(A)-binding protein, nuclear 1	0.04	0.82
25	320794	AA281993	Hs.91226	ESTs	2.96	4.33
	320822	AF100780	Hs.194679	WNT1 Inducible signaling pathway protein	0.10	0.79
	320824	AF120274	Hs.194689	artemin	1.16	1.11
	320830	AJ132445	Hs.266416	claudin 14	1.06 1.36	1.75 1.47
30	320843	AA317372	Hs.34744 Hs.34771	Homo sapiens mRNA; cDNA DKFZp547C136 (fr ESTs	5.30	7.49
30	320849 320853	D60031 Al473796	Hs.135904	ESTs	1.00	1.00
	320896	AB002155	Hs.271580	uroplakin 1B	5.90	2.55
	320921	R94038	Hs.199538	inhibin, beta C	2.20	1.17
	320927	Al205786	Hs.213923	ESTs	0.18	1.46
35	320957	A1878933	Hs.92023	core histone macroH2A2.2	1.67 3.26	2.18 3.62
	320997	H22544 W88483	Hs.293650	gb:yn69f11.r1 Soares adult brain N2b5HB5 ESTs	2.25	4.55
	321045 321046	H27794	Hs.269055	ESTs	2.69	4.25
	321052	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	2.14	2.56
40	321059	Al092824	Hs.126465	ESTs	1.69	0.53
	321062	R87955	Hs.241411	Homo sapiens mRNA full length insert cDN	2.76	5.20
	321067	AF131782	Hs.241438	Homo sapiens clone 24941 mRNA sequence	4.79 1.79	7.41 4.27
	321102	AA018306	Hs.125494	gb:ze40d08.r1 Soares retina N2b4HR Homo ESTs	1.00	3.14
45	321130 321142	H43750 AIB17933	Hs.298351	ASPL protein	8.73	15.36
10	321155	AA336635	Hs.99598	hypothetical protein MGC5338	3.04	5.03
	321158	AA700289		gb:yu76f11.r1 Soares fetal liver spleen	4.62	8.39
	321170	N53742	Hs.172982	ESTs	2.21	4.46
50	321199	AW385512	11- 226460	gb:yy56d10.s1 Soares_multiple_sclerosis_	5.69 4.00	8.01 7.32
20	321206 321225	H54178 AL080073	Hs.226469 Hs.251414	Homo sapiens cDNA FLJ12417 fis, clone MA Homo sapiens mRNA; cDNA DKFZp564B1462 (f	4.17	4.63
	321236	AW371941	Hs.18192	SerlArg-related nuclear matrix protein (1.00	1.00
	321244	AF068654	***************************************	gb:Homo sapiens isolate AN.1 immunoglobu	2.18	9.13
~ ~	321270	R83560		gb:yv76c06.s1 Soares fetal liver spleen	3.80	5.26
55	321317	AI937060	Hs.6298	KIAA1151 protein	1.81 1.00	1.65 1.00
	321318 321325	AB033041 AB033100	Hs.137507 Hs.300646	KIAA1215 protein KIAA protein (similar to mouse paladin)	0.44	0.93
	321342	AA127984	Hs.222024	transcription factor BMAL2	4.94	4.93
	321356	R93443	Hs.271770	ESTs	3.10	4.66
60	321418	AI739161	Hs.161075	ESTs	2.28	2.54
	321420	Al368667	Hs.132743	ESTs	1.13	0.97 3.35
	321430	U05890	U- 02045	gb:H.sapiens (DIG3) mRNA for immunoglobu	2.42 1.60	3.33
	321453 321467	N50080 X13075	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H gb:Human 2a12 mRNA for kappa-immunoglobu	0.42	0.72
65	321468	AA514198	Hs.38540	ESTs	2.46	6.50
••	321491	H70665	Hs.292549	ESTs	1.00	1,25
	321498	AW295517	Hs.255436	ESTs	3.19	6.24
	321504	W02356	Hs.268980	ESTs	2.28 2.14	3.86 3.94
70	321510	AA703650 H84972	Hs.255748 Hs.108551	ESTs ESTs	2.78	5.37
10	321513 321516	Al382803	Hs.159235	ESTs	3.06	7.19
	321565	AI525773	Hs.266514	hypothetical protein FLJ11342	4.89	7.82
	321577	H84260		gb:ys90g04.r1 Soares retina N2b5HR Homo	1.00	1.73
75	321581	AA019964	Hs.28803	ESTs	4.88	6.73 2.08
75	321582	AA143755 H95531	Hs.21858	trinucteolide repeat containing 3 gb;ys76e02.r1 Soares retina N2b4HR Homo	1.00 2.26	4.52
	321587 321626	AA295430	Hs.96322	hypothetical protein FLJ23560	1.95	3.83
	321628	H87064	Hs.161051	ESTs, Moderately similar to ALU6_HUMAN A	0.47	1.02
	321642	AW085917	Hs.247084	ESTs	1.52	1.38
80	321669	H95404	Hs.294110	ESTS	2.17	2.45
	321687	AA625149	Un 4904 CO	gb:af70c12r1 Soares_NhHMPu_S1 Homo sapi	4.31	6.95 3.28
	321688	H97646 AA700017	Hs.123158 Hs.173737	Homo sapiens cDNA FLJ12830 fis, clone NT ras-related C3 botulinum toxin substrate	2.82 0.51	1.08
	321693 321700	N55160	Hs.167260	ESTs	4.57	7.46
85	321701	AW390923	Hs.42568	ESTs	1.00	1.00
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	321709	N25847	Hs.108923	RAB38, member RAS oncogene family	1.00	1.00
	321710	N35682	Hs.259743	ESTs	2.97	5.26
	321775	Al694875	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	1.00	1.00
5	321777	A1637993	Hs.202312	Homo sapiens done N11 NTera2D1 teratoca ESTs	1.68 0.90	0.45 0.90
,	321779 321829	N42729 D81993	Hs.163835 Hs.8966	tumor endothetial marker 8	2.69	3.69
	321846	AA281594	Hs.87902	ESTs	5.11	7.64
	321879	AL109670	Hs.302809	ESTs	6.49	9.58
4.0	321883	AA426494	Hs.46901	KIAA1462 protein	0.28	0.95
10	321899	N55158	Hs.29468	ESTs	0.39	0.95
	321911	AF026944	Hs.293797	ESTs	6.20	10.76
	321949	R49202	Hs.181694 Hs.195689	EST	4.62 2.89	10.51 5.47
	321955 321956	Al651866 Al110177	Hs.132882	ESTs ESTs	0.32	1.25
15	321987	AL133612	Hs.272759	KIAA1457 protein	1.00	1.83
	321991	AL133627	Hs.158923	Homo sapiens mRNA; cDNA DKFZp434K0722 (f	4.00	6.47
	322002	AA328801	Hs.84522	ESTs	2.10	3.48
	322035	AL137517	Hs.306201	hypothetical protein DKFZp56401278	1.00	1.90
20	322044	AW340926	11- 454570	gb:xy51b10.x1 NCI_CGAP_Lu34.1 Homo sapie	3.20 1.55	9.67 1.07
20	322057 322060	N92197 Al341937	Hs.154679	synaptotagmin 1 gb:qt10e03.x1 NCI_CGAP_GC4 Homo sapiens	4.59	7.68
	322070	U80769	Hs.210322	Homo sapiens mRNA for KIAA1766 protein,	2.78	4.52
	322083	AF074982	Hs.226031	ESTs, Highly similar to KIAA0535 protein	3.10	5.52
~ ~	322091	AI819863	Hs.106243	ESTs	1.59	1.75
25	322125	R93901		gb:yq16c12_r1 Soares fetal liver spleen	2.06	5.27
	322130	R98978	Hs.117767	ESTs ESTs	10.12 0.94	16.49 0.64
	322147 322166	AF085919 AF085958	Hs.114176	gb:yr88b03.r1 Soares fetal liver spleen	4.09	6.67
	322173	H52567		gb.yt85d04.rt Soares_pineal_gland_N3HPG	3.46	4.85
30	322178	H56535		gb:yt88g03.r1 Soares_pineat_gland_N3HPG	0.44	2.54
	322179	H92891		gb:yt94c02.s1 Soares_pineal_gland_N3HPG	4.52	7.50
	322186	H67346	Hs.269187	ESTs	0.15	0.98
	322196	W87895	Hs.211516	ESTs	2.20 3.42	5.04 4.84
35	322212	AF087995	Hs.134877 Hs.179662	ESTs nucleosome assembly protein 1-like 1	0.82	2.14
55	322221 322277	AJ890619 AJ640193	Hs.226389	ESTs	3.62	3.98
	322278	AF086283	110.22.0000	gb:zd46f01.r1 Soares_fetal_heart_NbHH19W	1.00	1.00
	322284	A1792140	Hs.49265	ESTs	0.66	2.76
40	322288	AL037273	Hs.7886	pellino (Drosophila) homolog 1	0.71	0.70
40	322320	AF086419	11 75450	gb:zd78d03.r1 Soares_fetal_heart_NbHH19W	2.02	2.76
	322336	AA308526	Hs.76152	decorin gb:zb18c07.x5 Soares_fetal_lung_NbHL19W	2.92 8.50	4.44 11.56
	322339 322366	W17348 AW404274	Hs.122492	hypothetical protein	0.61	1.34
	322372	W25624	Hs.153943	ESTs	7.37	12.07
45	322374	AJ394663	Hs.122116	ESTs, Moderately similar to Osf2 [M.musc	4.78	10.50
	322378	AF064819	Hs.201877	DESC1 protein	1.00	1.00
	322388	AI815730	Hs.247474	hypothetical protein FLJ21032	7.09 3.20	6.49 5.80
	322416 322419	AA223183 AA248987	Hs.298442 Hs.14084	adaptor-related protein complex 3, mu 1 ring finger protein 7	1.64	1.57
50	322425	W37943	Hs.34892	KIAA1323 protein	0.83	1.00
50	322431	AA069222	Hs.141892	ESTs	3.96	5.22
	322450	AA040131	Hs.25144	ESTs	5.18	12.67
	322465	AA137152	Hs.286049	phosphoserine aminotransferase	3.41	2.23
55	322467	AF116826 AA744286	Hs.180340	putative protein-tyrosine kinase	1.00 1.75	1.30 2.03
55	322473 322509	T52172	Hs.266935 Hs.302213	tRNA selenocysteine associated protein ESTs	1.00	2.27
	322523	W80398	Hs.193197	ESTs	2.75	5.49
	322527	AF147359		gb:Homo sapiens full length insert cDNA	1.25	1.27
CO	322560	AI916847	Hs.270947	ESTs	4.57	8.81
60	322566	W87285	Hs.269587	ESTs	1.00	1.42 6.94
	322585 322635	AA837622 AA679084		gb:zh69c01.r1 Soares_fetal_liver_spleen_ qb:zh90h08.r1 Soares_fetal_liver_spleen_	4.18 2.40	4.85
	322641	AA007352	Hs.256042	ESTs	2.94	4.64
	322653	AI828854	Hs.258538	striatin, calmodulin-binding protein	0.48	0.38
65	322664	AA011522		gb:zi03g07,r1 Soares_fetal_liver_spleen_	1.92	2.18
	322687	AJ110759		gb:AF074666 Human fetal liver cDNA libra	4.14	6.75
	322692	AA018117	Hs.60843	potassium voltage-gated channel, shaker-	3.50	5.00
	322694	Al110872	Hs.279812	PRO0327 protein clone FLB1727	1.80 1.00	1.72 3.43
70	322708 322712	AF113674 AA021328	Hs.283773 Hs.23507	hypothetical protein FLJ11109	3.28	3.86
, ,	322766	AW068805	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	1.63	1.53
	322770	AA045796	Hs.122682	ESTs	1.53	1.06
	322794	AJ608591	Hs.38991	\$100 calcium-binding protein A2	12.06	1.94
75	322810	AI962276	Hs.127444	ESTs CCT-	4.09	6.90
75	322818 322820	AW043782 Al377755	Hs.293616 Hs.120695	ESTs ESTs	1.20 0.21	1.63 1.93
	322872	AA827228	Hs.126943	ESTS	2.04	1.63
	322882	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	5.26	1.22
0.0	322887	AI986306	Hs.86149	phosphoinositol 3-phosphate-blinding prot	2.80	2.24
80	322913	A1733737	Hs.68837	ESTs	2.38	6.61
	322926	AI825940	Hs.211192	ESTs	4.02	5.79
	322929 322968	A1365585 A1905228	Hs.146246 Hs.83484	ESTs SRY (sex determining region Y)-box 4	0.30 2.06	1.14 1.13
	322971	C15953	Hs.212760	hypothetical protein FU13649	1.18	2.00
85	322981	AA493252	Hs.159577	ESTs	2.28	2.61

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	322988	C18727	Hs.171941	ESTs	0.39	2.00
	323003	AJ733859	Hs.149089	ESTs	3.28 3.38	1.00
	323013	AA134042 AL157565	Hs.191451 Hs.315369	ESTs Homo sapiens cDNA: FLJ23075 fis, clone L	0.G6	5.68 1.10
5	323025 323032	AW244073	Hs.145946	ESTs	10.18	21,27
9	323052	R21124	Hs.85573	Homo sapiens DC29 mRNA, complete cds	1.46	1.90
	323064	AL119341	Hs.49359	Homo sapieris mRNA; cDNA DKFZp547E052 (fr	3.08	5.64
	323098	A1700025	Hs.270471	ESTS	2.31 5.38	4.49 11.64
10	323102 323155	AL119913 AL135041	Hs.163615	ESTs gb:DKFZp762K2310_r1 762 (synonym: hmel2)	2.38	5.56
10	323176	AW071648	Hs.82101	pleckstrin homology-like domain, family	1.06	1.41
	323191	AA195600	Hs.301570	ESTs	0.73	1.24
	323225	AA205654	Hs.24790	KIAA1573 protein	5.25 0.45	11.95 1.35
15	323232 323266	AA148722 AW003362	Hs.224680 Hs.243886	ESTs nuclear autoantigenic sperm protein (his	1.71	1.83
IJ	323281	AJ697556	Hs.292659	ESTs	1.24	3.21
	323283	AA256014	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	12.68	15.05
	323314	AA226310	Hs.191501	ESTs	4.42 2.58	9.61 5.93
20	323316	AL134620	Hs.280175	ESTs ras homolog gene family, member A	1.98	3.30
20	323334 323338	AJ335501 R74219	Hs.77273 Hs.23348	S-phase kinase-associated protein 2 (p45	1.62	1.00
	323348	AA233056	Hs.191518	ESTs	1.00	1.07
	323351	AA704103	Hs.24049	ESTs	1.43	1.68
25	323359	AA234172	Hs.137418	ESTS	0.34 3.01	1.18 3.71
23	323360 323405	AA716061 AW139550	Hs.161719 Hs.115173	ESTs ESTs	1.90	8.81
	323420	A1672386	Hs.263780	ESTs	0.29	1.01
	323434	AW081455	Hs.120219	ESTs	2.27	1.92
20	323445	AA253103	Hs.135569	ESTs, Weakly similar to NEUROD [H.sapien	0.43 3.19	0.80 3.85
30	323449 323492	AA282865 H00978	Hs.284153 Hs.20887	Fanconi anemia, complementation group A hypothetical protein FLJ10392	2.70	3.20
	323501	AA182461	Hs.84520	ESTs	2.04	3.31
	323505	AI652287		gb:EST382593 MAGE resequences, MAGK Homo:		3.08
25	323515	AA282274	Hs.256083	ESTs	2.69 1.20	3.40 1.09
35	323541 323545	Al185116 Al814405	Hs.104613 Hs.224569	RP42 homolog ESTs	1.25	1.55
	323635	R63117	Hs.9691	Homo sapiens cDNA: FLJ23249 fis, clone C	0.27	0.72
	323675	AA984759	Hs.272168	tumor differentially expressed 1	3.70	5.80
40	323678	AL042121	Hs.20880	ESTs	3.33 1.00	5.10 1.00
40	323591 323693	AA317561 AW297758	Hs.145599 Hs.249721	ESTs ESTs	2.01	1.54
	323746	AW298611	Hs.12808	MARK	4.11	5.53
	323774	AA329806	Hs.321056	Homo sapiens mRNA; cDNA DKFZp586F1322 (f	2.06	3.70
15	323856	AA355264	Hs.267604	hypothetical protein FLJ10450	3.42 5.97	8.13 12.51
45	323857 323870	T18988 AA341774	Hs.293668 Hs.129212	ESTs ESTs	3.17	4.52
	323876	AL042492	Hs.147313	ESTs	0.36	1.00
	323885	AA344308	Hs.128427	Homo sapiens BAC clone RP11-335J18 from	2.31	3.33
50	323911	AL043212	Hs.92550	ESTs	4.38 5.80	5.41 10.20
50	323919 323972	AA862973 AI869964	Hs.220704 Hs.182906	ESTs ESTs	3.10	5.14
	324005	AA610011	Hs.208021	ESTs	5.34	10.07
	324036	AI472078	Hs.303662	ESTs	1.00	5.03
55	324055	AA528794	Hs.128644	ESTs	0.86 0.45	1.00 0.91
22	324063 324072	AW292740 AA381829	Hs.272813	dual oxidase 1 gb:EST94855 Activated T-cells I Homo sap	2.82	5.12
	324092	AW269931	Hs.202473	Homo sapiens cDNA: FLJ22278 fis, clone H	2.40	2.52
	324095	AW377983	Hs.298140	Homo sapiens cDNA: FLJ22502 fis, clone H	1.32	4.30
60	324129	AI381918	Hs.285833	Homo sapiens cDNA: FLJ22135 fis, clone H	1.40 4.24	1.77 6.21
60	324132 324214	AW504860 AA412395	Hs.288836 Hs.225740	hypothetical protein FLJ12673 ESTs	6.96	10.69
	324227	AA295552	Hs.28631	Homo sapiens cDNA: FLJ22141 fis, clone H	0.81	0.53
	324266	AL047634	Hs.231913	ESTs	2.42	4.05
65	324275	AA429088	Hs.98523	ESTs	3.62	5.38 0.70
65	324281 324290	AL048026 AA432032	Hs.124675 Hs.304420	ESTs, Wealdy similar to T14742 hypotheti ESTs	0.14 3.71	4.34
	324303	AL118754	113.00-120	gb:DXFZp761P1910_r1 761 (synonym: hamy2)	0.95	0.91
	324312	Al198841	Hs.128173	ESTs	4.06	5.91
70	324325	AL138153	Hs.300410	ESTs	5.88	8.25
70	324338 324341	AL138357 AW197734	Hs.145078 Hs.99807	regulator of differentiation (in S. pomb . ESTs, Weakly similar to unnamed protein	0.87 1.28	1.25 1.00
	324343	AW452016	Hs.293232	ESTs	2.54	3.46
	324371	AA452305	Hs.270319	ESTs	5.85	8.36
75	324382	AW502749	Hs.24724	MFH-amplified sequences with leucine-ric	0.76 2.88	1.64 5.69
13	324384 324385	AA453396 F28212	Hs.127656 Hs.284247	KIAA1349 protein KIAA1491 protein	1.81	1.99
	324388	A1924963	Hs.306206	hypothetical protein FLJ11215	1.00	1.00
	324432	AA464510	Hs.152812	ESTs	2.73	2.17
80	324497	AW152624	Hs.136340	ESTs, Weakly similar to unnamed protein	0.71 1.00	1.90 1.00
80	324510 324580	AI148353 AA492588	Hs.287425	Homo sapiens cDNA FLJ11569 fis, clone HE gb:ng99c08.s1 NCL_CGAP_Thy1 Homo sapiens	1.00 2.18	3.50
	324582	AA506935	Hs.132036	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.96	11.35
	324633	AA572994	Hs.325489	ESTs	2.92	4.22
85	324640	AW295832	Hs.134798	ESTs, Moderately similar to TTL MOUSE TU	5.48 0.39	11.74 0.73
ره	324675	AW014734	Hs.157969	ESTs	9.43	4.13

	W	O 02/08	6 44 <i>3</i>			
	324699	AW504732	Hs.21275	hypothetical protein FLJ11011	0.93	0.93
	324747	AA603532	Hs.130807	ESTs	1.57	1.81
	324748	AA657457	Hs.292385	ESTs	1.55	1.34
	324801	AI819924	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	1.00	6.56
5	324804	AJ692552		gb:wd73f12.x1 NOL_OGAP_Lu24 Homo sapiens	1.00	7.53
_	324828	AA843926	Hs.124434	ESTs	2.00	3.25
	324855	AW152305	Hs.122364	ESTs	2.74	3.43
	324866	AI541214	Hs.46320	Small proline-rich protein SPRK (lauman,	1.07	0.95
	324871	AW297755	Hs.271923	Homo sagiens cDNA: FLJ22785 fis, clone K	1.68	1.21
10	324886	AA805794	Hs.131511	ESTs	2.56	5.61
	324889	D31010		gb:HUML12147 Human fetal lung Homo sapie	2.20	4.65
	324948	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN A	5.28	7.05
	324953	Al264628	Hs.125428	ESTs	3.37	5.51
	324958	AA625076	Hs.132892	protocadherin 20	5.12	9.81
15	324988	T06997	Hs.121028	hypothetical protein FLJ10549	2.52	1.08
13	325024	F13254	Hs.78672	taminin, atpha 4	5.24	10.22
	325105	H97109	Hs.105421	ESTs	1.00	1.00
	325108	AA401863	Hs.22380	ESTs	1.99	2.14
	325114	D83901	Hs.315562	ESTs	2.73	3.17
20	325146	Al064690	Hs.171176	ESTs	1.86	3.41
20	325149	D61117	Hs.187646	ESTs	0.42	0.93
	325187	AI653682	Hs.197812	ESTs	6.50	11.31.
	325228	7.000002	122107012	2010	6.18	15.76
	325235				2.64	4.12
25	325328				2.87	4.42
23	325340				0.29	0.33
	325367				16.56	24.29
		-			0.63	1.22
	325373 325389				0.88	1.05
30					5.75	14.14
30	325436				8.46	17.82
	325471				3.32	6.42
	325498				5.51	8.28
	325557				7.48	21.40
25	325559				4.08	6.25
35	325560				4.20	5.24
	325569				1.10	1.13
	325585				1.00	1.00
	325587				2.98	13.40
40	325597				0.78	0.78
40	325639					
	325685				0.46	0.66
	325686				0.95	1.55
	325735				4.48	9.20
4.0	325739				0.59	0.88
45	325740				2.42	6.61
	325792				7.88	9.83
	325819				4.74	7.18
	325883				2.02	2.64
~a ·	325895				7.78	15.98
50	325925				2.04	10.60
	325932				4.18	7.36
	325941				3.66	9.03
	325969				0.61	0.80
	325971				4.88	7.42
55	326025				0.55	1.07
	326046				7.21	14.72
	326099				3.60	5.98
	326108				1.27	1.06
C C	326163			•	3.27	5.70
60	326165				0.45	1.11
	326189				0.13	0.45
	326204				5.60	9.00
	326230				7.00	12.01
	326274				1.00	8.09
65	326360				9.86	15.35
	326393				0.52	0.77
	326505				1.00	1.42
•	326515				1.24	5.84
	326589				9.20	13.49
70	326592				2.77	4.01
	326605				2.01	2.53
	326692				1.00	1.00
	326693				1.00	1.31
	326720				0.19	0.65
75	326742				2.34	7.20
	326770				0.25	0.83
	326818				3.09	4.56
	326936				2.08	3.45
00	326964				0.41	1.70
80	326983				2.02	3.80
	326991				1.09	1.20
	327036				1.00	8.04
	327040				3.05	4.22
	327053				3.55	6.31
85	327075				1.59	1.40
	_					

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327085	2.50	12.57	
327130	5.38	8.04	

	W U 02/080443		
	327085	2.50	12.57
	327130	5.38	8.04
	327156	3.74	6.58
	327220	1.28	1.54
5			12.01
5	327224	6.56	12.91
	327268	2.61	5.40
	327321	2.42	3.11
	327332	6.62	10.58
	327361	2.69	4.41
10			
10	327377	2.04	6.72
	327395	2.61	4.50
	327414	1.00	8.01
	327442	5.91	9.65
		6.58	18.01
15	327467	0.30	
15	327473	3.79	7.48
	327483	4.08	8.87
	327562	0.68	2.86
	327568	1.00	2.00
		2.06	3.61
20	327606	2.00	44.00
20	327611	5.90	14.26
	327642	4.06	8.74
	327654	1.05	2.08
	327734	1.00	1.00
	327775	1.46	11.79
25			
23	327796	3.47	5.65
	327840	3.26	6.64
	327940	5.84	15.58
	327984	0.36	1.50
	328004	1.87	1.42
30		0.42	0.59
30	328021		0.55
	328068	2.83	4.68
	328100	3.04	5.39
	328101	3.54	5.20
	328113	0.72	0.91
35			0.91 5.16
33	328157	5.58	3.10
	328196	. 45.76	11.13
	328197	5.98	10.58
	328264	3.11	4.88
	328299	2.20	3.06
40	· 328342	1.49	1.94
70			1.00
	3283 65	1.00	1.00
	328369	4.40	7,36
	328381	1.86	7.36 4.93 7.56
	328451	5.51	7.56
45	328481	0.13	0.72
			3.97
	328500	2.71	3.31
	328530	5.41	7.62
	328600	3.14	10.68
	328608	4.56	8.17
50	328616	2.24	11.91
	328623	3.04	5.46
	328632	0.70	1.19
	328664	3.48	6.80
	328666	10.42	25.47
55	328698	9.68	14.56
	328700	2.74	10.22
	328708	0.15	0.57
		6.23	8.91
	328735		
60	328743	3.62	6.54
60	328806	0.22	0.78
	328861	3.68	10.54
	328908	5.42	16.36
	328933	2.02	5.29
65	328934	1.73	4.45
O)	328949	3.34	5.41
	329005	2.88	7.26
	329011	2.52	3.72
	329033	1.00	1.03
	329037	5.07	8.16
70		1.98	2.41
70	329067		241
	329134	2.24	3.25
	329157	2.30	11.04
	329178	2.64	5.02 15.27
	329192	6.41	15.27
75	329194	0.31	0.79
, ,			0.75
	329204	1.60	3.75
	329224	2.99	6.11
	329228	0.83	0.83
	329288	0.63	1.01
80	329337	1.00	1.00
50	329541		1.00
		0.76	1.68
	329560	1.34	2.02
	329588	1.68	2.22
	329643	4.18	11.77
85	329703	1.00	1.00
-55	******		

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	329764				5.78	15.50
	329816			•	2.09	5.44
	329860				3.13	10.77
-	329993				7.83	14.21
5	330020				5.58	13.12
	330036				3.32	5.57
	330052				4.31 1.34	7.97 1.76
	330085				4.70	12.46
10	330088				0.44	1.06
10	330093				3.47	4.83
	330100				2.14	3.61
	330106				3.17	6.87
	330107				5.61	11.89
15	330120				4.50	12.74
15	330123				1.55	7.62
	330208				13.10	23.38
	330263				2.81	4.98
	330300				3.00	4.41
20	330313				0.67	0.76
20	330366				4.76	11.82
	330372	A A 440740	Hs.182971	karyopherin alpha 5 (importin alpha 6)	2.14	2.15
	330385	AA449749	Hs.154387	KIAA0103 gene product	0.40	1.15
	330397	D14659	Hs.112341	protease inhibitor 3, skin-derived (SKAL	1.11	0.94
25	330468 330472	L10343 L24203	Hs.82237	ataxia-telangiectasia group D-associated	1.67	1.17
23	330472	L38486	Hs.296049	microfibrillar-associated protein 4	0.46	1.07
	330493	M27826	Hs.267319	endogenous retroviral protease	1.07	0.95
	330495	M31328	Hs.71642	guanine nucleolide binding protein (G pr	0.97	0.96
	330506	M61906	Hs.6241	phosphoinositide-3-kinase, regulatory su	0.17	3.66
30	330512	M80563	Hs.81256	S100 calcium-binding protein A4 (calcium	0.60	1.06
50	330537	U19765	Hs.2110	zinc finger protein 9 (a cellular retrov	2.81	2.07
	330547	U32989	Hs.183671	tryptophan 2,3-dioxygenase	3.91	1.49
	330551	U39840	Hs.299867	hepatocyte nuclear factor 3, alpha	1.15	1.03
	330568	U56244	113.230001	(NONE)	2.83	4.79
35	330599	U90437		gb:Human RP1 homolog mRNA, 3"UTR region	2.08	1.54
55	330601	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	0.89	1.35
	330605	X02419	Hs.77274	plasminogen activator, urokinase	1.87	1.55
	330609	X04741	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.83	1.30
	330617	X53587	Hs.85266	integrin, beta 4	1.54	1.15
40	330630	X78669	Hs.79088	reliculocalbin 2, EF-hand calcium bindin	1.39	1.19
	330644	Y07755	Hs.38991	S100 calcium-binding protein A2	3.83	1.13
	330650	Z68228	Hs.2340	junction plakoglobin	1.25	0.95
	330660	AA347868	Hs.139293	ESTs, Wealdy similar to ALU7_HUMAN ALU S	15.50	29.07
	330692	AA017045	Hs.6702	ESTs	1.00	1.00
45	330707	AA133891	Hs.293690	ESTs	0.20	1.35
	330715	AA233707	Hs.11571	Homo sapiens cDNA FLJ11570 fis, clone HE	0.12	1.40
	330717	AA233926	Hs.52620	integrin, beta 8	6.62	5.42
	330722	AA243560	Hs.34382	ESTs	1.40	1.65
	330740	AA297746	Hs.22654	Homo sapiens voltage-gated sodium channe	0.27	2.04
50	330742	AA400979	Hs.25691	receptor (calcitonin) activity modifying	0.44	0.90
	330744	AA406142	Hs.12393	dTDP-D-glucose 4,6-dehydratase	0.71	3.23
	330751	AA428286	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	1.66	1.52
	330760	AA448663	Hs.30469	ESTs	0.52	0.90
	330763	AA450200	Hs.274337	hypothetical protein FLJ20665	0.37	0.97
55	330786	D60374	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	0.78	0.84
	330790	T48536	Hs.105807	ESTs	0.23	3.17
	330814	AA015730	Hs.265398	ESTs, Weakly similar to transformation-r	0.37	2.07
	330827	AA040332	Hs.12744	ESTs	1.60	1.00
	330844	AA063037	Hs.66803	ESTs	0.93	1.16
60	330901	AA157818	Hs.267319	endogenous retroviral protease	1.02	1.03
	330931	F01443	Hs.284256	hypothetical protein FLJ14033 similar to	0.24	0.88
	330952	H02855	Hs.29567	ESTs	0.08	1.31
	330961	H10998	Hs.7164	a disintegrin and metalloproteinase doma	1.29	1.26
15	330968	H16568	Hs.23748	ESTs	0.48	0.96
65	331014	H98597	Hs.30340	hypothetical protein KIAA1165	0.29	0.74
	331046	N66563	Hs.191358	ESTS	0.99	8.56
	331060	N75081	Hs.157148	Homo saplens cDNA FLJ11883 fis, clone HE	1.24	1.00
	331099	R36671	Hs.83937	hypothetical protein	0.75	1.03
70	331108	R41408	Hs.21983	ESTs	1.00	2.75 10.68
70	331131	R54797	4407	gb:yg87b07.s1 Soares infant brain 1NIB H	6.04	
	331135	R61398	Hs.4197	ESTs	0.80	0.96 4.29
	331170	T23461	Hs.159293	ESTs	2.63	2.71
	331180	T32446	Hs.6640	Human DNA sequence from PAC 75N13 on chr	1.78 1.00	3.01
75	331183	T40769	Hs.8469	ESTs MONEY	1.70	3.80
13	331203	T82310	Un gaage	(NONE)	1.20	3.19
	331271	AA059347	Hs.82226	glycoprotein (transmembrane) nmb	0.31	1.30
	331306	AA252079	Hs.63931	dachshund (Drosophila) homolog	2.09	2.41
	331327	AA281076	Hs.109221	ESTs Homo sapiens cDNA FLJ13495 fis, clone PL	0.72	2.43
80	331341	AA303125	Hs.23240	KIAA1462 protein	0.09	0.91
ou	331359	AA416979	Hs.46901		1.02	0.87
	331363	AA421562	Hs.91011	anterior gradient 2 (Xenepus laevis) hom	1.03	1.23
	331378	AA448881	Hs.49282	hypothetical protein FLJ11088 NADPH oxidase 4	1.40	1.00
	331384	AA456001	Hs.93847		1.80	3.93
85	331402	AA505135	Hs.44037 He 163628	ESTs ESTs, Moderately similar to ALU7_HUMAN	1.65	1.89
G,	331422	F10802	Hs.163628	ental monorared assume as uncertification.		

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	331490	N32912	Hs.26813	CDA14	2.48	1.73	
	331531	N51343		ghtyz15g04.s1 Soares_multiple_sclerosis_	0.98	1.68	
	331547	N54811	11-040000	gb:od74f04.s1 NOI_CGAP_Ov2 Homo sapiens	3.80 0.11	5.75 0.67	
5	331578	N57960 N71027	Hs.249989 Hs.152618	ESTs ESTs	1.09	1.38	
,	331589 331608	N71027 N89851	Hs.112110	PTD007 protein	0.93	0.76	
	331614	N92293	Hs.240272	EST	0.17	1.34	
	331668	W69707	Hs.58030	EST	2.24	3.82	
	331671	W72033	Hs.194695	ras homolog gene family, member I	1.00	1.24	
10	331676	W79834	Hs.58559	ESTs, Weakly similar to rhotekin (Murrusc	0.08	1.07	
	331681	W85712	Hs.119571	collagen, type III, alpha 1 (Ehlers-Dani	8.72	4.27 0.54	
	331692	W93592	Hs.152213	wingless-type MMTV integration site fami Homo sapiens NY-REN-62 antigen mRNA, par	0.94 1.57	1.34	
	331717	AA190888	Hs.153881 Hs.104072	ESTs	6.80	11.77	
15	331718 331811	AA191404 AA404500	Hs.301570	ESTs	1.10	1.00	
13	331820	AA405970	Hs.97996	transcription termination factor, mitoc	0.73	0.59	
	331831	AA412031	Hs.97901	EST	2.77	4.08	
	331852	AA418988	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	0.23	0.93	
^^	331943	AA453418	Hs.21275	hypothetical protein FLJ11011	0.36 1.00	1.88 1.00	
20	331969	AA460702	Hs.82772	collagen, type XI, alpha 1	3.04	3.87	
	331990	AA478102 AA482009	Hs.139631 Hs.105104	ESTs ESTs	1.19	0.78	
	332002 332027	AA489671	Hs.65641	hypothetical protein FL120073	1.27	1.03	
	332029	AA489697	Hs.145053	ESTs	0.30	1.62	
25	332033	AA489840	Hs.251014	EST	2.30	3.70	
	332048	AA496019	Hs.201591	ESTs	0.17	0.52	
	332071	AA598594	Hs.205293	KIAA1211 protein	1.35 0.19	1.23 2.00	
	332074	AA599012	Un 1EEEAC	gb:ae41e11.s1 Gessler Wilms tumor Homo s KIAA1080 protein; Golgi-associated, gamm	0.15	1.18	
30	332083 332085	AA600200 AA600353	Hs.155546 Hs.173933	nuclear factor VA	0.30	1.50	
50	332125	AA609861	Hs.312447	ESTs	0.22	0.62	
	332177	F10812	Hs.101433	ESTs	8.21	18.03	
	332180	H03348	Hs.7327	claudin 1	2.27	1.57	
~~	332185	H10356	Hs.101689	ESTs	0.09	1.18	
35	332203	H49388	Hs.317769	EST	8.05 0.78	5.02 0.85	
	332232	N48891	Hs.101915	Stargardt disease 3 (autosomal dominant) ESTs, Wealdy similar to putative p150 [0.96	1.23	
	332240 332261	N54803 N70294	Hs.324267 Hs.269137	ESTs	2.40	3.74	
	332275	R08838	Hs.26530	serum deprivation response (phosphaticy)	0.27	0.75	
40	332280	R38100	Hs.146381	RNA binding motif protein, X chromosome	0.39	1.88	
	332299	R69250	Hs.21201	nectin 3; DKFZP566B0846 protein	5.24	12.76	
	332304	R74041	Hs.101539	ESTs	1.44	3.18	
	332314	T25862	Hs.101774	hypothetical protein FLJ23045	0.68 1.71	1.32 0.88	
45	332384 332434	M11433 N75542	Hs.101850 Hs.289068	retinol-binding protein 1, cellular Homo sapiens cDNA FLJ11918 fis, clone HE	0.43	0.86	
73	332445	T63781	Hs.11112	ESTs	0.68	1.00	
	332453	L00205	Hs.111758	keratin 6A	31.54	1.00	
	332458	M33493	Hs.250700	tryptase beta 1	0.51	1.00	
5 0	332504	AA053917	Hs.15106	chromosome 14 open reading frame 1	0.79	1.24	
50	332525	M17252	Hs.278430	cytochrome P450, subfamily XXIA (steroid	0.98	1.70 0.66	
	332530	M31682	Hs.1735	inhibin, beta B (activin AB beta polypep	0.88 0.22	1.46	
	332535 332539	N20284 AA412528	Hs.19280 Hs.20183	cysteine-rich motor neuron 1 ESTs, Weakly similar to AF164793 1 prote	0.93	1.49	
	332559	M13955	Hs.166189	cytokeratin 2	0.35	1.13	
55	332563	N92924	Hs.274407	protease, serine, 16 (thymus)	1.00	1.00	
	332565	AA234896	Hs.25272	E1A binding protein p300	0.36	1.05	
	332594	AA279313	Hs.3239	methyl CpG binding protein 2 (Rett syndr	0.53	0.59	
	332634	S38953	Hs.283750	tenascin XA	0.38 1.00	1.16 1.70	
60	332638 332640	AA283034 AA417152	Hs.50640 Hs.5101	JAK binding protein protein regulator of cytokinesis 1	6.15	1.16	
00	332654	AA001296	Hs.288217	hypothetical protein MGC2941	1.50	2.73	
	332665	AA223335	Hs.63788	propionyl Coenzyme A carboxylase, beta p	1.20	0.91	
	332692	AA496035	Hs.247926	gap junction protein, alpha 5, 40kD (con	0.17	1.12	
	332716	L00058	Hs.79070	v-myc avian myelocytomatosis viral oncog	1.00	1.44	
65	332736	L13773	Hs.114765	myeloid/lymphoid or mixed-lineage leukem	1.00 0.53	1.81 0.78	
	332758	X93921	Hs.296938	dual specificity phosphatase 7 hypothetical protein FLJ10902	1.44	1.56	
	332781 332792	AA233258	Hs.247112	nypodieticai piotein PLS 10502	1.70	1.19	
	332816				1.85	2.47	
70	332858				1.04	1.57	
	332906				3.48	8.04	
	332911				1.00	1.00	
	332912				1.06 1.00	4.40 1.00	
75	332922 332956				0.42	0.88	
, ,	332959				1.96	6.34	
	332982				0.56	0.99	
	332984				0.30	0.78	
00	332998				1.47	2.01	
80	333058				0.47	1.38	
	333097				2.14 2.76	3.19 3.70	
	333121 333122				1.92	1.21	
	333123				1.85	1.39	
85	333138				0.47	0.52	

	WO 02/086443		
	333139	1.88	0.84
	333140	0.21	0.64
	333221	1.51	1.11
	333260	0.75	1.01
5	333380	6.68	15.75
•	333387	4.56	12.61
	333512	5.05	8.01
	333524	2.28	3.98
	333585	2.31	1.53
10	333603	2.23	1.17
10	333604	2.51	1.58
	333618	0.52	0.98
	333627	1.44	1.36
	333628	1.90	1.90 2.10
15		1.85	2.10
13	333650	1.85	2.35
	333578	2.18	5.67
	333750	1.99	5.67 2.60
	333763 333767	1.02	0.96
20		1.78	1.65
20	333768	2.15	1.65 2.13
	333769	1.46	2.53
	333772	1.00	1.42
	333777	2.99	1.42 4.50
25	333846	0.47	0.94
25	333884	0.50	1.00
	333887	0.43	0.89
	333891 .	0.51	0.91
	333892	0.26	1.13
20	333904	0.55	0.98
30	333906		
	333948	1.70	2.15 1.09
	333954	0.37	1.05
	333966	8.10	14.30
~ ~	333968	0.63	1.38 12.30
35	334061	4.24	12.30
	334094	1.30	12.03
	334113	4.55	8.63 1.59
	334161	0.82	1.59
	334183	0.47	0.76
40	334187	1.36	3.70
	334219	0.69	1.04
	334222	1.88	1.70
	334223	4.72	3.14 0.62
	334239	0.79	0.62
45	334255	0.45	1.10
	334333	1.00	3.56
	334378	3.98	5.76
	334382	1.50	1.31
	334492	3.59	4.75
50	334562	5.94	15.40
	334588	8.14	19.53
	334616	1.55	1.56
	334633 .	5.16	8.07
	334648	0.59	2.13
55	334787	3.70	7.15
- •	334866	8.13	10.60
	334891	0.32	1.14
	334933	1.00	3.84
	334934	4.01	7.43
60	334945	1.04	2.96
- •	334967	0.29	1.14
	334990	1.50	1.39
	335015	5.88	18.65
	335093	0.55	1.75
65	335120	4.31	8.01
45	335125	0.38	1.97
	335179	1.24	1.98
	335188	0.46	1.47
	335211	1.61	1.42
70	335288	0.73	0.97
	335289	0.20	0.97 0.26
	335361	2.18	1.58 0.71 14.94
	335379	0.50	0.71
	335414	3.64	14.94
75	335416	293	3.98
, ,	335496	0.96	0.91
	335497	1.71	0.91 1.92
	335548	1.15	2.40
	335551 .	3.22	10.54
80	335558	3.42	4.89
50	335586	5.50	12.75
	3355619	2.99	. 3.07
	335620	3.80	8.29
	335521	0.28	0.57
85	335582	0.46	1.17
55	www.		
	•		

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7

	WO 02/086443			PC
	335686	2.55	3.81	
	335755	2.24	1.07	
	335784	0.20	0.97	
_	335814 335815	1.13	1.48 3.51	
5	335815	2.45 1.00	4.16	
	335823	0.49	1.70	
	335823 335835 335851	1.66	1.39	
	335858	2.98	6.43	
10	335000	0.98	0.99	
10	335036	12.10	21.93	
	33530 3350AR	1.00	1.64	
	335083	1.00	4.21	
	33596 335936 335938 335983 335995	0.37	1.17	
15	336021	1.04	0.84	
	336021 336034 336038	11.40	23.54	
	336038	1.19 0.54	1.21	
	336066 336107	0.95	1.63 0.70	
20	336107	3 13	6.29	
20	336205 336275 336292	3.13 3.20 2.34	10.10	
	335275	2.34	3.09	
	330232	1.00	3.09 1.00 0.79	
	336419	1.00 0.65	0.79	
25	336632	2.33 2.55	2.16	
	336633	2.55	2.23 2.03	
	336634	2.19	2.03	
	336331 336419 336632 336633 336634 336635 336636 336636 336637 336638	2.69	2.48	
20	336636	2.13 2.43	1.83	
30	338637	243	2.24 2.03	
	336638	2.31 0.60	131	
	335659	0.31	1.31 1.18	
	336675	1.50	1.14	
35	336684 336694	4.74	7.10	
<i>JJ</i>	336716	4.43	6.37	
	336721	2.20	0.74	
	336798	1.64	2.14	
	336900	6.14	12.73	
40	336900 336948	1.00	1.00	
	337028	1.30	2.09	
	337043 337046	4.01	11.53 1.84	
	337046	1.67 2.78	7.35	
45	337054 337128 337162	7.20	16.14	
73	33/120	3.45	5.34	
	337183	5.72	11.41	
	337183 337184	3.72	5.90	
	33/192	1.27	1.06	
50	337194 337229 337268	1.88	1.68	
	337229	0.22	1.03	
	337268	1.00	3.31	
	337299 337325 337389 337493 337497 337500	3.23 2.76	5.14	
55	337325	5.80	3.72 10.42	
55	337389	2.06	6.30	
	33/493	7.88	20.29	
	337437 3375M	3.80	4.48	
	337549	1.66	2.31	
60	337603	1.27	8.54	
-	337605	5.76	7.16	
	337671	0.73	0.97	
	337755	1.54	0.92	
65	337786	5.07	9.73	
65	337809	6.18 3.78	12.87 12.97	
	337862	2.66	8.16	
	337871	0.26	1.34	
	337958 338008 338033	1.48	1.12	
70	338033	2.38	14.59	
, ,	338083	0.65	2.16	
	338110	1.00	1.61	
	338112	5.86	8.25	
	338145	1.70	1.97	
75	338148	8.07	18.19	
	338158	1.30	4.55	
	338161	2.58	3.57	
	338179	1.00 3.32	1.00 4.63	
80	338182	1.00	3.34	
OV.	338189 338197	0.99	1.69	
	338199	4.58	7.62	
	338215	6.01	15.85	
	338279	0.53	0.95	
85	338316	20.58	38.66	

	WO 02/086443			PCT/US02/12476
	338322	3.23	7.39	
	338357	4.10	11.39	
	33839	10.12	21.59	
	338356	0.69	1.02	
5	338374	0.40	1.18	
,	338414	0.47	1.06	
	338418	6.12	13.86	
	338469	3.09	5.11	
	338501	6.28	10.32	
10	338506	6.97	12.41	
10	338523	3.10	5.84	
	338549	1.70	2.70	
	338561	0.79	0.81	
	338563	1.72	1.46	
15	22002	0.17	0.91	
10	338652 338671 338676 338726 338779	2.10	15.86	
	20070	1.20	1.09	
	200720	0.12	0.57	
	338804	0.99	1.67	
20	320004	1.00	1.00	
20	338936 338871	4.30	9.81	_
	338372	5.02	12.81	
	230070	0.23	1.12	
	338879 338937	6.55	12.26	
25	338966	1.76	5.42	
23	338993	1.00	2.40	
	339047	5.26	10.81	
	339100	5.10	6.88	
	339114	1.00	1.70	
30	339121	1.00	3.75	
50	339170	10.36	19.67	
	339229	4.08	13.48	
	339264	2.64	3.83	
	339293	1.73	1.94	
35	MARIA			
55				

TABLE 88 shows the accession numbers for those Pkeys in Table 8A lacking unigenelD's. For each probesel we have listed the gene cluster number from which the ofigonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oaldand California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

```
Unique Eos probeset identifier number
             CAT number: Gene cluster number
Accession: Genbank accession numbers
45
             Pkey
                              CAT number Accessions
                                              AW340926 AA249063 N86075
AI341937 AW003063 U34725 AA904742
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                              187363_1
             322060
                             44320_1
42705_1
50
             321430
                                               X57414 X57415
             321467
                              43034_1
                                              X13075 X13076
R93901 AF075073 R93902
             322125
                             46779_1
46861_1
             322166
                                               H69434 AF085958 H69846
                                              H52567 H52557 AF085970 H52164
H56535 AF085980 H56712
                              46873_1
46882_1
             322173
55
             322178
             322179
                              46885_1
                                               H92891 AF085982 H92777
                                              H84849 H84252 H84260 H86664 H85320
H95531 H95521 H84529
             321577
                              1615102_1
                              1615333_1
             321587
                             111953_1
627492_1
47271_1
             313723
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60
                                              H22544 H46842 Al204929
W69304 AF086283 W69200
             320997
             322278
                                              AA625149 AA313030 AA313052 H97453
AA665089 AA135130 AA484059 AA102419 AW877765
W79150 AF086419
             321687
                              218439_1
                             129439_1
47422_1
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             322320
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AW979268 AA878419 AA431342 AA431628
A1308300 A1308296
65
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300201
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682222_1
             305897
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                                              AL120701 AL135041 AL121524
AF147359 T58511 T58560
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38927_1
473768_2
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70
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             322585
                                              W88919 W89125
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322635
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                                              AA005129 AA679084 AA694399
AA011522 AA679084 AA011691 AA330797
AI239464 AI239473 AA625812 AI208703
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315454
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380580_1
75
                             37372_1
327472_1
             322687
                                              AF074666 Al110759 AF090902
                                              A1903735 AA491283 A1694953 AW976903 AA761352
A1347274 AW844024
             314852
307783
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                                              AA381722 AA381829 AW963906 AW963902 AA381242
AA488472 W27363 AA317053 BE082689 AW967036 BE079872
AW970512 AA280251 AI652287 BE466438 AI650725 AA551854 AA281574 AW571481
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AA847835 AA768376
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85
             300926
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	324530	328264_1	AA492588 AA492498 AA492571
	301882	275087_1	T78054 T79888 AA398185
	324804	398093_1	ALG92552 AL393343 AL800510 AL377711 F24263 AA661876
-	324889	1515978_1	
5	302697	43219_1	A3001409 A3001410
	302711	45419_1	L08442 D51348 L12061
	302742 318499	458_39 364430_1	T25451 AAS85296 AA585305
	310624	34624_4	U88396 U88898 AA916056 T03285 AI341594 AI359534 AI634031 U88397
10	302847	458_105	X98941 X98942 X98943 X98953 X98949
	304122	772715	H28966
	303598	270283_1	AA382814 AA402411 AA412355
	311409	837264_1	A1698839 A1909260 A1909259 Z78390 T97427
15	312094 319312	797889_1 1540116_1	Z45481 F12393 T74437
13	319407	1688823_1	R05329 R01555 R08276
	319425	1689571_1	T82930 R02424 T85145
	320007	229683_1	AA336314 T82938 AA327744 AW967388 AA639967 T10753
20	320018	1815987_1	
20	319484 318865	1691553_1 1535937_1	T91772 R07257 R07098 H10818 F07831 Z43072
	312220	1671607_1	N74613 T98756 T98589
	319546	243305_1	R09692 R09414 AA346353
	312389	902067_1	AI863140 W80703 R43474
25	319611	1566863_1	H14957 R56522 R11908 BE080180 AW827313 AW231970 AA995028 AA428584 AW872716 AW892508 AW854593 AA578441 AW975234 AA664937 AA984131
	312437	291472_1	AA528743 AA552874 AA564758 AW053245 AI267534 AW070190 AW893483 AA770330 AA906928 AA906582 AA758746 AA551717
			AW063311 AA429538
	311896	579192_1	AW206447 AI248530 AI084433 AI400976 R16553
30	319834	112523_1	AA071267 T65940 T64515 AA071334
	321102	80531_1	AA018306 H38925 AA001221
	321158	410938_1	H79670 H47798 AA700289 N34524 AA305071 AW954803 AA502335 Al433430 Al203597 AW026670 AW265323 AW850787 AA317554 AW993643 AW835572
	321199	212379_1	AW385512 AJ334966 W32951 H62656 H53902 R88904 AW835732
35	305528	288323	AA769156
-	321270	1662057_1	N59537 N78278 R83560
	314126	177666_1	AA226431 AA226569 AA488748
	320714	743644_1	R91883 AI445591
40	306442 306446	AA976899 AA977348	
40	306458	AA978186	
	306510	AA988546	
	306557	AA994530	
40	306572	AA995686	
45	306582	AA996248	
	306656 306686	A1004024 A1015615	
	306751	A1032589	
	308011	A1439473	
50	306892	Al092465	
	308106	A1476803	
	308154 306956	AJ500600 AJ125111	
	306958	Al125152	
55	308213	AI557041	
	308216	A1557135	
	308219	AI557246	
	308588 308599	AI718299 AI719893	
60	308643	AI745040	
	308673	A1760864	
	308697	A1767143	
	308778	AJ811109	
65	308808	A1818289 A1832332	
05	308875 308886	A1833240	
	308898	AI858845	
	308966	AI870704	·
70	308979	Al873111	
70	303011 303077	41689_1 44060_1	AF090405 AF090407 AF090406 AF163305 AF163307 AF163303
	305016	AA626876	A ILLUSTRA INSTITUTION
	305034	AA630128	
75	305072	AA641012	
75	305148	. AA654070	
	305190 303978	AA665955 AW513315	
	303978	AW515465	•
	303998	AW516449	
80	303999	AW516611	
	305235	AA670480	
	305312	AA700201	
	305413 305447	AA724659 AA737856	
85	321244	29327_1	AF068654 AF068656 AF068655

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	305637	AA805124	
	305639 305650	AA806138 AA807709	
5	305690	AA813477	•
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	305759 305792	AA635353 AA845256	
10	307041	A1144243	
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	305901	AAB72958	
	305910	AA875981	
15	307415 307426	AI242118 AI243364	
	307517	A)275055	
	307551	A1281556	
	307561 307608	A <u>1282207</u> A <u>129029</u> 5	
20	307691	Al318285 *	
	307730 307760	Al336092 Al342387	
	307764	AI342731	
25	307796	A1350556	
23	309045 309051	Al910902 Al911975	
	307807	A351799	
	307808 307820	Al351826 Al355761	
30	307852	Al365541	•
	309122	Al928178	
	309164 309177	Al937761 Al951118	
0.5	307902	Al380462	
35	309299 309303	AW003478 AW004823	
	309476	AW129368	
	309532	AW151119	
40	309747 309769	AW264889 AW272346	
	309799	AW276964	
	309866 302679	AW299916 311853_1 H65022 AA186889	
45	309923	AW340684	
45	309928	AW341418	
	309931 309933	AW341683 AW341936	
	302705	31765_1	
50	302789 304006	34161_1 AJ245067 AJ245070 AW517947	
	304024	T03036	
	304026 304028	T03160 T03265	
~ ~	304046	T54803	
55	304061 304063	T61521 T62536	
	302802	34487_1 Y08250 Y0824S	
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60	304155 304203	H68696 N56929	
•	304234	W81608	
	304348 304430	AA179868 AA347682	
	304456	AA411240	
65	304521	AA464716	
	304526 304607	AA476427 AA513322	
	304735	AA576453	
70	304760 306015	AA580401 AA897116	
, ,	306063	AA906316	
	306065 306104	AA906725 AA910956	
	306109	AA911861	
75	306242	AA932805	
	306288 306396	AA936900 AA970223	
	330568	NOT_FOUND_entrez U56244	
80	330599 331131	1532312 U90437 genbank_R54797 R54797	
-	331203	NOT_FOUND_entrez T82310	
	331531	genbank_N51343 N51343	
	331547 332074	457396_1 AA828597 N54811 genbank_AA599012 AA599012	
85			

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TABLE 8C shows the genomic position for those Pkeys in Table 8A lacking uniques ID's and accession numbers. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Unique number corresponding to an Eos probeset
Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham L et al., Nature (1999) 402-489-495.
Indicates DNA strand from which exons were predicted.

Strand:

	Nt_position			ficted exons.
10				
	Pkey	Ref Strand	Nt_position	
	332792	Dunham, L. et.al.	Plus	73381-73768
1.5	332816	Dunham, I. et.al.	Plus	359844-360030
15	332906	Dunham, I. et.al.	Plus	1923101-1923205
	332911 332912	Dunham, L et.al. Dunham, L et.al.	Plus Plus	1961767-1961858 1962120-1962246
	332922	Dunham, i. et.al.	Plus	2009620-2009738
00	332956	Dunham, i. et.al.	Plus	2510528-2510658
20	332959	Dunham, Let.al.	Ptus	2518145-2518213
•	333138 333139	Dunham, I. et.al. Ounham, I. et.al.	Plus Plus	3369205-3369323 3369495-3369571
	333221	Dunham, L. et.al.	Plus	3978070-3978187
25	333380	Dunham, I. et.al.	Plus	4904775-4904846
25	333387	Dunham, I. et.al.	Plus	4910935-4910997
	333512 333524	Dunham, L et.al. Dunham, l. et.al.	Pius Pius	5560510-5560564 5612620-5612780
	333585	Dunham, I. et.al.	Plus	6234778-6234894
20	333618	Dunham, I. et.al.	Plus	6562391-6562566
30	333627 333628	Dunham, I. et.al.	Plus Plus	6620584-6620903 6629004-6629233
	333650	Dunham, I. et.al. Dunham, I. et.al.	Plus	6795852-6797128
	333678	Dunham, I. et.al.	Plus	7068223-7068288
25	333750	Dunham, I. et.al.	Plus	7608165-7608234
35	333763 333767	Ounham, I. et.al. Ounham, I. et.al.	Plus Plus	7692491-7692630 7694407-7694623
	333768	Dunham, I. et.al.	Plus	7695440-7695697
	333769	Dunham, I. et.al.	Plus	7696625-7696707
40 .	333772	Dunham, I. et.al.	Plus	7706773-7706902
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20	337268	Dunham, L et.al.	Plus	28011979-28012034
	337299	Dunham, L. et.al.	Plus Plus	29022656-29022775 31401509-31401579
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	333121	Dunham, L et.al.	Minus	3308446-3308358
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	333260	Dunham, L et.al.	Minus	4308400-4308304
	333603 333604	Dunham, I. et.al. Ounham, I. et.al.	Minus Minus	6466335-6465727 6467090-6466768
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	334187	Dunham, I. et.al.	Minus	11921456-11921205
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90	334223 334255	Dunham, L. et.al. Dunham, L. et.al.	Minus Minus	12734365-12734269 13200776-13200692
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	334648 334787	Ounham, I. et.al. Ounham, I. et.al.	Minus Minus	15363301-15363222 16299093-16298937
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	338161	Dunham, L		Minus	12124716-12124658
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	338676	Dunham, I.		Minus	24637427-24637369
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	329560 329541	3962491 3983503	Plus Minus	2095-2990 2765-3059	
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	325340	6017033	Minus	166656-166	
	325373 325367	5866920 5866920	Minus Minus	1136686-11 922881-922	
	325389	5866921	Plus	239672-239	
75	325436	5866939	Minus	29778-2990	
	325498	5866967	Plus	173372-173	
	325471 325557	6017034 6056302	Minus Plus	289268-289 50921-5105	
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	325587 325585	6682462 6682462	Plus Plus	126724-126 73476-7357	
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	326108	5867187	Minus	23784-23903
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73	330085 330120	6671864	Minus	127553-127656
	330123	6671869	Minus	35311-35406
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	326720	6552456	Plus	84525-84677
	326770 326692	6598307 6682502	Minus Ptus	513603-513668 117697-117899
~ ~	326693	6682502	Minus	335002-335095
55	326983	5867657 5007660	Minus	16023-16581
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	326964	6469836	Plus	75340-75456
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OU	327075	6531965	Plus	4041318-4041431
	327085	6531965	Plus	4734947-4735069
	327036 327130	6531965 6531976	Plus Plus	319951-320040 20247-22343
65	327156	5866841	Minus	2462-2620
	327288	5867481	Plus	48583-48773
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	327224	5867534	Plus	188468-188544
70	327321	6249562 6552412	Minus Minus	99745-99836
	327361 327396	5867743	Plus	61013-62130 8702-8820
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75	327442 327467	5867759 5867772	Plus Plus	111483-111618 88030-88151
,,	327467 327473	5867775	Plus	75101-75181
	327483	5867783	Plus	181573-181662
	327377 327562	5867793 5867804	Minus Minus	37610-37676 343989-344474
80	327568	5867811	Minus	46152-46287
	327606	6004463	Plus	200262-200495
	327611 327642	5867868 5867891	Minus Minus	175053-175392 2513-2743
^-	327654	5867910	Minus	97564-97710
85	327734	5867940	Minus	31003-31583

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	327796	5867982	Plus	85267-85405			
	327840	6249578	Minus	73065-73206			
_	330208	6013599	Ptus	66517-66931			
5	330263	6671884	Minus	101503-101634			
	323004	5867993	Minus	157407-157887			
	328101	5858020	Plus	289920-290014			
	328100	5868020	Minus	263545-263635			
10	328113	5868024	Minus	80378-80491			
10	328157	5868064	Ptus	73326-73615			
	328196	5868080	Minus	16551-16729 42133-42438			
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13	328068	6117819	Plus	253903-254022			
	328264	6381912	Plus	55086-55404			
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	328616	5868239	Plus	293920-294224			
	328623	5868246	Minus	120020-120126			
	328632	5868247	Plus	76734-76853			
25	328666	5858254	Minus	778-901 625555-625633			
23	328698 328700	5868264 5868264	Minus Plus	764089-764203			
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•	328735	5868289	Plus	89389-89455			
	328743	5868289	Plus	274638-274726			
30	328806	5868324	Plus	29408-29684			
	328299	5868366	Minus	149708-149889			
	328342	5868383	Plus	59955-60094			
	328365	5868387	Minus	270724-270798			
35	328369	5868388 5868392	Plus Plus	75371-75583 662758-662848			
22	328381 328451	5868425	Minus	217275-217336			
	328481	5868449	Minus	8987-9180			
	328500	5868464	Plus	59098-59481			
	328530	5868482	Plus	334973-335406			
40	328664	6004473	Plus	1193739-1193866			
	328861	6381928	Minus	108317-108403			
	328908	5868493	Plus	117002-117059			
	328933	5868500	Plus	771755-771889			
45	328934	5868500 6456765	Plus Minus	846342-846448 43552-43619			
43	328949 330313	6042030	Minus	33642-33775			
	329005	5868542	Plus	85470-85673			
	330366	2944106	Plus	151837-151914			
	330372	6580495	Minus	317461-317688			
50	329033	5868561	Minus	5390-5479			
	329037	5868562	Minus	32466-32562			
	329067	5868591	Minus	146417-147652			
	329134	5868679	Plus	29959-30018			
55	329157 329178	5868687 5868704	Minus Plus	145940-146155 179177-179463			
JJ	329170	5868716	Plus	166936-167020			
	329194	5868716	Minus	304450-304559			
	329204	5868720	Minus	3050-3190			
	329224	5868728	Plus	27422-27664			
60	329228	5868728	Minus	50118-50287			
	329288	5868771	Plus	25554-26299			
	329337	5868806	Minus	467155-467222			
	329011	6682532	Plus	48658-48741			

TABLE 9A: Potential Therapeutic, Diagnostic and Prognostic targets for Therapy of Lung Cancer

Table 9A shows about 1312 genes up-regulated in lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) relative to normal body tissues. These genes were selected from about 59680 probesets on the Eos/Afrymetrix Hut03 Genechip array.

Table 99 show the accession numbers for those Pixey's tacking UnigenetD's for table 9A. For each probeset we have tisted the gene cluster number from which the objourndeotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (Double Twist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the

Table 9C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 9A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number Unigene number 15 Pkey: ExAccn:

UnigenelD: Unigene Title:

5

10

20

Unigene gene title

Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granufomatous and carcinoid tumors) divided by the average of normal lung samples

Average of non-malignant lung disease samples (including bronchilis, emphysema, fibrosis, atelectasis, asihma) divided by the average of normal lung samples R1:

R2:

	142,	Alaas	10 th 11011 11123	nan ang ordere various (man-mg or man-		•
	Pkey	ExAcon	Unigene!D	Unigene Title	R1	R2
	400195			NM_007057*:Homo sapiens ZW10 interactor	1.03	1.00
25	400205			NM_006265":Homo sapiens RAD21 (S. pomba)	15.80	396.00
	400220			Eos Control	2.28	2.84
	400277			Eos Control	7.68	9.72
	400285			Eos Control	1.00	1.00
	400268	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	1.04	2.24
30	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	132.45	4.00
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	43.86	74.00
	400301	X03635	Hs.1657	estrogen receptor 1	1.00	1.00
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	1.75	1.65
~ ~	400328	X87344	Hs.180062	transporter 2, ATP-binding cassette, sub	0.87	1.80
35	400419	AF084545		Target	156.55	253.00
	400512			NM_030878*:Homo sapiens cytochrome P450,	1.00	2.00
	400517	AF242388		lengsin	3.67	87.00
	400560			NM_030878*:Homo sapiens cytochrome P450,	1.00 20.26	1.00 45.00
40	400664			NM_002425:Homo sapiens matrix metallopro	1.36	1.07
40	400665			NM_002425:Homo sapiens matrix metallopro	3.26	3.22
	400666			NM_002425:Homo sapiens matrix metallopro NM_003105*:Homo sapiens sortilin-related	1.00	91.00
	400749				7.63	24.00
	400763			Target Exon Target Exon	1.00	1.00
45	401027 401093			C12000586*:gi]6330167 dbj BAA86477.1] (A	1.00	155.00
73	401203			Target Exon	1.00	86.00
	401212			C12000457*:gi[7512178]pir[[T30337 polypr	1.00	400.00
	401411			ENSP00000247172°:HYPOTHETICAL 126.2 kDa	1.00	72.00
	401435			C14000397*:gl]7499898[pir][T33295 hypoth	1.00	64.00
50	401464	AF039241		histone deacelylase 5	3.82	49.00
•	401714			ENSP00000241802*:CDNA FLJ11007 FIS, CLON	2.02	40.00
	401747			Homo sapiens keratin 17 (KRT17)	128.43	68.00
	401760			Target Exon	1.74	35.00
	401780			NM_005557*:Homo sapiens keratin 16 (foca	26.47	10.50
55	401781			Target Exon	10.33	4.61
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	4.13	270
	401797			Target Exon	1.44	2.10
	401961			NM_021626:Homo sapiens serine carboxypep	1.41	1.86
~	401985	AF053004		class I cytokine receptor	1.00	177.00
60	401994			Target Exon	61.84	47.00
	402075			ENSP00000251056*:Plasma membrane calcium	1.00	1.00 1.39
	402260			NM_001436*:Homo sapiens fibrillarin (FBL	1.58 2.09	35.00
	402265			Target Exon	1.00	92.00
65	402297			Target Exon NM_030920*:Homo sapiens hypothetical pro	28.87	13.00
UJ	402408 402420			C1000823*:gij10432400(emb)CAC10290.1] (A	1.00	1.44
	402420			Target Exon	7.44	243.00
	402802			NM_001397:Homo sapiens endothelin conver	1.00	70.00
	402994			NM_002463*:Homo sapiens myxovirus (influ	1.37	1.43
70	403137			NM_005381*:Homo saplens nucleolin (NCL),	1.00	19.00
, 0	403306	NM_006825		transmembrane protein (63kD), endoplasmi	1.00	43.00
	403329			Target Exon	1.00	61.00
	403381			ENSP00000231844*:Ecotropic virus integra	1.00	119.00
	403478			NM_022342:Homo sapiens kinesin protein 9	28.13	136.00
75	403485			C3001813*:gi 12737279 ref XP_012163.1 k	20.23	76.00
	403627			Target Exon	6.30	29.33
	403715			Target Exon	1.30	35.00
	404044			ENSP00000237855*:DJ398G3.2 (NOVEL PROTEI	1.00	54.00
00	404076			NM_016020*:Homo sapiens CGI-75 protein (14.29	91.00
80	404101			C8000950:gi[423560]pir[]A47318 RNA-bindi	1.00	1.00
	404140			NM_006510:Homo sapiens ret finger protei	1.42	1.44
	404165			ENSP00000244562:NRH dehydrogenase (quino	1.00	54.00
	404185			Target Exon	1.00	117.00 13.77
85	404210			NM_005936:Homo sapiens myeloid/lymphoid	5.93 1.00	1.00
05	404253			NM_021058*:Homo sapiens H2B histone fami	1.00	1.00

	W	O 02/0864	143			
	404287		•	C6001909:gi[704441]dbj[BAA18909.1] (D298	29.71	42.00
	404298			C6001238*spi121715 spiP26697 GTA3_CHBCK	1.30	1.00
	404347			Target Exon	1.00	1.00
-	404440			NM_021048:Homo saplans metanoma antigen,	1.00	15.00
5	404721			MM_005596°:Homo sepiens nuclear factor I	1.00	60.00
	404794	NM_000078		chotesteryl ester transfer protein, plas	1.07	1.38
	404854			Target Exon	1.61 1.00	2.01 1.00
	404877			NM_005365:Homo sapiens melanoma antigen,	1.00	1.00
10	404927			Target Exxon Target Exxon	1.00	1.00
10	404996 405449			CY000047:gi]11427234 ref XP_009399.1 z	1.00	1.00
	405568			NM_031413°:Homo sapiens cat eye syndrome	1.00	78.00
	405572			Target Exxon	0.76	1.14
	405646			C12000200:qi]4557225[ref]NP_000005.1] al	1.01	1.28
15	405676	BE335714		cytochrome c-1	1.13	2.89
	405770			NM_002362:Homo sapiens melanoma antigen,	45.52	37.00
	405932			C15000305:0f3806122fgb[AAC69198.1] [AF0	1.99	1.99
	406137			NM_000179°:Homo sapians mutS (E. coli) h	2.77	2.38
20	406360			Target Exon	1.00 1.00	35.00 39.00
20	406399			NM_003122*:Horno sapiens serine protease	1.00	1.00
	406467	VE3000	11- 404405	Target Exon immunoglobulin lambda locus	1.41	1.74
	406621 406642	X57809	Hs.181125	ob:Homo sapiens mRNA for immunoglobulin	2.16	3.91
	406663	AJ245210 U24683	Hs.293441	immunoglobulin heavy constant mu	2.07	2.93
25	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	15.00	51.00
23	406673	M34996	Hs.198253	major histocompatibility complex, class	0.98	3.09
	406676	X58399	Hs.81221	Human L2-9 transcript of unrearranged im.	1.30	1.53
	406578	U77534		gb:Human clone 1A11 immunoglobulin varia	1.33	1.45
	405685	M18728		gb:Human nonspecific crossreacting antig	1.46	2.85
30	406587	M31126	Hs.272822	pregnancy specific beta-1-glycoprotein 9	8.61	8.50
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	226.37	350.00
	406698	X03068	Hs.73931	major histocompatibility complex, class	1.01	2.52 32.00
	406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transferas	20.25 0.75	1.91
25	406851	AA609784		major histocompatibility complex, class	38.15	1114.00
35	406964 406967	M21305		gb:Human alpha satellite and satellite 3 gb:Human parathyroid hormone-like protei	1.00	1.00
	406974	M24349 M57293		gb:Human parathyroid hormone-related pep	1.00	1.00
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	1.77	1.10
	407128	R83312	Hs.237260	EST	1.00	1.00
40	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	142.70	135.00
	407168	R45175	Hs.117183	ESTs	2.16	18.00
	407239	AA076350	Hs.67846	leukocyte immunoglobulin-like receptor,	1.10	1.57
	407242	M18728		gb:Human nonspecific crossreacting antig	1.12	2.85
45	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	3.24	15.38
45	407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MA	3.53 19.74	3.68 73.00
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93 gb:Homo sapiens cig33 mRNA, partial sequ	0.06	8.25
	407366 407378	AF026942 AA299264	Hs.271530 Hs.57776	ESTs, Moderately similar to 138022 hypot	1.00	26,00
	407430	AF169351	113.37770	gb:Homo sapiens protein tyrosine phospha	1.00	25.00
50	407453	AJ132087		gb:Homo sagiens mRNA for axonemal dynein	1.00	75.00
-	407577	AW131324	Hs.246759	hypothetical protein MGC12538	1.00	1.00
	407634	AW016569	Hs.136414	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	111,20	228.00
	407710	AW022727	Hs.23616	ESTs	1.00	28.00
c c	407720	AB037776	Hs.38002	KIAA1355 protein	1.89	1.31
55	407746	AK001962		hypothetical protein FLJ11100	1.00 4.51	1.00
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	1.00	5.00 28.00
	407758	D50915 AA608956	Hs.38365	KIAA0125 gene product ESTs, Moderately similar to PURKINJE CEL	0.97	1.14
	407782 407788	BE514982	Hs.112619 Hs.38991	S100 calcium-binding protein A2	7.88	3.83
60	407790	AI027274	Hs,288941	Homo sapiens cDNA FLJ14866 fis, clone PL	3.63	42.00
00	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	89.96	109.00
	407839	AA045144	Hs.161566	ESTs	173.91	108.00
	407944	R34008	Hs.239727	desmocollin 2	111.30	70.00
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	151.17	8.00
65	408031	AA081395	Hs.42173	Homo sapiens cONA FLJ10366 fis, clone NT	9.91	93.00
	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	195.78	231.00
	408070	AW148852	14. 400070	gb:xf05d05.x1 NCI_CGAP_Bm35 Homo sapien	1.00 37.84	1.00 61.00
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7 hypothetical protein FLJ10718	0.85	1.71
70	408122 408212	A1432652 AA297567	Hs.42824 Hs.43728	hypothetical protein	5.88	7.91
70	408243	Y00787	Hs.624	interleukin 8	4.27	9.98
	408349	BE546947	Hs.44276	homeo box C10	3.79	3.46
	408353	BE439838	Hs.44298	mitochondrial ribosomal protein S17	1.88	1.65
	408354	AI382803	Hs.159235	ESTs	1.00	73.00
75	408369	R38438	Hs.182575	solute carrier family 15 (H??? transport	1.41	16.50
	408380	AF123050	Hs.44532	diubiquitin	15.19	37.22
	408482	NM_000676	Hs.45743	adenosine A2b receptor	1.65	1.19
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	1.98 1.55	1.24 1.50
80	408536	AW381532	Hs.135188	ESTs	1.00	1.00
ov	408545 408572	AW235405	Hs.253690 Hs.226568	ESTs ESTs, Moderately similar to ALU4_HUMAN A	1.00	44.00
	408572	AA055611 AW963372	Hs.46677	PRO2000 protein	107.16	56.00
	408560	AA525775	. 44.70077	ESTs, Moderately similar to PC4259 ferri	1.00	1.00
	408761	AA057264	Hs.238936	ESTs, Weakly similar to (defline not ava	52.24	141.00
85	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	3.05	109.00

	W	O 02/086	443			
	408783	AF192522	Hs.47701	NPC1 (Niamann-Pick disease, type C1, gen	1.02	1.07
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	41.19 24.67	61.00 45.00
	408805 408341	H69912 AW438865	Hs.48269 Hs.256862	vaccinia related kinase 1 ESTs	1.00	58.00
5	408873	AL046017	Hs.182278	calmodufin 2 (phosphorylase kinase, delt	1.00	89.00
-	408908	BE296227	Hs.250822	serine/threonine kinase 15	7.76	1.00
	408992	AA059325	Hs.71642	guanine nucleotide binding protein (G pr	1.00	1.00
	408996	A1979168	Hs.344096	glycoprotein (transmembrane) nmb	3.71	5.50
10	409015	BE389387	Hs.49767	NM_004553:Homo sapiens NADH dehydrogenas	1.44 4.28	1.24 5.32
10	409038 409041	T97490 AB033025	Hs.50002 Hs.50081	smati inducible cytokine subfamily A (O) Hypothetical protein, XP_051860 (KIAA119	112.42	195.00
	409077	AA401369	Hs.190721	ESTs	1.00	17.00
	409093	BE243834	Hs.50441	CGI-04 protein	2.02	1.93
	409103	AF251237	Hs.112208	XAGE-1 protein	80.44	40.00
15	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	14.87	6.00
	409187	AF154830	Hs.50966	carbampyl-phosphate synthetase 1, mitoch	1.00 1.22	1.00 1.00
	409228 409234	AI654298 AI879419	Hs.271695 Hs.27206	ESTs, Wealdy similar to 2109260A B cell ESTs	1.00	1.00
	409268	AA625304	Hs.187579	ESTs	11.90	23.00
20	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	1.00	1.00
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	168.91	35.00
	409404	BE220053	Hs.129056	ESTs	1.00	1.00
	409420	Z15008	Hs.54451 Hs.346735	taminin, gamma 2 (nicein (100kD), kalini	79.74 1.45	96.00 2.10
25	409430 409446	R21945 Al561173	Hs.67688	splicing factor, arginine/serine-rich 5 ESTs	1.00	4.00
	409506	NM_006153	Hs.54589	NCK adaptor protein 1	3.97	28.00
	409522	AA075382		gb:zm87b03.s1 Stratagene ovarian cancer	15.98	141.00
	409582	AA401369	Hs.190721	ESTs	1.00	17.00
20	409532	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	292.12 1.00	79.00 82.00
30	409705 409719	M37762 Al769160	Hs.56023 Hs.108681	brain-derived neurotrophic factor Homo sapiens brain tumor associated prot	1.00	1.00
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	0.12	18.12
	409744	AW675258	Hs.56265	Homo sapiens mRNA; cDNA DKFZp586P2321 (f	20.75	51.00
	409757	NM_001898	Hs.123114	cystatin SN	22.46	15.80
35	409866	AW502152		gb:UI-HF-BR0p-air-f-11-0-UI.r1 NIH_MGC_5	1.00	1.00
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	1.50 25.92	1.09 50.00
	409902 409935	AJ337658 AW511413	Hs.156351 Hs.278025	ESTs ESTs	2.63	2.11
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	2.17	4.01
40	409958	NM_001523	Hs.57697	hyaturonan synthase 1	0.91	2.07
	410001	AB041036	Hs.57771	kalikrein 11	1.04	2.28
	410032	BE065985	11- 50000	gb:RC3-BT0319-120200-014-a09 BT0319 Homo	1.00 1.00	58.00 34.00
	410037 410044	AB020725 BE566742	Hs.58009 Hs.58169	KIAA0918 protein highly expressed in cancer, rich in teuc	1.00	1.00
45	410048	W76467	Hs.58218	profine oxidase homolog	1.03	1.44
	410076	T05387	Hs.7991	ESTs	1.12	1.50
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	9.89	1.00 1.00
	410153 410166	BE311926 AK001376	Hs.15830 Hs.59346	hypothetical protein FLJ12691 hypothetical protein FLJ10514	1.00 1.00	1.00
50	410193	AJ132592	Hs.59757	zinc finger protein 281	42.01	51.00
•	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	1.72	1.32
	410309	BE043077	Hs.278153	ESTs	1.00	2.00
	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	32.08	75.00 1.00
55	410348 410407	AW182663 X66839	Hs.95469 Hs.63287	ESTs carbonic anhydrase IX	1.00 1.40	1.11
55	410418	031382	Hs.63325	transmembrane protease, serine 4	4.30	2.03
	410438	AB037756	Hs.45207	hypothetical protein KIAA1335	1.00	18.00
	410553	AW016824	Hs.255527	hypothetical protein MGC14128	1.34	1.04
60	410555	W27235	Hs.64311	a disintegrin and metalloproteinase doma	23.99	1.41
60	410561 410681	BE540255 AW246890	Hs.6994 Hs.65425	Homo sapiens cDNA: FLJ22044 fis, clone H calbindin 1, (28kD)	10.04 10.8B	1.00 18.92
	410781	Al375672	Hs.165028	ESTs	1.00	57.00
	411027	AF072099	Hs.67846	leukocyte Immunoglobulin-like receptor,	1.62	3.78
	411074	X60435	Hs.68137	adenylate cyclase activating polypeptide	1.00	1.15
65	411089	AA456454		cell division cycle 2-like 1 (PITSLRE pr	1.56	1.58
	411152	BE069199	11- 22400E	gb:QV3-BT0379-010300-105-g03 BT0379 Homo	1.00 1.82	84.00 1.45
	411248 411252	AA551538 AB018549	Hs.334605 Hs.69328	Homo sapiens cDNA FLJ14408 fis, clone HE MD-2 protein	7.32	12.74
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	3.44	2.55
70	411365	M76477	Hs.289082	GM2 gangiloside activator protein	1.35	2.02
	411402	BE297855	Hs.69855	NRAS-related gene	1.00	46.00
	411573	AB029000	Hs.70823	KIAA1077 protein	11.40 1.08	11.35 1.90
	411579 411617	AC005258 AA247994	Hs.70830 Hs.90063	U6 snRNA-associated Sm-like protein LSm7 neurocalcin delta	1.74	2.57
75	411732	AA059325	Hs.71642	guanine nucleotide binding protein (G pr	1.02	1.00
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	1.34	2.19
	411789	AF245505	Hs.72157	Adlican	2.19	2.79
	411800	N39342	Hs.103042	microtubule-associated protein 18	23.34 1.00	34.00 8.00
80	411945 412115	AL033527 AK001763	Hs.92137 Hs.73239	v-myc avian myelocytomatosis viral oncog hypothetical protein FLJ10901	2.07	1.64
55	412113	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	118.48	92.00
	412276	BE262621	Hs.73798	macrophage migration inhibitory factor (1.98	1.49
	412464	T78141	Hs.22826	ESTs, Weakly similar to 155214 salivary	1.16	1.34
05	412530	AA766268	Hs.266273	hypothelical protein FLJ13346	41.52	84.00
85	412537	AL031778		nuclear transcription factor Y, alpha	17.90	55.00

	W	O 02/086	443			
	412659	AW753865	Hs.74376	olfactomedin related ER localized protei	14.65 382.46	47.00 128.00
	412719	AW015610	Hs.816 Hs.335951	ESTs hypothetical protein AF301222	54.S0	1.00
	412723 412811	AA648459 H06382	ID.333331	ESTs	1.60	11.00
5	412817	AL037159	Hs.74619	proteasome (prosome, macropain) 26S subu	1.63 17.63	1.42 56.00
	412663	AA121673	Hs.59757 Hs.75258	zinc finger protein 281 H2A histone family, member Y	1.00	22.00
	412924 413004	BE018422 T35901	Hs.75117	interleukin enhancer binding factor 2, 4	2.19	2.05
10	413011	AW068115	Hs.821	biglycan	1.22 0.30	1.88 6.23
10	413048 413063	M93221 AL035737	Hs.75182 Hs.75184	mannose receptor, C type 1 chifinase 3-like 1 (cartilage glycoprote	3.43	8.71
	413129	AF292100	Hs.104613	RP42 homolog	4.67	4.77
	413142	M81740	Hs.75212	omithine decarboxylase 1	1.92 5.73	2.59 27.00
15	413223 413248	AI732182 · T64858	Hs.191866 Hs.21433	ESTs hypothetical protein DKFZp547J036	0.99	1.06
13	413273	U75679	Hs.75257	stem-loop (histone) binding protein	1.00	18.00
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.10 95.94	1.09 69.00
	413281 413364	AA861271 BE536218	Hs.222024 Hs.137516	transcription factor BMAL2 fidgetin-like 1	1.00	1.00
20	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	0.95	2.09
	413409	Al638418	Hs.1440	DEAD/H (Asp-Glu-Ala-Asp/His) box potypep	1.00 1.00	1.00 31.00
	413453 413527	AA129640 BE250788	Hs.128065 Hs.179882	ESTs hypothetical protein FLJ12443	1.08	1.46
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	79.15	114.00
25	413573	AI733859	Hs.149089	ESTs	1.00 8.80	1.00 10.00
	413582 413597	AW295647 AW302885	Hs.71331 Hs.117183	hypothetical protein MGC5350 ESTs	1.00	1.00
	413690	BE157489	110.111.00	gb:RC1-HT0375-120200-011-e06 HT0375 Homo	1.00	1.00
20	413691	AB023173	Hs.75478	ATPase, Class VI, type 118	3.15 2.88	2.32 9.52
30	413719 413753	BE439580 U17760	Hs.75498 Hs.75517	small inducible cytokine subfamily A (Cy taminin, beta 3 (nicein (125kD), katinin	144.10	108.00
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	1.00	17.00
	413833	Z15005	Hs.75573	centromere protein E (312kD) ESTs	1.00 64.24	1.00 148.00
35	413882 413926	AA132973 AA133338	Hs.184492 Hs.54310	ESTs	1.00	67.00
-	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, done NT	43.42	42.00 1.11
	413995	BE048146	Hs.75671 Hs.75716	syntaxin 1A (brain) serine (or cystelne) proteinase inhibito	1.23 2.02	2.51
	414035 414142	Y00630 AW368397	Hs.334485	Homo sapiens cDNA FLJ14438 fis, clone HE	1.00	102.00
40	414180	AI863304	Hs.120905	Homo sapiens cDNA FLJ11448 fis, clone HE	6.92 1.00·	77.00 1.00
	414245 414275	BE148072 AW970254	Hs.75850 Hs.889	WAS protein family, member 1 Charot-Leyden crystal protein	1.00	59.00
	414317	BE263280	Hs.75888	phosphogluconate dehydrogenase	1.52	1.73
A =	414334	AA824298	Hs.21331	hypothetical protein FLJ10036	1.78 33.90	1.72 151.00
45	414341 414368	D80004 W70171	Hs.75909 Hs.75939	KIAA0182 protein uridine monophosphale kinase	171.60	97.00
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.32	1.85
	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	226.15 1.64	66.00 1.98
50	414570 414618	Y00285 A1204600	Hs.76473 Hs.96978	insulin-like growth factor 2 receptor hypothetical protein MGC10764	1.87	72.00
	414675	R79015	Hs.296281	interleukin enhancer binding factor 1	1.51 43.61	1.39 64.00
	414683	S78296 AF002020	Hs.76888 Hs.76918	hypothetical protein MGC12702 Niemann-Pick disease, type C1	28.63	71.00
	414696 414711	AI310440	Hs.288735	Homo sapiens cDNA FLJ13522 fis, clone PL	14.86	42.00
55	414718	H95348	Hs.107987	ESTs	1.00 1.64	5.00 1.44
	414732 414747	AW410976 U30872	Hs.77152 Hs.77204	minichromosome maintenance deficient (S. centromere protein F (350/400kD, mitosin	65.01	74.00
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	130.35	121.00
60	414774	X02419	Hs.77274	plasminogen activator, urokinase	2.24 1.63	2.19 1.53
60	414805 414809	D14694 A1434699	Hs.77329 Hs.77356	phosphatidylserine synthase 1 transferrin receptor (p90, CD71)	1.97	2.60
	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.48	10.60
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian DNA (cytosine-5-)-methyltransferase 1	103.22 1.80	143.00 1.69
65	414839 414883	X63692 AA926960	Hs.77462	CDC28 protein kinase 1	14.29	10.06
-	414907	X90725	Hs.77597	polo (Drosophia)-like kinase	1.95 3.00	2.20 2.90
	414914 414945	U49844 BE076358	Hs.77613 Hs.77667	ataxia telangiectasia and Rad3 related tymphocyte antigen 6 complex, locus E	1.02	1.21
	414972	BE263782	Hs.77695	KIAA0008 gene product	1.00	1.00
70	415014	AW954064	Hs.24951	ESTs	1.42 1.00	2.84 30.00
	415091 415138	AL044872 C18356	Hs.77910 Hs.295944	3-hydroxy-3-methylglutaryl-Coenzyme A sy tissue factor pathway inhibitor 2	34.72	107.00
	415227	AW821113	Hs.72402	ESTs	1.87	49.00
75	415238	R37780	Hs.21422	ESTs ESTs	1.00 1.00	1.00 1.00
75	415263 415295	AA948033 R41450	Hs.130853 Hs.6546	ESTs ESTs	1.00	1.00
	415339	NM_015156	Hs.78398	KIAA0071 protein	51.18	165.00
	415669	NM_005025	Hs.78589 Hs.78596	serine (or cysteine) proteinase Inhibito proteasome (prosome, macropain) subunit,	30.84 1.48	63.00 1.39
80	415674 415709	BE394784 AA649850	Hs.278558	ESTs	1.00	1.00
	415735	AA704162	Hs.120811	ESTs, Wealdy similar to 138022 hypotheti	1.00	72.00 31.00
	415799 415817	AA653718 U88967	Hs.225841 Hs.78867	DKFZP434D193 protein protein tyrosine phosphatase, receptor-t	6.23 24.30	1.00
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	32.51	35.00
85	415989	Al267700		ESTs	78.89	1.00

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	416018	AW138239	Hs.78977	proproteia convertase subfilisin/kexin t	1.00	1.00
	416065	BE267931	Hs.78996 Hs.79018	proliferating cell nuclear antigen chromatin assembly factor 1, subunit A (3.35 39.03	2.32 3.00
	416111 416177	AA033813 AA174069	Hs.187607	ESTs	1.00	9.00
5	416178	AI808527	Hs.192822	serologically defined breast cancer anti	3.83	3.76
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.67 9.70	1.00 1.00
	416209 416239	AA236776 AL038450	Hs.79078 Hs.48948	MAD2 (mitotic arrest deficient, yeast, h ESTs	83.87	129.00
	416250	AA581386	Hs.73452	hypothetical protein MGC10791	1.96	2.12
10	416322	BE019494	Hs.79217	pyrroline-5-carboxytate reductase 1	2.08 1.00	1.73 89.00
	416423 416448	H54375 L13210	Hs.268921 Hs.79339	ESTs lectin, galactoside-binding, soluble, 3	1.28	1.54
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	27.29	67.00
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	53.29	51.00
15	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3 hypothetical protein FLJ23017	9.96 3.68	5.00 33.00
	416722 416819	AA354604 U77735	Hs.122546 · Hs.80205	pim-2 oncogene	1.59	1.84
	416936	N21352	Hs.42987	ESTs, Wealty similar to S21348 probable	1.00	1.00
20	417034	NM_006183	Hs.80962	neurotensin Homo sapiens cDNA FLJ12033 fis, clone HE	1.00 32.95	1.00 156.00
20	417061 417079	A1675944 U65590	Hs.188691 Hs.81134	interleukin 1 receptor antagonist	3.91	4.93
	417218	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	1.00	51.00
	417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	3.38 82,94	2.05 25.36
25	417308 417315	H60720 Al080042	Hs.81892 Hs.180450	KIAA0101 gene product ribosomal protein S24	106.61	121.00
	417324	AW265494	120100100	ESTs	1.20	1.28
	417356	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	8.97 2.59	3.27 1.82
	417389 417428	BE260964 N87579	Hs.82045 Hs.278871	midkine (neurite growth-promoting factor gb:LL2030F Human fetal heart, Lambda ZAP	1.00	52.00
30	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	304.75	173.00
	417466	AI681547	Hs.59457	hypothetical protein FLJ22127	1.24	1.34
	417512	A1979168	Hs.344095	glycoprotein (transmembrane) mmb ataxia-telangiectasia group D-associated	2.14 2.66	5.50 1.68
	417515 417542	L24203 J04129	Hs.82237 Hs.82269	progestagen-associated endometrial prote	1.28	1.35
35	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	42.76	51.00
	417715	AW969587	Hs.86366	ESTs	6.35 113.31	2.75 56.00
	417720 417791	AA205625 AW965339	Hs.208057 Hs.111471	ESTs ESTs	39.98	16.00
	417830	AW504786	Hs.122579	hypothetical protein FLJ 10461	2.61	31.00
40	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	2.35 1.52	2.44 1.11
	417900 417933	BE250127 X02308	Hs.82906 Hs.82962	CDC20 (cell division cycle 20, S. cerevi thymidylate synthetase	4.74	2.55
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	3.61	5.21
45	417975	AA641836	Hs.30085	hypothetical protein FLJ23186	12.49 1.00	38.00 26.00
45	417991 418004	AA731452 U37519	Hs.190008 Hs.87539	ESTs aldehyde dehydrogenase 3 family, member	3.02	2.12
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	187.59	1.00
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.85	2.63 1.69
50	418057 418113	NM_012151 AJ272141	Hs.83363 Hs.83484	coagulation factor VIII-associated (intr SRY (sex determining region Y)-box 4	1.54 6.82	5.22
50	418140	BE613836 .	Hs.83551	microfibrillar-associated protein 2	1.26	1.46
	418203	X54942	Hs.83758	CDC28 protein kinase 2	134.19 1.00	144.00 1.00
	418207 418216	C14685 AA662240	Hs.34772 Hs.283099	ESTs AF15q14 protein	64.66	61.00
55	418236	AW994005	Hs.337534	ESTs	18.53	147.00
	418249	H89226	Hs.34892	KIAA1323 protein	30.53	106.00 3.00
	418281 418283	U09550 S79895	Hs.1154 Hs.83942	oviductal glycoprotein 1, 120kD (mucin 9 cathepsin K (pycnodysostosis)	1.00 3.96	5.16
	418300	AJ433074	Hs.86582	Homo sapiens cDNA: FLJ21578 fis, clone C	3.18	2.91
60	418322	AA284166	Hs.84113	cyclin-dependent kinase Inhibitor 3 (CDK	11.96	6.68
	418327	U70370	Hs.84136 Hs.241407	paired-like homeodomain transcription fa serine (or cysteine) proteinase inhibito	9.23 1.00	2.22 1.00
	418345 418379	AJ001696 AA218940	Hs.137516	fidgetin-like 1	21.68	44.00
	418397	NM_001269	Hs.84746	chromosome condensation 1	1.00	8.00
65	418403	D86978	Hs.84790 Hs.85266	KIAA0225 protein integrin, beta 4	16.91 1.56	18.98 1.16
	418462 418478	BE001596 U38945	Hs.1174	cyclin-dependent kinase Inhibitor 2A (me	3.22	2.38
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	2.66	2.22
70	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxyllc	2.04 1.33	2.21 37.00
70	418538 418543	BE244323 NM_005329	Hs.85951 Hs.85962	exportin, tRNA (nuclear export receptor hyakıronan synthase 3	1.04	1.23
	418574	N28754		M-phase phosphoprotein 9	48.60	85.00
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	18.24	26.00 1.41
75	418641 418661	BE243136 NM_001949	Hs.86947 Hs.1189	a disintegrin and metalloproteinase doma E2F transcription factor 3	1.19 29.05	43.00
	418663	AK001100	Hs.41690	desmocollin 3	112.17	19.00
	418678	NM_001327	Hs.87225	cancer/testis antigen	1.18	1.10
	418686 418689	Z36830 Al360883	Hs.87268 Hs.274448	annexin A8 hypothetical protein FLJ11029	1.54 1.19	1.98 1.04
80	418712	Z42183	113-61 4440	gb:HSC0BF041 normalized infant brain cDN	1.00	12.00
	418727	AA227609	Hs.94834	ESTs	1.00	49.00
	418738	AW388633	Hs.6682 Hs.191721	solute carrier family 7, (cationic amino ESTs	49.85 1.00	1.00 140.00
4.0	418819 418830	AA228776 BE513731	Hs.88959	hypothetical protein MGC4816	20.97	23.00
85	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	57.09	35.00

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	418971	AA360392	Hs.87113	ESTs	1.00	12.00 28.00
	418973	AA233056	Hs. 191518	ESTs insufinoma-associated 1	. 4.89 1.00	10.00
	419078 419079	M93119 AW014836	Hs.89584 Hs.18844	ESTs	1.09	1.98
5	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	2.06	1.68
_	419088	AJ538323	Hs.52620	integrin, beta 8	15.60 1,11	51.00 1.83
	419092 419121	J05581 AA374372	Hs.89603 Hs.89626	mucin 1, transmembrane parathyroid hormone-like hormone	1.00	1.00
	419171	NM_002846	Hs.89655	protein tyrosine phosphatase, receptor t	1.10	1.14
10	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	1.00	1.00
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	3.18 1.00	2.43 34.00
	419288 419335	AA256106 AW960146	Hs.87507 Hs.284137	ESTs hypothetical protein FLJ12688	1.00	8.00
	419354	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	22.63	54.00
15	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	2.50 1.00	1.98 7.00
	419423	D26488	Hs.90315	KIAA0007 protein ob:HUM316G10B Clontech human aorta polyA	1.00	12.00
	419443 419452	D62703 U33635	Hs.90572	PTK7 protein tyrosine kinase 7	1.64	1.84
	419474	AW968619	Hs.155849	ESTs	13.63	62.00
20	419485	AA489023	Hs.99807	ESTs, Wealty similar to unnamed protein	4.27 3.66	2.26 3.63
	419488	AA316241 AU076704	Hs.90691	nucleophosmin/nucleoplasmin 3 fibrinogen, A alpha polypeptide	13.05	115.00
	419502 419539	AF070590	Hs.90869	Homo sapiens clones 24622 and 24623 mRNA	74.60	117.00
	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	1.47	4.98
25	419569	AI971651	Hs.91143	jagged 1 (Alagille syndrome) topoisomerase (DNA) II binding protein	1.00 94.30	4.00 94.00
	419594 419703	AA013051 AI793257	Hs.91417 Hs.128151	ESTs	15.26	50.00
	419721	NM_001650	Hs.288650	aquaporin 4	1.00	191.00
20	419729	AA586442	Hs.21411	gb:no53a03.s1 NCI_CGAP_SS1 Homo sapiens	1.00 2.02	59.00 1.08
30	419741	NM_007019	Hs.93002 Hs.93005	ubiquilin carrier protein E2-C shug (chicken homolog), zinc finger prot	1.00	1.00
	419745 419752	AF042001 AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	29.87	77.00
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	50.99	214.00
36	419936	Al792788		gb:ol91d05.y5 NCI_CGAP_Kid5 Homo sapiens	1.00 1.64	1.00 2.47
35	419937 419983	AB040959 W55956	Hs.93836 Hs.94030	DKFZP434N014 protein Homo sapiens mRNA; cDNA DKFZp586E1624 (f	15.72	94.00
	420005	AW271106	Hs.133294	ESTs	3.15	1.43
	420047	AJ478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	12.45 1.00	39.00 117.00
40	420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT cyclin-dependent kinase 4	1.43	1.21
40	420162 420251	BE378432 AW374968	Hs.95577 Hs.348112	Human DNA sequence from clone RP5-1103G7	2.35	3.23
	420259	AF004884	Hs.96253	calcium channel, voltage-dependent, P/Q	0.77	1.15
	420281	Al623693	Hs.323494	ESTS	45.04 49.22	54.00 31.00
45	420309 420332	AW043637 NM_001756	Hs.21766 Hs.1305	ESTs, Weakly similar to ALU5_HUMAN ALU S serine (or cysteine) proteinase inhibito	0.05	2.82
7,7	420380	AA640891	Hs.102406	ESTs	0.99	2.74
	420462	AF050147	Hs.97932	chondromodulin I precursor	1.00 49.74	1.00 133.00
	420520	AK001978	Hs.98510 Hs.98806	similar to rab11-binding protein hypothetical protein	94.65	88.00
50	420552 420560	AK000492 AW207748	Hs.59115	ESTs	1.00	17.00
-	420610	Al683183	Hs.99348	distal-less homeo box 5	1.00	13.00
	420689	H79979	Hs.88678	ESTs	50.09 1.00	95.00 31.00
	420721 420759	AA927802 T11832	Hs.159471 Hs.127797	ZAP3 protein Homo sapiens cDNA FLJ11381 fis, clone HE	1.00	48.00
55	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	3.04	1.25
	420900	AL045633	Hs.44269	ESTs	2.24	7.00
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy transcription factor 17	1.00 1.00	8.00 27.00
	421002 421027	AF116030 AA761198	Hs.100932 Hs.55254	ESTs	2.87	38.00
60	421037	A168480B	Hs.197653	ESTs	1.00	46.00
	421041	N36914	Hs.14691	ESTs, Moderately similar to 138022 hypot	1.00 1.34	98.00 1.46
	421073	NM_004689	Hs.101448 Hs.1355	metastasis associated 1 cathepsin E	119.47	427.00
	421110 421133	AJ250717 AA401369	Hs.190721	ESTs	1.10	17.00
65	421150		Hs.189902	ESTs	1.45	1.63
	421155		Hs.102267	lysyl oxidase	1.00 1.37	15.00 1.10
	421307 421316	BE539976 AA2872 03	Hs.103305 Hs.324728	Homo sapiens mRNA; cDNA DKFZp434B0425 (f SMA5	1.00	21.00
	421379		Hs.103982	small inducible cytokine subfamily B (Cy	1.92	3.94
70	421451	AA291377	Hs.50831	ESTs	5.89	14.00 1.76
	421474		Hs.104637 Hs.105097	solute carrier family 1 (glutamate trans thymidine kinase 1, soluble	1.46 1.56	1.08
	421506 421508		Hs.105115	absent in melanoma 2	5.11	5.23
~-	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	1.00	3.00
75	421524	AA312082	Hs.105445	GDNF family receptor alpha 1	2.63 1.46	10.58 1.88
	421526 421552		Hs.105460 Hs.105700	DKFZP56400823 protein secreted frizzled-related protein 4	30.21	50.32
	421574		Hs.105924	defensin, beta 2	1.67	1.74
00	421582	Al910275		trefoil factor 1 (breast cancer, estroge	1.23	1.00
80	421633		Hs.106260	sorting nexin 10	1.00 0.05	116.00 6.33
	421659 421677		Hs.106511 Hs.38282	protocadherin 17 ESTs	1.31	1.42
	421753		Hs.107911	ATP-binding cassette, sub-tamily B (MDR/	1.41	1.20
0.5	421773	W69233	Hs.112457	ESTs	1.12	1.14 1.29
85	421777	BE562088	Hs.108196	HSPC037 protein	1.97	1.23

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	421800	AA298151	Hs.222969	ESTs	1.03	1.30
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.88	1.59
	421896	N62293	Hs.45107	ESTs	11.84	22,80 90.00
_	421928	AF013758	Hs.109543	polyadenylate binding protein-Interactin	45.89	
5	421931	NM_000814	Hs.1440	gamma-aminobutyric acid (GABA) A recepto	1.13	1.49 20.25
	421948	L42583	Hs.334309	kerafin 6A	51.83 1.17	1.15
	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	1.00	52.00
	422026	U80736	Hs.110826	trinucleotide repeat containing 9	67.61	62.00
10	422094	AF129535	Hs.272027	F-box only protein 5	4.37	2.34
10	422095	A1868872	Hs.282804	hypothetical protein FL/22704	4.18	95.50
	422109	\$73265	Hs.1473	gastrin-releasing peptide gb:QV0-OT0033-010400-182-a07 OT0033 Homo	40.89	71.00
	422128	AW881145	Un 4470	serine (or cysteine) proteinase inhibito	1.13	1.38
	422129	AU076635	Hs.1478 Hs.112110	mitochondrial ribosomal protein L42	41.59	96.00
15	422134	AW179019		protease inhibitor 3, skin-derived (SKAL	2.37	1.10
15	422158	L10343	Hs.112341	S100 calcium-binding protein A7 (psorias	3.29	1.68
	422168	AA586894	Hs.112408 Hs.114218	frizzled (Drosophita) homolog 6	4.93	5.73
	422278 422282	AF072873	Hs.114309	apolipoprotein L	1.49	1.71
	422283	AF019225 AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	25.99	10.91
20	422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS, polypept	1.54	1.41
20	422310	AF073515	Hs.114948	cytokine receptor-like factor 1	1.15	1.78
	422330	D30783	Hs.115263	epiregulin	1.00	112.00
	422364	AF067800	Hs.115515	C-type (calcium dependent, carbohydrate-	9.39	60.00
	422406	AF025441	Hs.116206	Opa-interacting protein 5	18.33	53.00
25	422424	AI186431	Hs.295638	prostate differentiation factor	1.71	3.21
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	47.53	32.00
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	73.68	35.54
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	173.97	26.00
	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	4.68	2.92
30	422656	AI870435	Hs.1569	LIM homeobox protein 2	1.00	1.00
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Dani	3.89	4.55
	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	1.05	1.46
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	3.88	1.53
	422809	AK001379	Hs.121028	hypothetical protein FLJ 10549	99.56	53.00
35	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.69	3.17
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	70.46	61.00
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	77.74	3.00
	422960	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	5.88	8.55
	422963	AA401369	Hs.190721	ESTs	171.41	17.00
40	422976	AU076657	Hs.1600	chaperonin containing TCP1, subunit 5 (e	2.12	1.62
	422981	AF026445	Hs.122752	TATA box binding protein (TBP)-associate	10.49	35.00 32.47
	422986	AA319777	Hs.221974	ESTs	12.40 16.41	60.00
	423034	AL119930		gb:DKFZp761A092_r1 761 (synonym: harny2)	1.00	1.00
15	423049	X59373	Hs.188023	ESTs, Moderately similar to HXDA_HUMAN H	1.82	2.96
45	423081	AF262992	Hs.123159	sperm associated antigen 4	1.14	1.53
	423184	NM_004428	Hs.1624	ephrin-A1 collagen, type VII, alpha 1 (epidermolys	2.14	1.69
	423217	NM_000094	Hs.1640	ribulose-5-phosphate-3-epimarasa	7.18	14.00
	423248	AA380177 BE006775	Hs.125845 Hs.126782	sushi-repeat protein	21.90	64.00
50	423309 423361	AW170055	Hs.47628	ESTs	1.00	1.00
30	423453	AW450737	Hs.128791	CGI-09 protein	55.52	66.00
	423511	AF036329	Hs.129715	gonadotropin-releasing hormone 2	0.88	1.17
	423516	AB007933	Hs.129729	ligand of neuronal nitric oxide synthase	1.76	5.40
	423551	AA327598	Hs.233785	ESTs	3.54	4.33
55	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	1.00	50.00
-	423575	C18863	Hs.163443	Horno sapiens cDNA FLJ11576 fis, clone HE	38.88	70.00
	423624	AI807408	Hs.166368	ESTs	1.00	67.00
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	76.02	1.00
	423542	AW452650	Hs.157148	hypothetical protein MGC13204	19.14	58.00
60	423562	AA642452	Hs.130881	B-cell CLL/tymphoma 11A (zinc finger pro	3.61	13.57
	423573	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	240.73	40.00
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	1.00	59.00
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.20	1.00
	423761	NM_006194	Hs.132576	paired box gene 9	1.00	1.00
65	423787	AJ295745	Hs.236204	nuclear pore complex protein	7.18	6.64
	423816	AF151064		hypothetical protein	1.00	44.00
	423826	U20325	Hs.1707	cocaine- and amphetamine-regulated trans	1.00	1.00
	423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	1,00	1.00
70	423887	AL080207	Hs.134585	DKFZP434G232 protein	1.00	1.00 31.00
70	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription f	31.33 5.81	10.87
	423954	AW753164	Hs.288604	KIAA1632 protein	3.55	3.30
	423961	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin	233.42	68.00
	424012	AW368377	Hs.137569	tumor protein 63 kOa with strong homolog	0.93	1.01
75	424016	AW163729	Hs.6140	hypothetical protein MGC15730 Homo sapiens cDNA FLJ14354 fis, clone Y7	21,30	52.00
13	424028	AF055084	Hs.153692		1.00	1.00
	424046	AF027866	Hs.138202 Hs.102267	serine (or cysteine) proteinase inhibito lysyl oxidase	21.91	70.00
	424086 424098	AI351010 AF077374	Hs.139322	small proline-rich protein 3	137.82	54.00
	424120	T80579	Hs.290270	ESTs	1.00	1.00
80	424165	AW582904	Hs.142255	islet amytoid polypeptide	1.00	34.00
50	424200	AA337221		gb:EST41944 Endometrial turnor Homo sapie	13.06	48.00
	424279	L29306	Hs.171814	tryptophan hydroxylase (tryptophan 5-mon	1.00	1.00
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	164.58	87.00
	424326	NM_014479	Hs.145296	disintegrin protesse	53.72	302.00
85	424340	AA339036	Hs.7033	ESTs	0.88	1.15
-5	1010			· -		

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	424351	BE622117	Hs.145567	hypothetical protein	0.93	1.03
	424364	AW383226	Hs.201189	ESTs, Wealdy similar to G01763 atrophin-	7.02	3.24
	424381	AA285249	Hs.146329	protein kinase Chk2	95.55 1.63	92.00 3.25
5	424411 424420	NM_005209 BE614743	Hs.146549 Hs.146688	crystaffin, beta A2 prostaglandin E synthase	1.63	1.33
,	424441	X14850	Hs.147097	H2A histone family, member X	1.82	1,29
	424502	AF242388	Hs.149585	tengsin	1.60	1.00
	424503	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor, mitochondrial translational initiation f	1.02 1.00	2.24 17.00
10	424513 424539	8E385864 L02911	Hs.149894 Hs.150402	Activin A receptor, type I (ACVR1) (ALK	32.46	108.00
10	424568	AF005418	Hs.150595	cytochrome P450, subfamily XXVIA, polype	3.40	2.58
	424502	AK002055	Hs.151045	hypothetical protein FLJ11193	31.87	25.00
	424529	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.58 1.00	2.37 1.00
15	424645 424687	NM_014682 J05070	Hs.151449 Hs.151738	KIAA0535 gene product matrix metalloproteinase 9 (gelatinase B	2.12	2.23
10	424717	AW992292	Hs.152213	wingless-type MMTV integration site fami	1.00	1.00
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	56.19	12.00 1,30
	424840	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo Noi56 (D. melanogaster)-like protein	2.65 1.23	1.05
20	424867 424905	AI024860 NM_002497	Hs.153591 Hs.153704	NIMA (never in mitosis gene a)-related k	21.35	1.00
-0	424979	D87989	Hs.154073	UDP-galactose transporter related	1.36	1.35
	424999	AW953120		gb:EST365190 MAGE resequences, MAGB Horno	1.24	1.41 11.00
	425048 425057	H05468 AAB26434	Hs.164502 Hs.1619	ESTs achaeta-scute complex (Orosophila) homol	1.00 7.46	87.00
25	425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	2.52	3.82
	425118	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	4.84	4.03
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	3.62 1.00	2.73 53.00
	425202 425234	AW962282 AW152225	Hs.152049 Hs.165909	ESTs, Wealdy similar to 138022 hypotheti ESTs, Wealdy similar to 138022 hypotheti	100.77	44.00
30	425234	AW067800	Hs.155223	sianniocatcin 2	3.30	2.90
-	425245	A1751768	Hs.155314	KIAA0095 gene product	1.91	2.32
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	1.41 1.00	1.49 68.00
	425266 425274	J00077 BE281191	Hs.155421 Hs.155462	alpha-fetoprotein minichromosome maintenance deficient (mi	1.97	1.63
35	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	141.49	123.00
	425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	1.00	84.00
	425371	D49441	Hs.155981	mesothelin	0.87 14.90	1.59 5.76
	425397 425420	J04088 BE536911	Hs.156346 Hs.234545	topoisomerase (DNA) II alpha (170kD) hypothetical protein NUF2R	1.00	1.00
40	425424	NM_004954	Hs.157199	ELKL motif kinase	10.58	9.74
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homoto	1.74	1.40
	425566	AW162943	Hs.250618	UL16 binding protein 2	1.49 53.29	1.14 233.00
	425580 425650	L11144 NM_001944	Hs.1907 Hs.1925	galanin desmoglein 3 (pemphigus vulgaris antigen	33.45	1.00
45	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	1.00	55.00
	425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-recept	1.00	10.00
	425734 425776	AF056209 U25128	Hs.159396 Hs.159499	peptidylglycine alpha-amidating monooxyg parathyroid hormone receptor 2	1.00 1.00	41.00 48.00
	425810	A)923627	Hs.31903	ESTs	27.39	98.00
50	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.99	1.58
	425849	AJ077288	Hs.296323	serum/glucocorticoid regulated kinase	71.16 1.35	3.42 1.34
	425852 426067	AK001504 AA401369	Hs.159651 Hs.190721	death receptor 6, TNF superfamily member ESTs	1.01	17.00
	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	26.26	47.00
55	426215	AW067800	Hs.155223	stanniocalcin 2	1.91	2.90
	426227	U67058	Hs.154299 Hs.168950	Human proteinase activated receptor-2 mR Homo sapiens mRNA; cDNA DKFZp566A1046 (f	22.40 1.00	25.00 1.00
	426269 426283	H15302 NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	91.39	229.00
	426329	AL389951	Hs.271623	nucleoparin 50kD	4.34	4.08
60	426427	M86699	Hs.169840	TTK protein kinase	7.02	1.00
	426432 426440	AF001601 BE382756	Hs.169857 Hs.169902	paraoxonase 2 solute carrier family 2 (facilitated glu	1.16 2.59	1.68 1.71
	426459	AF151812	Hs.169992	hypothetical 43.2 Kd protein	1.56	1.66
<i>~</i> -	426471	M22440	Hs.170009	transforming growth factor, alpha	20.60	26.00
65	426496	D31765	Hs.170114	KIAA0061 protein	9.81 19.23	22.00 17.00
	426501 426514	AA401369 BE616633	Hs.190721 Hs.170195	ESTs bane marphogenetic protein 7 (asteogenic	103.74	41.00
	426536	AI949749	Hs.44441	ESTs	4.65	23.00
20	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	1.00	43.00
70	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	160.06 1.51	8.00 1.35
	426691 426746	NM_006201 J03626	Hs.171834 Hs.2057	PCTAIRE protein kinase 1 uridine monophosphate synthetase (orotat	2.13	1.68
	426752	X69490	Hs.172004	tün	0.02	5.14
75	426784	U03749	Hs.172216	chromogranin A (parathyroid secretory pr	1.72	1.71
75	426807 426812	AA385315 AF105365	Hs.156682 Hs.172613	ESTs solute carrier family 12 (potassium/chlo	1.30 1.47	1.64 1.53
	426814	AF036943	Hs.172619	myelin transcription factor 1-like	1.00	1.00
	426831	BE296216	Hs.172673	S-adenosylhomocysteine hydrolase	1.51	1.25
90	426897	AA401369	Hs.190721	ESTs	141.56	17.00
80	426925 426935	NM_001196 NM_000088	Hs.315689 Hs.172928	Homo sapiens cONA: FLJ22373 fis, clone H collagen, type I, alpha 1	32.61 2.65	38.00 3.16
	426955 426964	AA393739	Hs.287416	Homo sapiens cDNA FLJ11439 fis, clone HE	1.97	3.49
	426966	Al493134		sclerostin	1.00	1.00
85	426991	AK001536	Un 470CCO	Homo sapiens cDNA FLJ10574 fis, clone NT	3.39 4.24	2.28 17.00
O)	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.44	17.00

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	427239	BE270447	Hs_174070	ubiquitin carrier protein gb:ae70b06.s1 Stratagene schizo brain S1	1.58 1.34	1.60
•	427260 427281	AA663848 AA906147	Hs.102869	ESTs	1.00	66.00
_	427335	AA448542	Hs.251677	Gantigen 78	51.83	4.00
5	427354	T57896	Hs.191095	ESTs	1.17 7.31	1.95 41.00
	427355 427376	AW023482 AA401533	Hs.97849 Hs.19440	ESTs ESTs	1.00	57.00
	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	0.42	1.32
	427427	AF077345	Hs.177936	lectin, superfamily member 1 (cartilage-	1.00	20.00 1.00
10	427441	AA412605	Hs.343879 Hs.178078	SPANX family, member C quitamate receptor, metabolropic 4	1.00 0.97	1.03
	427445 427505	X80818 AA361562	Hs.178761	26S proteasome-associated pad1 homolog	4.60	4.04
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	22.00	45.00 92.00
1.5	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S. hypothetical protein FLJ23188	97.45 1.50	3.24
15	427546 427562	AA188763 R56424	Hs.36793 Hs.26534	ESTs	6.81	40.00
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	69.91	62.00
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLI23228 fis, clone C	2.70 1.37	49.00 1.88
20	427666	A1791495	Hs.180142 Hs.180191	calmodulin-like skin protein hypothetical protein FLJ14904	29.55	67.00
20	427668 427677	AA298760 NM_007045	Hs.180296	FGFR1 oncogene partner	3.52	2.63
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	7.41	34.00 70.00
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial ESTs	15.84 7.03	4.52
25	427719 427722	Al393122 AK000123	Hs.134726 Hs.180479	hypothetical protein FLJ20116	2.92	1.74
23	427747	AW411425	Hs.180655	serine/threonine kinase 12	1.76	1.26
	427912	AL022310	Hs.181097	tumor necrosis factor (ligand) superfami	9.63 41.97	59.00 118.00
	427961 428004	AW293165 AA449563	Hs.143134 Hs.151393	ESTs gtutamate-cysteine ligase, cetalytic sub	23.82	1.00
30	428023	AL038843	10	Homo sapiens cDNA: FLJ23602 fis, clone L	1.40	1.33
	428045	AW812795	Hs.337534	ESTs, Moderately similar to 138022 hypot	96.28 1,25	167.00 1.29
	428093	AW594506 AU077258	Hs.104830 Hs.182429	ESTs protein disulfide isomerase-related prot	1.86	1.60
	428098 428129	AJ244311	Hs.26912	ESTs	1.00	42.00
35	428169	Al928984	Hs.182793	golgi phosphoprotein 2	2.76	2.11 1.00
	428182	BE386042	Hs.293317 Hs.2248	ESTs, Weakly similar to GGC1_HUMAN G ANT small inducible cytokine subfamily B (Cy	1.00 85.59	181.00
	428227 428242	AA321649 H55709	ns.2240 Hs.2250	leukemia inhibitory factor (cholinergic	8.57	21.64
	428330	1,22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	7.77	15.90
40	428434	A1909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	0.58 237,53	1.43 204.00
	428450 428471	NM_014791 X57348	Hs.184339 Hs.184510	KIAA0175 gene product stratifin	6.00	4.60
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	56.54	16.00
45	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.53 1.00	2.15 1.00
45	428505 428532	AL035461 AF157326	Hs.2281 Hs.184786	chromogranin B (secretogranin 1) TBP-interacting protein	1.00	58.00
	428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	1.00	16.00
	428664	AK001656	Hs.189095	similar to SALL1 (sal (Drosophila)-like	1.00 187.37	1.00 255.00
50	428698 428728	AA852773 NM_016625	Hs.334838 Hs.191381	KIAA1866 protein hypothetical protein	47.24	80.00
50	428748	AW593206	Hs.98785	Ksp37 protein	1.00	87.00
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	1.06 1.98	1.13 92.00
	428771 428801	AB028992 AW277121	Hs.193143 Hs.254881	KIAA1069 protein ESTs	1.67	6.15
55	428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible, hep	1.03	1.27
	428839	A1767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	124.17 1.00	43.00 1.00
	428845	AL157579 AF100779	Hs.153610 Hs.194680	KIAA0751 gene product WNT1 inducible signaling pathway protein	15.16	27.00
	428959 428969	AF120274	Hs.194689	arternin	1.36	1.24
60	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like	0.97	3.31 16.47
	429065	AJ753247	Hs.29643 Hs.116586	Horno sapiens cONA FLJ13103 fis, clone NT ESTs	6.82 19.08	67.00
	429164 429170	A1688663 NM_001394	Hs.2359	dual specificity phosphatase 4	16.18	105.00
	429183	AB014604	Hs.197955	KIAA0704 protein	79.72	104.00
65	429201	X03178	Hs.198246	group-specific component (vitamin D bind gap junction protein, beta 5 (connexin 3	1.00 1.33	1.00 1.09
	429211 429220	AF052693 AW207206	Hs.198249	ESTs	1.00	7.00
	429228	A1553633	Hs.326447	ESTs	39.47	29.25
70	429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.01 1.07	1.18 1.00
70	429263 429276	AA019004 AF056085	Hs.198396 Hs.198612	ATP-binding cassette, sub-family A (ABC1 G protein-coupled receptor 51	3.70	142.00
	429359	W00482	Hs,2399	matrix metalloproteinase 14 (membrane-in	1.30	1.94
	429412		Hs.2407	POU domain, class 2, associating factor	94.09 41.91	86.00 10.00
75	429413 429486	NM_014058 AF155827	Hs.201877 Hs.203963	DESC1 protein hypothetical protein FLJ10339	12.19	1.00
, ,	429504		Hs.204238	lipocalin 2 (oncogene 24p3)	1.61	1.08
	429538	BE182592	Hs.11261	small proline-rich protein 2A	4.43	2.90
	429547	AA401369 AW450624	Hs.190721 Hs.220931	ESTs ESTs	1.06 2.89	17.00 65.00
80	429551 429563		Hs.2437	eukaryotic translation initiation factor	1.49	1.37
- •	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	61.86	100.00
	429610		Hs.211092	LUNX protein; PLUNC (palate lung and nas pituitary tumor-transforming 1	1.59 2.78	1.69 1.74
	429612 429616		Hs.252587 Hs.120845	ESTs	1.00	1.00
85	429656		Hs.211584	neurofilament, light polypeptide (68kD)	1.00	4.00

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	429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	69.95 1.25	104.00 1.21
	429736	AF125304 NM_005754	Hs.212680 Hs.220689	turnor necrosis factor receptor superfami Ras-GTPase-activating protein SH3-domain	1.00	7.00
	429782 429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	44.50	1.00
5	429918	AW873986	Hs.119383	ESTs	1.00	78.00
	429978	AA249027	11- 22727	ribosomal protein S6	1.98 1.00	3.09 48.00
	429986 430044	AF092047 AA464510	Hs.227277 Hs.152812	sine oculis homeobox (Drosophila) homolo ESTs	69.27	59.00
	430114	AA847744	Hs.99640	ESTs	1.00	1.00
10	430134	BE350149	Hs.105223	ESTs, Weakly similar to T33188 hypotheti	1.00 1.10	51.00 2.22
	430147	R60704 AW182459	Hs.234434 Hs.125759	hairy/enhancer-of-split related with YRP ESTs, Wealdy similar to LEU5_HUMAN LEUKE	1.00	127.00
	430287 430294	AI538226	Hs.32976	guarrine nucleotide binding protein 4	3.80	1.47
	430300	U60805	Hs.238648	oncostatin M receptor	1.00	35.00
15	430315	NM_004293	Hs.239147	guanine dearninase	92.31 1.18	28.00 1.08
	430337 430378	M36707 229572	Hs.239600 Hs.2556	calmodulin-like 3 humor necrosis factor receptor superfami	5.28	66.00
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	16.76	38.00
20	430393	BE185030	Hs.241305	estrogen-responsive B box protein	1.63 1.00	1.50 1.00
20	430439 430451	AL133561 AA836472	Hs.297939	DKFZP434B061 protein cathepsin B	1.64	2.12
	430454	AW469011	Hs.105635	ESTs	63.35	44.00
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	2.47	1.91
25	430481	AA479678	Hs.203269	ESTs, Moderately similar to ALU8_HUMAN A	1.00 12.28	31.00 41.00
23	430486 430508	BE052109 A1015435	Hs.241551 Hs.104637	chloride channel, calcium activated, fam ESTs	4.75	7.27
	430533	AA480895	Hs.57749	ESTs, Weakly similar to T17288 hypotheti	1.00	1.00
	430563	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.00	1.59
30	430677	Z26317 AA401369	Hs.94560 Hs.190721	desmoglein 2 ESTs	1.72 0.90	1.30 17.00
30	430678 430686	NM_001942	Hs.2633	desmoglein 1	1.00	1.00
	430788	A1742925	Hs.7179	ESTs, Weakly similar to 2004399A chromos	1.62	1.84
	430890	X54232	Hs.2699	glypican 1	1.58 90.28	1.40 132.00
35	430935 430985	AW072916 AA490232	Hs.27323	zinc finger protein 131 (clone pHZ-10) ESTs, Weakly similar to 178885 serine/th	0.94	1.28
33	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	60.25	28.00
	431089	BE041395		ESTs, Weakly similar to unknown protein	23.32	941.00
	431092	Al332764	Hs.125757	ESTs doublesex and mab-3 related transcriptio	13.46 49.43	63.00 62.00
40	431124 431164	AF284221 AA493650	Hs.59506 Hs.94367	Homo sapiens cDNA: FLJ23494 fis, clone L	0.44	2.20
10	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	182.26	101.00
	431221	AW207837	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	4.15 1.00	13.97 86.00
	431277 431322	AA501806 AW970622	Hs.345824	gb:EST382704 MAGE resequences, MAGK Homo	40.55	200.00
45	431342	AW971018	Hs.21659	ESTs	1.00	53.00
	431384	BE158000	Hs.285026	gb:MR2-HT0377-150200-202-e03 HT0377 Homo	0.94	1.14
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu hypothetical protein DKFZp434A1315	1.30 3.90	1.25 26.00
	431494 431515	AA991355 NM_012152	Hs.298312 Hs.258583	endothelial differentiation, lysophospha	1.41	1.87
50	431548	AIB34273	Hs.9711	novel protein	5.66	15.00
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CO49C, alpha	0.99 0.99	1.44 3.51
	431745 431770	AW972448 BE221880	Hs.163425 Hs.268555	ESTs 5-3' exoribonuclease 2	67.12	91.00
	431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	3.36	4.71
55	431846	BE019924	Hs.271580	uroplakin 1B	4.49	2.51 3.32
	431890 431934	X17033 AB031481	Hs.271986 Hs.272214	integrin, alpha 2 (CD49B, alpha 2 subuni STG protein	2.20 1.01	1.04
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	51.17	46.35
	432006	AL137382	Hs.272320	Homo sapiens mRNA; cDNA DKFZp434L1226 (f	0.94	1.65
60	432023	R43020	Hs.236223 Hs.298241	EST	0.94 1.10	47.00 2,24
	432201 432210	AJ538613 AJ567421	Hs.273330	Transmembrane protease, serine 3 Homo sapiens, clone IMAGE:3544662, mRNA,	1.42	1.45
	432226	AW182766	Hs.273558	phosphale cytidylytransferase 1, cholin	1.00	1.00
<i>(</i>	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	18.67	1.00
65	432265 432281	8E382679 AK001239	Hs.285753 Hs.274263	SCG10-like-protein hypothetical protein FLJ10377	1.09 40.98	1.21 58.00
	432365	AK001106	Hs.274419	hypothetical protein FLJ10244	1.00	214.00
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	157.34	37.00
70	432375	BE536069	Hs.2962	S100 calcium-binding protein P	1.65 73.71	1.06 75.00
70	432407 432441	AA221036 AW292425	Hs.163484	gb:zr03f12.r1 Stratagene NT2 neuronal pr ESTs	56.35	72.00
	432489	AI804855	Hs.207530	ESTs	1.00	24.00
	432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, ctone C	137.72	98.00 31.00
75	432552 432583	AI537170 AW023624	Hs.173725 Hs.162282	ESTs, Weakly similar to ALU8_HUMAN ALU S potassium channel TASK-4; potassium chan	1.00 0.27	35.18
15	432606	NM_002104	Hs.3066	granzyme K (serine protesse, granzyme 3;	2.87	6.22
	432625	Al243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	26.63	56.00
	432653	N62096	Hs.293185	ESTs, Wealthy similar to JC7328 amino aci	1.92	5.29 48.00
80	432677 432715	NM_004482 AA247152	Hs.278611 Hs.200483	UDP-N-acetyl-alpha-D-galactosamine:polyp ESTs, Wealdy similar to KIAA1074 protein	1.00 45.13	48.00 31.00
00	432753	NM_014075	Hs.336938	Homo sapiens PRO0593 mRNA, complete cds	1.00	68.00
	432788	AA521091	Hs.178499	Homo sapiens cDNA: FLJ23117 fis, clone L	2.69	3.67
	432842 432867	AW674093 AW016936	Hs.334822 Hs.233364	hypothetical protein MGC4485 ESTs	1.22 1.00	1.34 1.00
85	432917	NM_014125	Hs.241517	PRO0327 protein	10.25	6.62
		- '				

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	432920	U37689	Hs.3128	polymerase (RNA) II (DNA directed) polyp	1.44	1.30
	433001	AF217513	Hs.279905	done HQ0310 PR00310p1	154.79 20.96	85.64 100.00
	433023	AW864793	Hs.87409	thrombospondin 1 Homo sapiens cDNA FLJ11660 fis, clone HE	1.00	10.00
5	433042 433091	AW193534 Y12642	Hs.281895 Hs.3185	lymphocyte antigen 6 complex, locus D	1.20	1.09
,	433159	AB035898	Hs.150587	kinesin-like protein 2	13.82	39.00
	433183	AF231338	Hs.222024	transcription factor BMAL2	1.00	69.00
	433258	AA622788	Hs.203613	ESTs, Weakly similar to ALUB_HUMAN !!!!	1.00 44.81	1.25 117.00
10	433409	A1278802	Hs.25661	ESTs caspase 6, apoptosis-related cysteine pr	70.39	105.00
10	433437 433485	U20536 A1493076	Hs.3280 Hs.201967	aldo-keto reductase family 1, member C2	11.55	2.00
	433537	Al733692	Hs.112488	ESTs	8.65	55.00
	433547	W04978	Hs.303023	beta tutrufin 1, class VI	25.16	83.00
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	1.00 20.30	19.00 49.00
15	433647	AA603367	Hs.222294	ESTs	20.30 5.92	10.03
	433658	L03678	Hs.156110 Hs.135150	immunoglobufin kappa constant tung type-I cell membrane-associated gly	2.29	2.22
	433800 433819	AI094221 AW511097	Hs.112765	ESTs	3.71	8.00
	433862	D86960	Hs.3610	KIAA0205 gene product	62.08	104.00
20	433980	AA137152	Hs.286049	phosphoserine aminotransferase	108.91 1.00	47.00 1.00
	434088	AF116677	Hs.249270	hypothetical protein PRO1956 hypothetical protein PRO2013	121,27	87.00
	434094 434105	AA305599 AW952124	Hs.238205 Hs.13094	preseniins associated momboid-like pro	1.22	1.23
	434217	AW014795	Hs.23349	ESTs	14.11	57.00
25	434340	Al193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	2.10	2.56
	434360	AA401369	Hs.190721	ESTs	40.98 1.48	17.00 1.56
	434414	Al798376	U- 225225	gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens Homo sapiens cDNA: FLJ23523 fis, ctone L	1.00	64.00
	434424 434467	AI811202 BE552368	Hs.325335 Hs.231853	Homo sapiens cONA FLJ 13445 fis, chone PL	54.91	85.00
30	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	2.46	2.00
50	434627	AJ221894	Hs.39311	ESTs	1.00	1.00
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	1.00 7.08	23.00 56.00
	434769	AA648884	Hs.134278	Homo sapiens cDNA FUJ12676 fis, clone NT ESTs	8.52	44.00
35	434792 434808	AA649253 AF155108	Hs.132458 Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	11.33	1.00
55	434828	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced	1.00	1.00
	434876	AF160477	Hs.61460	lg superfamily receptor LNIR	1.25	1.29
	434891	AA814309	Hs.123583	ESTs	1.00 1.00	6.00 1.00
40	434928	AW015595	Hs.4267	Homo sapiens clones 24714 and 24715 mRNA Target CAT	1.26	1.10
40	435013 435066	H91923 BE261750	Hs.110024 Hs.4747	dyskeratosis congenita 1, dyskerin	1.69	1.37
	435087	AW975241	Hs.23567	ESTs	1.00	1.00
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.90	1.93
45	435159	AA668879	Hs.116649	ESTs	1.00 1.02	1.00 1.46
45	435205	X54136	Hs.181125	immunoglobulin lambda locus cyclin-dependent kinase inhibitor 2C (p1	2.04	2.70
	435232 435304	NM_001262 H10709	Hs.4854 Hs.269524	ESTs	27.58	139.00
	435313	A1769400	Hs.189729	ESTs	1.00	14.00
	435505	AF200492	Hs.211238	interleukin-1 homolog 1	1.00	38.00
50	435509	A1458679	Hs.181915	ESTs	1.00 1.00	1.00 56.00
	435525	AI831297	Hs.123310 Hs.117305	ESTs Homo sapiens, clone IMAGE:3682908, mRNA	1.00	2.00
	435532 435550	AW291488 Al224456	Hs.324507	H.sapiens polyA site DNA	3.42	3.92
	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	3.95	1.80
55	435766	R11673	Hs.186498	ESTs	1.00	28.00
	435793	AB037734	Hs.4993	KIAA1313 protein	23.68 1.00	42.00 58.00
	436069 435170	A)056879 AW450381	Hs.263209 Hs.14529	ESTs ESTs	1.00	18.00
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	5.84	22.00
60	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	1.42	1.27
	436217	T53925	Hs.107	fibrinogen-like 1	57.97	31.00
	436238	AK002163	Hs.301724	hypothetical protein FLJ11301	2.51 2.33	1.71 1.64
	436251	BE515065	Hs.296585 Hs.344037	nucleolar protein (KKE/D repeat) protein regulator of cytokinasis 1	108.99	52.00
65	436291 436302	BE568452 AL355841	Hs.99330	hypothetical protein FLI23588	0.75	2.81
05	436396	AW992292	Hs.152213	wingless-type MMTV integration site fami	60.01	1.00
	436414	BE264633	Hs.143638	WD repeat domain 4	2.50	2.19 1.33
	435419	Al948626	Hs.171356	ESTs	0.95 1.12	9.26
70	436443		Hs.128746 Hs.199887	ESTs ESTs	1.00	1.00
70	436474 436481	AJ270693 AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.28	1.56
	436486	AA742221	Hs.120633	ESTs	1.00	19.00
	436511	AA721252	Hs.291502	ESTs	16.76	14.00
75	436553	X57809	Hs.181125	immunoglobulin lambda locus	1.08 19.20	1.74 9.75
75	436557	W15573 AA628980	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr down syndrome critical region protein DS	33.92	25.00
	436608 436667	AW025183	Hs.127680	ESTs	0.89	1.19
	436771	AW975687	Hs.292979	ESTs	1.00	10.00
00	436839	AA401369	Hs.190721	ESTs	1.00	17.00
80	436887		Hs.193235	hypothetical protein DKFZp547D155	1.06	1.15 1.00
	436944		Hs.5840	ESTs ESTe	1,00 25,13	25.00
	436961 436972	AW375974 AA284679	Hs.156704 Hs.25640	ESTs claudin 3	1.59	1.46
	430972		Hs.5398	guanine monphosphate synthelase	2.35	1.78
85	437044		Hs.69517	cONA for differentially expressed CO16 g	1.34	1.13

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	437181	Al306515	Hs.125343	ESTs, Wealdy similar to KIAA0758 protein	1.00	17.00
	437204	AL110216	Hs.22826	ESTs, Weakly similar to 155214 salivary	40.55	82.00
	437205	AL110232	Hs.279243	Homo sapiens mRNA; cDNA DKFZp564D2071 (f	1.00	112.00
_	437259	Al377755	Hs.120695	ESTs COO	1.00 1.56	205.00 1.54
5	437270	R18087	Hs.323769 Hs.28846	cisplatin resistance related protein CRR Homo sapiens mRNA: cDNA DKFZp5660134 (fr	113.25	125.00
	437271 437370	AL137445 AL359567	Hs.161962	Homo sapiens mRNA; cDNA OKFZp5470023 (fr	1.82	4.57
	437390	Al125859	Hs.112607	ESTs	1.35	1.75
	437412	BE059268	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	3.58	3.20
10	437435	AJ306152	Hs.27027	hypothetical protein DKFZp762H1311	3.03 1.00	1.08 39.00
	437444	H46008 A1954795	Hs.31518 Hs.156135	ESTs ESTs	1.00	19.00
	437568 437623	063880	Hs.5719	chromosome condensation-related SMC-asso	1.95	1.57
	437789	AI581344	Hs.127812	ESTs. Weakly similar to T17330 hypotheti	1.00	3.00
15	437814	AJ088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	1.00 1.07	45.00 1.78
	437840	AA884836	Hs.292014	ESTs ESTs, Wealdy similar to dJ365012.1 [H.sa	1.68	3.26
	437852 437879	BE001836 BE262082	Hs.256897 Hs.5894	hypothetical protein FLJ10305	1.87	2.52
	437915	Al637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	74.05	35.00
20	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	23.15	89.00
	437937	AI917222	Hs.121655	ESTs	1.00 12.28	1.00 31.00
	437942 438091	A1888256 AW373062	Hs.307526	ests nuclear receptor subfamily 1, group I, m	1.53	10.85
	438113	AJ467908	Hs.8882	ESTs	1.80	2.39
25	438119	AW963217	Hs.203961	ESTs, Moderately similar to AF116721 89	22.67	36.90
	438274	Al918906	Hs.55080	ESTs	1.00 38.92	1.00 38.00
	438378	AW970529	Hs.86434 Hs.292206	hypothetical protein FLJ21816 ESTs	1.00	1.00
	438403 438494	AA806607 AA908678	Hs.130183	ESTs	2.05	80.00
30	438545	AW297204	Hs.125811	ESTs	1.00	131.00
	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	1.43	1.45
	438702	A1879064	Hs.54618	ESTS	1.00 1.33	34.00 1.10
	438724 438746	AW612553 Al885815	Hs.114670 Hs.184727	Human DNA sequence from clone RP11-16L21 Human melanoma-associated antigen p97 (m	2.42	1.59
35	438779	NM_003787	Hs.6414	nucleolar protein 4	1.00	18.00
	438821	AA826425	Hs.192375	ESTs	2.03	2.57
	438885	A1886558	Hs.184987	ESTs	6.42 22.41	88.00 17.00
	438898	AA401369 AA280174	Hs.190721 Hs.285681	ESTs Williams-Beuren syndrome chromosome regi	1.00	1.00
40	438915 438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9	2.20	1.88
	439000	AW979121		gb:EST391231 MAGE resequences, MAGP Homo	2.78	4.81
	439023	AA745978	Hs.28273	ESTs	1.17	1.31
	439024	R96696	Hs.35598 Hs.153089	ESTs ESTs	1.00 1.00	28.00 67.00
45	439128 439146	A/949371 AW138909	Hs.156110	immunoglobulin kappa constant	1.38	1.41
	439223	AW238299	Hs.250618	UL16 binding protein 2	1.93	1.64
	439285	AL133916		hypothetical protein FLJ20093	46.23	139.00
	439318	AW837046	Hs.6527	G protein-coupled receptor 56	2.00 6.10	2.20 7.37
50	439343 439394	AF086161 AA401369	Hs.114611 Hs.190721	hypothetical protein FLJ11808 ESTs	3.39	17.00
50	439410	AA632012	Hs.188746	ESTs	1.83	3.07
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	23.28	52.00
	439452	AA918317	Hs.57987	B-cell CLL/ymphoma 11B (zinc finger pro	18.76 2.78	122.00 1.58
55	439453 439477	8E264974 W69813	Hs.6566 Hs.58042	thyroid hormone receptor interactor 13 ESTs, Moderately similar to GFR3_HUMAN G	1.22	1.44
55	439492	AF086310	Hs.103159	ESTs	7.46	39.00
	439523	W72348	Hs.185029	ESTs	1.00	1.19
	439592	AF086413	Hs.58399	ESTs	1.00	1.00 1.00
60	439606	W79123 AF088076	Hs.58561 Hs.59507	G protein-coupled receptor 87 ESTs, Weakly similar to AC004858 3 U1 sm	33.61 1.00	1.00
UU	439670 439702	AW085525	Hs.134182	ESTs	4.30	10.00
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	86.55	11.00
	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (lg),	2.36	1.88
65	439750	AL359053	Hs.57664	Homo sapiens mRNA full length Insert cON Homo sapiens mRNA full length Insert cON	2.02 1.00	6.08 21.00
03	439759 439780	AL359055 AL109688	Hs.67709	gb:Homo sapiens mRNA full length insert	7.27	25.00
	439840	AW449211	Hs.105445	GDNF family receptor alpha 1	1.00	1.00
	439926	AW014875	Hs.137007	ESTs	32.58	71.00
70	439963	AW247529	Hs.6793	platelet-activaling factor acetylhydrola	21.28 68.83	9.55 61.00
70	439979 440006	AW600291 AK000517	Hs.6823 Hs.6844	hypothetical protein FLJ10430 hypothetical protein FLJ20510	1.83	4.02
	440028	AW473675	Hs.125843	ESTs, Weakly similar to T17227 hypotheti	1.42	2.54
	440106	AA864968	Hs.127699	KIAA1603 protein	1.00	54.00
75	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	24.18	52,00 4.72
75	440273 440289	Al805392 AW450991	Hs.325335 Hs.192071	Homo sapiens cDNA: FLJ23523 fis, clone L ESTs	3.21 38.63	113.00
	440269	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	62.88	147.00
	440492	R39127	Hs.21433	hypothetical protein DKFZp547J036	2.35	3.62
00	440527	AV657117	Hs.184164	ESTs, Moderately similar to \$65657 alpha	10.84	57.00 2.37
80	440659 440704	AF134160 M69241	Hs.7327 Hs.162	claudin 1 insulin-like growth factor binding prote	3.18 2.89	2.37 2.09
	440943	AW082298	Hs. 146161	hypothelical protein MGC2408	2.02	1.41
	440994	AJ160011	Hs.272068	ESTs	1.29	1,14
0.5	441020	AA401369	Hs.190721	ESTs 21 to a bound to	142.99	17.00
85	441031	Al110684	· Hs.7645	fibrinogen, B beta polypeptide	1.41	99.00

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	441128	AA570256		ESTs, Wealdy similar to T23273 hypothesi	4.13 1.00	3.50 1.00
	441290 441362	W27501 BE614410	Hs.89605 Hs.23044	cholinergic receptor, nicotinic, alpha p RAD51 (S. cerevisiae) homolog (E coli Ra	130.23	43.00
	441377	BE218239	Hs.202656	ESTs	22.03	1.00
5	441390	A1692560	Hs.131175	ESTs	3.65	7.70 1.00
	441497	RS1064	Hs.23172 Hs.127728	ESTs ESTs	1.00 1.53	1.42
,	441525 441553	AW241867 AA281219	Hs.121296	ESTs	1.89	1.57
_	441507	NM_005010	Hs.7912	neuronal cell adhesion molecule	1.47	211
10	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1 Homo sapiens mRNA; cDNA DKFZp566E183 (fr	216.22 2.31	363.00 2.05
	441636 441737	AA081846 X79449	Hs.7921 Hs.7957	adenosine dearninase, RNA-specific	1.30	1.49
	441790	AA401369	Hs.190721	ESTs	44.15	17.00
1.5	441801	AW242799	Hs.86366	ESTs	1.00 1.00	1.00 122.00
15	441919 441937	AJ553802 R41782	Hs.128121 Hs.22279	ESTs ESTs	0.86	1.37
	441954	AJ744935	Hs.8047	Fanconi anemia, complementation group G	1.48	1.39
	442025	AW887434	Hs.11810	CDA11 protein	1.00 9.92	46.00 45.00
20	442029	AW956698	Hs.14456 Hs.12311	neural precursor cell expressed, develop Homo sapiens clone 23570 mRNA sequence	25.05	77.00
20	442072 442108	AJ740832 AW452649	Hs.166314	ESTs	3.61	3.14
	442117	AW664964	Hs.128899	ESTs	3.00	5.49 1.00
	442137	AA977235	Hs.128830	ESTs, Wealthy similar to Z192_HUMAN ZINC heterochromatin-like protein 1	1.00 1.92	1.66
25	442159 442179	AW163390 AA983842	Hs.278554 Hs.333555	chromosome 2 open reading frame 2	27.22	50.00
25	442328	AI952430	Hs.150614	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.00	3.42
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	181.59 10.59	76.00 144.00
	442530 442547	A1580830 AA306997	Hs.176508 Hs.217484	Homo sapiens cDNA FLJ14712 fts, clone NT ESTs, Weakly simitar to ALU1_HUMAN ALU S	109.23	98.00
30	442556	AL137761	Hs.8379	Homo saplens mRNA; cDNA DKFZp586L2424 (f	1.00	53.00
-	442619	AA447492	Hs.20183	ESTs, Weakly similar to AF164793 1 prote	29.02	50.00 19.00
	442710	AJ015631	Hs.23210	ESTs ESTs, Weakly similar to T23976 hypotheti	1.00 1.00	5.00
	442717 442875	R88362 BE623003	Hs.180591 Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	22.85	50.00
35	442914	AW188551	Hs.99519	hypothetical protein FLJ14007	25.33	82.00
	442932	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	3.18 8.45	4.41 64.00
	442942 443068	AW167087 AL188710	Hs.131562	ESTs ESTs	1.00	27.00
	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	1.00	24.00
40	443211	Al128388	Hs.143655	ESTs 1704	12.42 128.84	2.00 96.00
	443247 443324	BE614387 R44013	Hs.333893 Hs.164225	c-Myc target JPO1 ESTs	0.02	4.59
	443383	A1792453	Hs.166507	ESTs	1.00	47.00
4.5	443400	R28424	Hs.250648	ESTs	18.52 4.02	61.00 1.75
45	443426	AF098158 AA025610	Hs.9329 Hs.9605	chromosome 20 open reading frame 1 cleavage and polyadenylation specific fa	2.98	2.57
	443572 443575	AA023010 Al078022	Hs.269636	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.00	29.00
	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	1.00	16.00 39.00
50	443633	AL031290	Hs.9654 Hs.143610	simitar to pregnancy-associated plasma p ESTs	1.00 39.81	70.00
50	443648 443715	A1085377 A1583187	Hs.9700	cyclin E1	48.74	7.00
	443723	A1144442	Hs.157144	syntaxin 6	1.29	1.30
	443802	AW504924	Hs.9805 Hs.9914	KIAA1291 protein foliistalin	1.75 1.35	1.61 1.13
55	443859 443892	NM_013409 AA401369	Hs.190721	ESTS	1.00	17.00
•	443947	W24187		gb:zb47f09.r1 Soares_fetal_hing_NbHL19W	1.33	1.64
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	5.71 1.47	6.87 1.92
	444006 444009	BE395085 Al380792	Hs.10086 Hs.135104	type I transmembrane protein Fn14 ESTs	1.00	77.00
60	444017	U04840	Hs.214	neuro-oncological ventral antigen 1	1.00	1.00
	444127	N63620	Hs.13281	ESTs	1.00 1.00	29.00 1.00
	444129 444279	AW294292 U62432	Hs.256212 Hs.89605	ESTs cholinergic receptor, nicolinic, alpha p	0.60	7.80
	444371	BE540274	Hs.239	forkhead box M1	2.91	1.14
65	444378	R41339	Hs.12569	ESTs	1.00 469.00	1.00 556.00
	444381 444461	BE387335 R53734	Hs.283713 Hs.25978	ESTs, Weakly similar to S64054 hypotheti ESTs, Weakly similar to 2109260A B cell	12.88	105.00
	444471	AB020684	Hs.11217	KIAA0877 protein	24.91	90.00
20	444489	AJ151010	Hs.157774	ESTs	1.00	111.00 70.00
70	444619	BE538082	Hs.8172 Hs.47783	ESTs, Moderately similar to A46010 X-lin B aggressive lymphoma gene	1.00 30.56	139.00
	444665 444707	BE613126 Al188613	Hs.41690	desmocollin 3	1.00	1.00
	444735	BE019923	Hs.243122	hypothetical protein FLJ 13057 similar to	77.02	90.00
75	444781 444783	NM_014400	Hs.11950 Hs.62180	GPI-anchored metastasis-associated prote anillin (Drosophila Scraps homolog), act	1,57 77,55	1.31 2.00
13	445236	AK001468 AK001676	Hs.12457	hypothetical protein FLJ 10814	1.00	27.00
	445258	Al635931	Hs.147613	ESTs	1.00	73.00
	445413	AA151342	Hs.12677	CGI-147 protein	28.14	50.00 2.62
80	445417 445443	AX001058 AV653838	Hs.12680 Hs.322971	Homo sapiens cDNA FLJ10196 fis, clone HE ESTs	1.81 1.00	1.00
-00	445462	AA378776	Hs.288649	hypothetical protein MGC3077	2.09	1.70
	445517	AF208855	Hs.12830	hypothetical protein	1.87	70.00 2.72
	445537 445580	AJ245671 AF167572	Hs.12844 Hs.12912	EGF-like-domain, multiple 6 skb1 (S. pombe) homolog	1.71 1.52	1.34
85	445654	X91247	Hs.13046	thioredoxin reductase 1	1.51	1.52

## 45553 AST/6209 He. 174570 ## 45573 AA/25277 He. 251545 ## 45573 AA/25277 He. 151754 ## 45573 AA/25278 He. 151754 ## 45773 AA/25277 He. 151754 ## 45773 AA/2527		WO 02/086443					
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	449157	T05095	Hs.19597	KIAA1594 protein	1.61 2.36	2.36 1.56	
	449207 · 449228	AL044222 AJ403107	Hs.23255 Hs.148590	nucleoporin 155kD protein related with psoriasts	1.15	1.15	
	449230	BE613348	Hs.211579	metanoma cell adhesion molecule	206.65	151.00	
5	449305	A1638293		ghttD3b07x1 NCI_CGAP_GC6 Homo sapiens	17.28 26.39	45.00 35.00	
	449318 449448	AW235021 060730	Hs.78531 Hs.57471	Homo sapiens, Similar to RIKEN cDNA 5730 ESTs	1.00	1.00	
	449467	AW205006	Hs.197042	ESTs	1.00	1.00	
10	449523	NM_000579	Hs.54443	chemokine (C-C molif) receptor 5	56.80	216.86 1.00	
10	449722	BE280074	Hs.23960 Hs.135056	cyclin 81 Human DNA sequence from clone RP5-850E9	150.03 2.16	2.85	
	449976 450001	H06350 NM_001044	Hs.406	solute carrier family 6 (neurotransmitte	1.17	1.45	
	450098	W27249	Hs.8109	hypothetical protein FLJ21080	1.79	2.38	
15	450101	AV649989	Hs.24385 Hs.132863	Human hbc647 mRNA sequence Zic family member 2 (odd-paired Drosophi	1.00 1.00	69.00 1.00	
12	450149 450193	AW969781 AI916071	Hs.15607	Homo sapiens Fanconi anemia complementat	29.85	34.00	
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	1.00	1.00	
	450372	BE218107	Hs.202436	ESTs a disintegrin and metalloproteinase doma	1.00 51.26	1.00 93.00	
20	450375 450447	AA009647 AF212223	Hs.8850 Hs.25010	hypothetical protein P15-2	123.20	181.00	
20	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	1.00	19.00	
	450589	AI701505	Hs.202526	ESTs	1.00 1.00	23.00 100.00	
	450684 450701	AA872605 H39960	Hs.25333 Hs.288467	Interleukin 1 receptor, type II Homo sapiens cDNA FLJ12280 fis, ctone MA	1.89	1.55	
25	450705	U90304	Hs.25351	iroquois homeobox protein 2A (IRX-2A) (1.00	45.00	
	450832	AA401369	Hs.190721	ESTS	25.17 90.92	17.00 90.00	
	450937 450983	R49131 AA305384	Hs.26267 Hs.25740	ATP-dependant interferon response protei ERO1 (S. cerevisiae)-like	3.33	1.70	
	451105	A1761324	10.20140	gbwi60b11.x1 NCI_CGAP_Co16 Homo saplens	15.02	124.00	
30	451110	AJ955040	Hs.265398	ESTs, Weakly similar to transformation-r	1.00 3.02	143.00 2.29	
	451253 451291	H48299 R39288	Hs.26126 Hs.6702	claudin 10 ESTs	1.00	1.00	
	451320	AW498974	72.0702	diacytgtycerol kinase, zeta (104kD)	2.92	18.00	
25	451380	H09280	Hs.13234	ESTs	6.90 35.75	6.67 72.00	
35	451386 451437	AB029006 H24143	Hs.26334 Hs.31945	spastic paraplegia 4 (autosomal dominant hypothetical protein FLJ11071	1.00	69.00	
	451462	AK000367	Hs.26434	hypothetical protein FLJ20360	1.83	2.10	
	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	1.13 1.88	1.07 1.33	
40	451541 451592	BE279383 AI805416	Hs.26557 Hs.213897	plakophilin 3 ESTs	1.00	1.00	
40	451635	AA018899	Hs.127179	cryptic gene	1.52	1.92	
	451743	AA401369	Hs. 190721	ESTs	4.95 13.55	17.00 31,00	
	451806 451807	NM_003729 W52854	Hs.27076	RNA 3-terminal phosphate cyclase hypothetical protein FL123293 similar to	1.55	35.00	
45	451871	AI821005	Hs.118599	ESTs	1.81	2.53	
	451952	AL120173	Hs.301663	ESTs	1.00 3.43	22.00 2.26	
	452012 452046	AA307703 AB018345	Hs.279766 Hs.27657	kinesin family member 4A KIAA0802 protein	56.59	19.00	
	452194	AI694413	Hs.332649	olfactory receptor, family 2, subfamily	1.67	4.09	
50	452206	AW340281	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	9.31 13.42	53.00 17.00	
	452240 452256	AA401369 AK000933	Hs.190721 Hs.28661	ESTs Homo sapiens cDNA FL/10071 fis, clone HE	39.03	94.00	
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	153.01	340.00	
65	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	1.95 42.33	23.00 61.00	
55	452295 452304	BE379936 AA025386	Hs.28866 Hs.61311	programmed cell death 10 ESTs, Wealdy similar to S10590 cysteine	1.17	2.14	
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	1.00	13.00	
	452349	AB028944	Hs.29189	ATPase, Class VI, type 11A	1.09 54.49	1.42 53.00	
60	452367 452401	U71207 NM_007115	Hs,29279 Hs,29352	eyes absent (Drosophila) homolog 2 tumor necrosis factor, alpha-induced pro	1.00	32.00	
00	452410	AL133619		Homo sapiens mRNA; cDNA DKFZp434E2321 (f	1.26	1.99	
	452461	N78223	Hs.108106	transcription factor	24.47 54.61	35.00 102.00	
	452571 452613	W31518 AA461599	Hs.34665 Hs.23459	ESTs ESTs	1.39	1.32	
65	452699	AW295390	Hs.213062	ESTs	1.00	26.00	
	452705	H49805	Hs.246005	ESTS	1.00 112,87	1.00 1.29 ·	
	452747 452787	AF160477 AW294022	Hs.61460 Hs.222707	tg superfamily receptor LNIR KIAA1718 protein	1.00	1.00	
	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	1.00	1.00	
70	452823	AB012124	Hs.30596	transcription factor-like 5 (basic helix	7.91 3.16	75.00 1.92	
	452833 452838	BE559681 U65011	Hs.30736 Hs.30743	KIAA0124 protein preferentially expressed antigen in mala	174.35	1.00	
	452862	AA401369	Hs.190721	ESTs	98.26	17.00	
75	452865	AW173720	Hs.345805	ESTs, Weakly similar to A47582 B-cell gr	1.55 1.73	1.00 1.19	
75	452934 452946	AA581322 X95425	Hs.4213 Hs.31092	hypothetical protein MGC16207 EphA5	1.00	1.00	
	452976	R44214	Hs.101189	ESTs	1.58	1.98	
	453028	AB006532	Hs.31442	RecQ protein-like 4	1.80 0.77	1.60 1.50	
80	453095 453102	AW295660 NM_007197	Hs.252756 Hs.31664	ESTs frizzled (Drosophila) homolog 10	1.00	1.00	
	453103	A1301052	Hs.153444	ESTs	1.00	1.00	
	453120	AA292891	Hs.31773	pregnancy-induced growth inhibitor ESTs	1.23 1.00	1.20 83.00	
	453153 453160	N53893 A1263307	Hs.24360 Hs.239884	H28 histone family, member L	1.00	30.00	
85	453197	Al916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU S	1.00	134.00	

	11/	O 03/096	442				PCT/I	US02/12476
		O 02/0864 AL133161	44.3 Hs.32360	hypothetical protein FLJ 19667	1.69	1.93	101/	0502/121/0
	453240	AI969564	Hs.166254	hypothetical protein DXFZp5661133	1.00	1.00		
		NI.1_002277	Hs.41696	keratin, hair, acidic, 1	1.19	1.27		
~		AF034102	Hs.32951	solute carrier family 29 (nucleoside tra	4.90	4.11		
5		AI240865	Hs.8850	ESTs	199.42 1.00	340.00 16.00		
	453392		Hs.32964	SRY (sex determining region Y)-box 11 glycine receptor, beta	1.00	1.00		
	453431 453439		Hs.32973 Hs.32976	guarine nucleotide binding protein 4	3.44	5.17		
	453459		Hs.257789	ESTs	2.84	5.58		
10	453563	AW608906.co		Hs.181163	hypothetical	protein MGC5629	4.58	90.00
• •	453633		Hs.34045	hypothetical protein FLJ20764	1.74	1.60		
	453775		Hs.35120	replication factor C (activator 1) 4 (37	19.49	1.00		
	453830		Hs.20953	ESTs	24.92 167.59	25.00 66.00		
15	453857		Hs.35861 Hs.33032	DKFZP586E1621 protein hypothetical protein DKFZp434N185	1.00	39.00		
13	453867 453883		Hs.347524	cofactor required for Sp1 transcriptiona	1.97	1.58		
	453884	AA355925	Hs.36232	KIAAD185 gene product	63.89	20.00		
	453900		Hs.226414	ESTs, Wealdy similar to ALUB_HUMAN ALU S	20.41	16.00		
00	453922		Hs.36708	budding uninhibited by benzimidazoles 1	7.09	22.00 19.00		
20	453941	U39817	Hs.36820	Bloom syndrome	29.75 1.00	1.00		
	453964 453968		Hs.12744 Hs.62711	ESTs Horno sapiens, clona IMAGE:3351295, mRNA	2.05	1.81		
	453976		Hs.163714	ESTs	3.02	131.00		
	454024		Hs.293907	hypothetical protein FLJ23403	1.00	131.00		
25	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	1.23	1.02		
	454042	T19228	Hs.172572	hypothetical protein FLJ20093	30.63	171.00 1.00		
	454059	NH_003154	Hs.37048	statherin	1.00 1.01	1.45		
	454066 454098	X00356 W27953	Hs.37058 Hs.292911	calcitonin/calcitonin-related polypeptid ESTs, Highly similar to S60712 band-6-pr	1.26	1.11		
30	454241		15.22211	gb:CM2-HT0176-041099-017-c02 HT0176 Homo	6.33	5.04		
50	454417		Hs.110826	trinucleofide repeat containing 9	4.30	7.82		
	454439	AW819152	Hs.154320	DKFZP566O1646 protein	1.00	1.00		
	455175			gb:RC2-BN0033-180200-014-h09 BN0033 Homo	13.75 206.11	103.00 1.00		
35	455601		Hs.816	SRY (sex determining region Y)-box 2 gb:zx52e07.r1 Soares_fetal_fiver_spleen_	1.00	1.00		
33	456237 456321		Hs.87225	cancer/testis antigen	1.14	1.10		
	456475		Hs.95998	Friedreich ataxia	1.00	48.00		
	456508		Hs.123469	ESTs, Wealdy similar to AF208855 1 BM-01	162.25	189.00		
40	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	2.12	1.80		
40	456736		Hs.1619	achaete-scute complex (Drosophila) homol	1.15 1.00	1.94 1.00		
	456759		Hs.127792	delta (Drosophila)-like 3 HIV-1 Rev binding protein	16.42	84.00		
	456990 457200		Hs.171545 Hs.197764	thyroid transcription factor 1	0.57	1.76		
	457234		Hs.14355	Homo sagiens cDNA FLJ13207 fis, clone NT	2.71	4.15		•
45	457465		Hs.122908	DNA replication factor	46.37	47.00		
	457489		Hs.127179	cryptic gene	1.12	1.35		
	457646		Hs.112948	ESTs	1.55 1.00	2.51 55.00		
	457733 457819		Hs.291971 Hs.35406	ESTs ESTs, Highly similar to unnamed protein	4.36	3.18		
50		BE545684	Hs.343566	KIAA0251 protein	1.00	1.32		
	458098			metallothionein 1E (functional)	1.00	22.00		
	458207		Hs.7655	U2 small nuclear ribonucleoprotein auxil	2.06	1.88		
	458242		Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone H	1.00 7.00	1.00 9.85		
55	458247	R14439 AW975460	Hs.209194 Hs.142913	ESTs ESTs	1.00	3.00		
33	458778		Hs.326525	arylsulfatase D	1.31	2.01		
	458933	A1638429	Hs.24763	RAN binding protein 1	1.98	1.71		
	459352	AW810383	Hs.206828	ESTs	12.60	63.00		
60	459670	F01020	Hs.172004	titin	1.00	1.00 237.00		
60	459702	A1204995		gb:an03c03.x1 Stratagene schizo brain S1	1.00	231.00		
	TABLE 9	18		•				
65	Pkey:		is probeset ide	entifier number	•			
		nber: Gene clus	ter number accession num	ham				
	Accessio	ni: Genbank	accession non	ioeis				
	Pkey	CAT Number	er Access	sion				
70	407746	10125_1	AK001	962 R69415 BE464605 AA418699 AA053293 AA1490	75 AA058396 AW3	38226 AW272659 AA4	54607 AI139535	AW469852 Al275461
				1982 AA730033 AA576507 AA991217 AA782067 AI985	851 AA805864 AA	505598 AVV469857 Rb	,9546 AA9882/9	AWUU1097 NG332U
	400000	4000000 *		1 T27343 AA306950 AA360989 R58778				
	408070 408660	1036688_1 107294_1		8852 BE350895 1775 AA056342 Al538978 AW975281 AA664986				
75	408660	113735_1		382 AA075431				
, ,	409866	1156522_1		2152 H41202 H29772				
	410032	1170435_1	BE065	985 RE065944 RE066008 BE066083 RE066093				410EPROD 4109C
	411089	123172_1	AA456	454 AA713730 AA091294 AA584921 N86077 AW8367	81 AA601031 AA57	798/6 AA551106 AA63	13188 AW905577	A19558U8 A1679386
80	44450	1024000 4	A16798	895 AA514764 AA454562 A1082382 AA595822 AA5513 1199 AW936012 AW877466 AW819782 AW935798 AW	はんしゅうしゅうしゅうしゅう	00304 MA 1889334 AAbt 1 RE060121 AMR36624	5 AW877536 AW	935885 BE069202
δU	411152	1234028_1	AWR2	0019 AW935937 RE160180 AW935946 RE069101 BEC	69125 AW877527 I	BE160316 BE160398 /	AW935794 AW83	35701 AW935784
	412537	1304_1	A) 031	778 X59711 NM 002505 M59079 AIR70439 AI494259	AW664010 AA4050	163 AA436132 BE1745	516 AA412691 AH	400314 AA436024
	772001		TOPACT	3 RE079412 RE07942R N90322 AIR31202 AI141758 AI	016793 Al167566 A	NB62075 Al375230 AL	208445 AW23576	3 AL044113 AA382556
			AW95	3918 AA927051 AA889823 BE003094 AW390155 AW3	60805 AW360823	AW360810 AA425472	A1694282 AL044	114 AJ584577 AJ809865

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	WU	02/080443	A478773 A1160445 A1674630 N69088 AW665529 N49278 A1129239 A1457890 A1621264 AW7297152 A1266215 AA907787 A1286170 A1017982
	412811	132943_1	AR/87/3 A150433 A6/4530 R6509 A736741 AA382555 AW075811 AW252076 H05382 AW957730 AA352014 R13591 AA121201 D60420 BE263253 BE047862 Z41952 A424991 A1693507 AI663108 AA599060 AI091148 AA593869 R39887 AA813482 AW016452 H06383 R41807 A1364268 AA620528 AI241940 AW089149 AW090733 AW088375 Z38240
5	413590 414883	1383256_1 15024_1	AA121202 R17734 BE157489 BE157550 AA000000 NR6396 AA001348 BE535736 AA081745 BE566245
10			AABS2438 H75526 H77575 NA9786 W50565 H78746 BE569065 W04339 R98127 T55938 BE279271 AW960304 T29812 AA476873 BE297387 AA952753 AA177048 NM, O01826 X54941 BE314366 AA908783 A719075 BE270172 BE269319 AA859355 AL204630 W325243 AB35150 AAB72039 W72395 T99630 A4422691 H98450 N31428 BE255916 H03265 A4857576 AA716920 AA910644 AA495922 AA2931404 AW514667 R79953 AW662396 AA662522 AI865147 A4423153 AW782230 AA594410 AA583187 AW082734 AW082734 AI826996 AA282397 AA876046
15			AW613002 AA527373 AW972459 AB31360 AA621337 AA100926 AA772418 AA594628 AU33892 W95095 AU334317 AA398727 AU603031 N95210 AA59432 AU041437 AA932124 AA627584 AA938292 AU04827 AU23513 AU094597 H42079 R54703 AL630359 AA617681 AA978045 AA643280 W44567 AU991288 AL537692 AU090262 AA740817 AL312104 AP911822 AA746871 A1185409 AA129784 AA701623 AU075239 AA643280 W44567 AU991288 AU326092 AU326992 AA76383 AU69128 AU69128 AU79128 AU
13			A13939 A48320 A278887 AA962596 A1492600 W80433 AA001979 R97424 A1129015 N24127 AA157451 AA235549 AA459292 AA037114 AA129785 A4494211 AW059601 AW386710 R972790 N59755 A361128 AW589407 H47725 H97534 H48076 H48450 T99631 AW300758 H03431 R76789 AA964344 H77576 R96823 A4457100 N92845 N45682 H42038 BE220698 BE220715 H99552 AA701624 N74173 R54704 H79520 H72923 H03266 BE261919 AA769633 AA480310 AA507454 AA910586 A1203723 AW104725 W25611 W25071 T88980 H03513 T77589 R99156
20			H03256 BE261919 AA702275 T77551 AA911952 H52956 N83673 AA283672
20	44 5000	156454_1	A1267700 A1720344 AA191424 A1023543 A1459633 AA172056 AW958465 AA172236 AW953397 AA355086
	415989 417324	166714 1	414PGE 10.4 A A FERRA A A 105E77 A14PSE 432 A14PQE1605 AA45E370
	418574	17690_1	N28754 N28747 AL568146 AI979339 AA322671 AA322672 AW955043 AI990326 AA776406 AL016250 AA843678 AW451882 N23137 N23129
	410074	1,000_1	W70051 Al038748 AA831327 Al925845 AW945895
25	418712	1784125_1	Z42183 T31621 T97478
	419443	184788_1	D62703 AA242966 D79798 AU076704 T74854 T74860 T72098 T73265 T73873 T69180 T74658 T58786 T60385 T73410 T68781 T67845 T67593 T73952 T67864 T60630
	419502	18535_1	AU076704 T74854 T74850 172098 173265 173873 199180 174658 153676 160565 150565 173610 16057 16057 16057 174572 T68367 168401 T53959 T72360 T72099 T60377 T58961 T71712 T72821 T64738 T74545 T72077 T68868 T72065 173258 T72826 T64242 T68220 T74673 T71800 T68355 T61227 T62738 T63317 T53850 T64692 T73768 T73962 T73382 T68914 T70975 173400 T60631 T73277 T73203 T70498 T61409 T58925 NM_000508 M64982 T68301 T73729 T69445 T60424 T67922 T67736 T68716 T67755 T74765 T73819 T58719
30			774755 160477 174863 161109 168329 158850 171857 173425 163736 168607 158899 164309 172031 172079 164305 171905 160107 171916 173787 156035 164425 171870 160476 161875 167820 171895 1741006 169441 168170 174617 171995 169440 161875 17676 177916 177916 1779 178976 1789
35			A 24 2010 TADLES DECORD AVECORD LIBROR DORSOL AVECTORD ROSTON WORDS WINDS A A344135 AV660126 ROJ921 AA343000
55			ANNUTOTE AND CARCO ALCAST A ARRIPOSO ANNURSOS ANNURSOS ANNURSOS HISTORIAS HISTORIAS HISTORIAS AND CARCO AND ANNUAS AND CARCO ANNUAS AND CARCO AND
			AADEDED TOTOED TATTO DOETAS UTOSON AATOLISS AWSTISS ROBATS (201925 AVS57287 1/1959 1/1313 1/3920 1/3333 101010 103293
			T69283 T73931 T72178 T72456 AV645639 AV653476 T72957 T72300 T58906 T71457 T70494 T72956 T70495 T68267 T74407 T85778
40			18968 17391 17218 172367 17368 174101 173668 174518 172304 AA34326 17399 168070 172065 H72149 173493 173495 AV645993 R02293 170475 164751 AA344441 AA343657 AA3445732 AA344328 A1110639 AA344603 AF063513 164695 168516 172223 160507 167633 R29500
40	_		170475 164751 AA344441 AA343637 AA344732 AA344732 AA111053 AA344005 AF003513 10053 1
			TENZEN TENZEN TENZEN AVIGENAZO T733A1 TE1702 T74598 T40095 K02272 T40106 AA343045 AA341908 AA34190/ AA34280/ AA341904
			TESTAT TROOKS TESTEA MICKAGO AARAGO TETRIS TROAM TOUTO TERROL TESTOL 17/249 16916/ 1/1289 168251 AV654844 1943/5
			AARAGRAA TETEOR AAAAAA TERARE WARRE AARAGRA MARRES AARAGRA TERRI WARRAN TERRI
45			AARAAGO TEARGO USBIRA TOSTII TYRBAR TERRIS T71715 R29036 T72793 T69122 T64595 T62888 169139 168291 164652 1679/1 140802
			AA693592 AI248502 R29454 T64764 T57001 T73052 T71429 T51176 T58866 AV655414 H90426 AA342489 173666 167848 172512 153635
			T67837 T73317 T74273 T69420 T68245 T74380 T67862 T74474 T56068
	419936 421582	189181_1 2041_1	A1792788 BE142230 AA252019 A1910275 X00474 X52003 X05030 NM_003225 AA314325 AA308400 AA506787 AA314825 A1571948 AA507595 AA614579 AA587613 R83818
50	421302	2041_1	A ACCOSTO A ACTARDO A AGOTETO ALOGESTO ALADERISE ALOGERISA MALOGESTA ALOGESTA MALOGESTA ALOGESTA ALOGE
50			RED7414D AAS14776 AASRRO34 RED74DS1 RED74D68 AWD09769 AW050690 AA858276 R55389 AU001051 AW050700 AW750210 AA614539
			BE074045 Al307407 AW602303 BE073575 Al202532 AA524242 Al970839 Al909751 BE076078 Al909749 R55292
	422128	211994_1	AW881145 AA490718 M95637 AA304575 T06067 AA331991
55	423034	224122_1	Al.11930 Aa320596 AW752565 Al.031985 Al.137241 A1792386 A1733664 A1857654 A1049911
22	423816 424200	23234_1 236595_1	ALUSTISCS AL 13/241 ALISZOOD AI 13/3004 AIGS/034 AIGS/811 AA337221 AA336756 AW966196
	424999	245835 1	AW953120 R56325 AA349562
	426966	273896_1	AJ493134 AJ498691 AW771508 AJ498457 AJ768408 AJ783624 AJ383985 AJ580267 D79813 AA393768
	426991	27415_1	AK001536 AA191092 AW510354 AI554256 AL353968 AA134266
60	427260	276598_1	AA663848 AA400100 AA401424 AL038843 AA161338 BE268213 AA425597 N87306 AA092969 BE566038 AA247451 N47392 AI928802 AW182584 AW027872 AI819831
	428023	28589_2	41000004 MECOCO A100346 A1070611 A1002667 A1002006 AMP338658 AM150899 A 6887514 NA7393 NZYKKS AA973469 ANJ36599 ALZSZUD9
			41024220 AMERICA ED 2 NIZO EC ANOTOTAR ANOTOCO ANOTOCO ANOTOCO AA QUI SON AAA
			ANDROSS ANDROS AND
65			Al932767 W02632 BE396786 R37261
	429220	301384_1	AW207206 AW341473 AA448195 Al951341 AA249027 AL038984 AK001993 AL080066 AV652725 BE566226 AA345557 AA315222 AA090585 AA375688 AA301092 AA298454 W05762
	429978	31150_1	AA249027 AL038984 AK001993 AL030066 AV652725 BES60226 AA345357 AA313222 AA3901780 A33004 AA5712275 R31663 A354441 AW607939 H51658 D83880 N84323 BE296821 AW947007 D61461 AW079261 AA329482 AW901780 A354442 AA772275 R31663 A354441
			417C7E9E LINDADA AINAEDDE LINDETE AIROADEE AIROADEE AIRINATAA AIETRINGI CINEAUS AWRIDTA AWRIDD AIR 1955 AIRINADE AIR
70			AISR9705 AW055215 AI336532 AI338051 AA806547 C75509 C00618 AW071172 AW769904 AA630381 AI678018 AI865985 D79662 BE221049
			AW265018 AI589700 AW196655 N76573 AI370908 BE042393 N75017 AI698870 AW960115
	430439	31808_1	AL133561 AL041090 AL117481 AL122069 AW439292 AI968826 AW072916 AI184913 AA489195 AW466994 AW469044 N59350 AI819642 AI280239 AI220572 AA789302 AI473611 AW841126 D60937
	430935	325772_1	
75	431089 431322	327825_1 331543_1	BE041395 AA491826 AA621946 AA715980 AA666102 AW970622 AA503009 AA502998 AA502989 AA502805 T92188
, 5	431322	34624 1	AA221036 R87170 RES37068 RE544757 C18935 AW812058 T92565 AA227415 AA233942 AA223237 AA668403 AA601627 AW869639
		- · - · - ·	BE061833 BE000620 AW961170 AW847519 AA308542 AW821833 AW945688 C04699 AA205504 AA377241 AW821667 AA055720
			AWR170R1 AWR5646R AA155719 AA17992R T03007 AW75429R AA227407 AA11392B AA307904 C16859
٥٥	434414	38585_1	AT793376 S46400 AW311617 AW811616 W00557 BE142245 AW358232 AW361851 AW358362 AA232351 AA218567 AA055556 AW858231 AW357541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174
80			TG1130 AA140776 AA600900 AWR791RR AWR13567 AWR13538 AI26716R AA157718 AA157719 AA100472 AA100/74 AA130/56 AA15/705
			AA157730 AA157715 AA053524 AWR49581 AWR54566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE155909 AA226824
			AIB29309 AW991957 NG6951 AA527374 HG6215 AA045564 AIG94265 HG0808 AA149726 AW195620 BE081333 BE073424 AW817662
0.5			AW817705 AW817703 AW817659 BE081531 H59570
85	436608	42361_3	AA628980 A1126603 BE504035

				W CONTENS AND AREA
	W	O 02/086	443	PCT/US02/12476
5	438091	44954_1		AW373052 T55662 AI299190 BE174210 AW579001 H01811 W40186 R67100 AI923886 AW952164 AA628440 AW898607 AW898616 AA709126 AW898628 AW898544 AA947932 AW898625 AW898622 AI276125 A1185720 AW510698 AA987230 T52522 BE467708 AW243400 AW043642 AI288245 A1186932 D52654 D55017 D52715 D52477 D53933 D54679 AI288739 A1146984 AI922204 N98943 BE174213 AA845571 AI813854 AI214518 AI635262 A1193455 AI707807 AI698862 AW884528 AI024768 A1004723 AW087420 AI565133 N94964 A1268939 AW513280 AI061126 AI435818 AI859106 AI560506 AI024767 AA513019 AA757988 X56196 AA902959 AI334784 AI860794 AA010207 AW890091 AW513771 AI951391 AI337671 T52499 AA890205 AI644908 H75966 AA463487 AA358688 AI961767 AI665295 AA780994 AI985913 BE174196 AA029094 AW592159 T55581 N79072 AI611201 AA910812 AI220713 AW149306 AI758412 AA045713 R79750 N76096
	439000	#C7716 1		
	439285	467716_1 47065_1		AL 133016 N79113 AFRESIO1 N76721 AW950828 AA364013 AW955684 AI345341 AI86/454 N54/84 AI8552/0 AM212/3 ATM 14662
10	403200	41000_1		AA775552 N62351 N59253 AA626243 AI341407 BE175639 AA455968 AI358918 AA457077
••	439780	47673_1		AN ARROSO TRACCE PACETO
	441128	51021_2		ALTUS688 RC3965 RC3970 AA570256 AW014761 AA573721 AW73237 AU022165 AA554071 AA127551 N90525 AW973523 AA447991 AA243852 BE328850 Al148171
				A1359627 A1005068 A1356557 AA232991 AW016855 AA906902 AA233101 AA127550 BE512923 A1188710 A1032142 AW078833 N30308 AW675632 A1219028 A1341201 N22181 H95390
1.5	443068	558874_1		14 m 14 m 14 m 14 m 1 m 17 m 1
15	443947	586160_1		W24187 W24194 R17789 Y10043 NM_005342 L05085 AL034450 BE614226 AW749053 AA379173 AA248230 BE514634 AA334622 R70656 AA367593 AA214649
	447636	7301_1		Y10043 NM_00542 105053 ALIDS430 BED 14226 NNY-3505122 AAS05264 AAAH 1527 R01145 Al088588 BE463637 AA398795 Al354883 AA369318 AW957031 R35760 AA039903 AB85697 AW530122 AAS05264 AAAH 1527 R01145 Al088588 BE463637 AA398795 Al354883 AY768938 AL669996 Al452952 Al168582 Al189869 Al086670 AW262560 AW613854 AA862839 AA435840 AA670197 Al024032 Al990659 AJ990089 N81095 AA847919 AW960150 AA211075 AA044704 AA367594 AW582587 AW858854 AW818630 AW818281 AW818433 AW582595
20				
20	448993	79225_1		
	410000			A471630 BE540537 BE253451 KM4077 10 BE31030 EDE31030 A393504 A1559741 A1527478 AA399460 A1760441 AA346416 BE047245 AW340858 BE207794 AA053085 RE9173 AA292343 AA454908 AA293504 A1559741 A1527478 AA399460 A1760441 AA346416 BE047245 AA730380 AA394063 AA454833 A1982791 A1567270 A1813332 A1767858 AA427705 D20284 A1221458 BE048537 A1263048 AA346417 AA311497 BE537702
25	449305	804424_1		AI638293 AW813561
	451105	859083_1		A1704004 A18000044 A18000027
	451320°	86576_1		A1/613/4 AW080/941 AW080/941 AW080/941 AW080/94 A224195 A1/701458 W20198 F26326 AA890570 N90552 AW071907 A1671352 A1375892 T03517 R88265 A1124088 AA224388 A1084316 A1354686 T33652 A1140719 A1720/211 T03490 A1372637 T15415 AW205836 AA630384 T03515 T33230
				4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
30	454007	8865 1		WEARS AT 44 TORR DEPROASE DEPROASE DEPROASE DEPROASE DEPROASE AND
30	451B07 .	0003_1		
	452410	9163_1		
25				AASUZ4UI AASUS43 AL20459 AVV105931 A
35				AIZESSUS AISECUSZ AISU/USS AI4/16223 AASOSUS AISOSAIS AUGUST/ AUGUSZSC ATTOMATICA AIA AIA AIA AIA AIA AIA AIA AIA AIA
	454241	1067807_1		BE144666 BE184942 AW238414 BE184946
	455175	1257335_1		AW993247 AW851464
	456237	168730_1		A A GOOGGO TA A G C G
40	458098	47395_1		AAZUSBEZ KT199 BE505224 AAB32519 N45402 AW885857 N29245 BE455409 W07677 AW970089 AI299731 AA482971 BE503548 H18151 W79223 AF086393 BE5505224 AAB32519 N45402 AW0885857 N29245 BE456182 N206395 AA461301 W74510 R34182 AI090689 N46003 BE071550 R28075 AW134982 AI2240204 AI138906 AW026179 AI572316 BE466182 AI206395 AI276154 AI273269 A422817 AI371014 AI421274 AI188525 AA939164 BE549810 AW137865 AI694996 SE503841 AA459718 BE327407 BE437534 BE218421 BE467767 AA939054 BE467063 AI797130 BE327781
45				•
	TABLE 9	C		
	Pkey:	Unique n	umber	corresponding to an Eos probeset
	Ref:	Sequence	e sourc	e. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I, et al. Terers to the publication entities" The DAX
50		sequence	e of hun	nan chromosome 22." Dunham I. et al., Nature (1999) 402/489-495.
	Strand:	Indicates	DNAs	trand from which exons were predicted.
	Nt_positio	on: Indicates	nucleo	tide positions of predicted exons.
	Pkey	Ref	Stran	d NL position
55	400512	9796593	Minus	
	400517	9796686	Minus	49996-50346
	400560	9843598	Plus	94182-94323,97056-97243,101095-101236,102824-103005
	400664 400665	8118496 8118496	Plus	13558-13721,13942-14090,14554-14679 16879-17023
60	400666	8118496	Plus	17982-18115,20297-20456
-	400749	7331445	Minus	9162-9293
	400763	8131616	Minus	
	401027	7230983	Minus	
65	401093 401203	8516137 9743387	Minus Minus	
05	401213	9858408	Plus	87839-88028
	401411	7799787	Minus	s 144144-144329
	401435	8217934	Minus	
70	401464	6682291	Minus	
70	401714 401747	6715702 9789672	Plus Minus	96484-96681 118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-
	401747	3103012	search.	131932_132451_132575_133580-134011
	401760	9929599	Plus	83126-83250,85320-85540,94719-95287
75	401780	7249190	Minus	s 28397-28617-28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
75	401781	7249190	Minus	
	401785 401797	7249190 6730720	Minus Plus	6973-7118
	401757	4581193	Minus	
00	401985	2580474	Phus	61542-61750
80	401994	4153858	Minu	s 42904-43124,43211-43336,44507-44763,45199-45281,46337-45732
	402075 402260	8117407	Plus Minus	
	402260	3399565 3287673	Ptus	
	402297	6598824	Plus	35279-35405,35573-35659
85	402408	9796239	Minu	

	W	0 02/08	6443		PCT/US02/12476
				129750-129919	
	402420	9796339	Plus	39290-39502	
	402674	8077108	Minus	53242-53432	
	402802	3287156	Minus	53242-33432 4727-4969	
	402994	2996643	Minus	92349-92572,92958-93094,93579-93712,93949-94072,94591-94748,95214-95337	
5	403137	9211494	Minus		
	403306	8099945	Plus	127100-127251	
	403329	8516120	Plus	96450-96598	
	403381	9438267	Minus	26009-26178	
10	403478	9958258	Plus	116458-116564	
10	403485	9966528	Plus	2888-3001,3198-3532,3655-4117	
	403627	8569879	Minus	23868-24342	
	403715	7239669	Plus	8512B-85292	
	404044	9558573	Minus	225757-225939	
	404076	9931752	Minus	3948-3967	
15	404101	8076925	Minus	125742-125997	
	404140	9843520	Plus	37761-38147	
	404165	9926489	Minus	69025-69128	
	404185	4572584	Minus	129171-129327	
	404210	5006246	Plus	169925-170121	
20	404253	9367202	Minus	55675-56055	
	404287	2326514	Plus	53134-53281	
	404298	9944263	Minus	73591-73723	
	404347	9838195	Plus	74493-74829	
	404440	7528051	Plus	80430-81581	
25	404721	9856548	Minus	173763-174294	
	404794	4826439	Plus	101619-101698	
	404854	7143420	Plus	14260-14537	
	404877	1519284	Plus	1095-2107	
	404927	7342002	Plus	68690-69563	
30	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450	
	405449	7622497	Plus	42236-42570	
	405568	6006906	Plus	35912-36065	
	405572	3800891	Plus	85230-85938	
	405646	4914350	Plus	741-969	
35	405676	4557087	Plus	73195-73917	
	405770	2735037	Plus	61057-62075	
	405932	7767812	Minus	123525-123713	
	406137	9166422	Minus	30487-31058	
	406360	9256107	Minus	7513-7673	
40	406399	9256288	Minus	63448-63554	
	406467	9795551	Plus	182212-182958	

TABLE 10A: Potential Therapeutic, Diagnostic and Prognostic targets for Therapy of Lung Cancer and Non-malignant Lung Disease
Table 2A shows about 307 genes up-regulated in non-malignant lung disease relative to lung tumors and normal body tissues and/or down-regulated in lung tumors relative to
normal lung and non-malignant lung disease. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. 45

Table 108 show the accession numbers for those Pkey's tacking UnigenetD's for table 10A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column. 50

Table 10C show the genomic positioning for those Pkey's tacking Unigene ID's and accession numbers in table 10A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

55

Unique Eos probeset identifier number Exemptar Accession number, Genbank accession number Unigene number Pkey:

UnigenelD: 60 Unigene Title:

unigene gene title
Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the
average of normal tung samples
Average of non-malignant tung disease samples (including bronchilis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal tung R1:

R2:

65	Pkey 404394	ExAcon	UnigenalD	Unigene Tille ENSP00000241075:TRRAP PROTEIN.	R1 0.79 1.00	R2 3,10 159,00
	404916 405257			Target Exon Target Exon	1.00	422.00
	407228	M25079	Hs.155376	hemoglobin, bela	0.47	2.33
70	407568	AA740964	Hs.62699	ESTs	1.00	123.00
, 0	408562	Al436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	1.00	230.00
	409031	AA376836	Hs.76728	ESTs	1.00	128.00
	410434	AF051152	Hs.63668	toll-like receptor 2	39.65	149.00
	410467	AF102546	Hs.63931	dachshund (Orosophila) homolog	1.00	109.00
75	410808	T40326	Hs.167793	ESTs	1.14	13.14
	412351	AL135960	Hs.73828	T-cell acute lymphocytic laukemia 1	0.37	2.27
	412372	R65998	Hs.285243	hypothetical protein FLJ22029	1.00	173.00
	413795	AL04017B	Hs.142003	ESTs	0.10	11.90
	414154	AW205314	Hs.323060	ESTs .	0.62	2.09
80	414214	D49958	Hs.75819	glycoprotein M6A	0.03	4.55
	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	0.64	2.97
	415122	D60708	Hs.22245	ESTs	0.07	8.97
	415765	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and	0.67	1.65
	415775	H00747	Hs.29792	ESTs, Wealdy similar to 138022 hypotheti	0.29	2.64
85	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	1.00	145.00

	w	O 02/086	443			
	416319	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i	15.32	237.00 4.00
	416402	NM_000715	Hs.1012	complement component 4-binding protein, endofhelin receptor type 8	0.64 0.01	3.90
	41 <i>7</i> 355 417421	D13168 AL138201	Hs.82002 Hs.82120	mudear receptor subfamily 4, group A, m	35.30	357.00
5	417511	AL049176	Hs.82223	chordin-like	1.00	179.00
•	418489	U76421	Hs.85302	adenesine dearninase, RNA-specific, B1 (h	0.02 1.00	6.00 113.00
	418726	BE241812	Hs.87860	protein tyrosine phosphatase, non-recept ESTs, Weakly similar to S41044 chromosom	0.44	1.90
	418741 418883	H83265 BE387036	Hs.8881 Hs.1211	acid phosphatase 5, tartrale resistant	0.96	2.04
10	419086	NM_000216	Hs.89591	Kalmann syndrome 1 sequence	0.62	2.74
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	0.03	6.90 5.13
	419235	AW470411	Hs.288433	neurotrimin hypothetical protein FLJ21276	1.48 37.55	336,00
	419407 420556	AW410377 AA278300	Hs.41502 Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	0.80	3.65
15	420656	AA279098	Hs.187636	ESTs	1.65	8.07
	420729	AW964897	Hs.290825	ESTs SULL SUFFE COSMOSSIS	2.99	25.82 1.95
	421177	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f ESTs, Moderately similar to ALU5_HUMAN A	0.46 1.00	156.00
	422060 422426	R20893 W79117	Hs.325823 Hs.58559	ESTs	0.03	7.44
20	422652	AW967969	Hs.118958	syntaxin 11	0.14	3.62
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	0.01 0.75	3.16 141.75
	424433	H04607	Hs.9218	ESTs ESTs	1.00	167.00
	424585 424711	AA464840 NM_005795	Hs.131987 Hs.152175	calcitonin receptor-like	0.43	3.01
25	424973	X92521	Hs.154057	matrix metalloproteinase 19	0.37	19.45
	425023	AW956889	Hs.154210	endothelial differentiation, sphingospi	0.14 1.00	3.35 94.00
	. 425664 425998	AJ006276 AU076629	Hs.159003 Hs.165950	transient receptor potential channel 6 fibroblast growth factor receptor 4	0.68	1.42
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	0.03	3.74
30	426753	T89832	Hs.170278	ESTs	1.00	141.00
	427558	D49493	Hs.2171	growth differentiation factor 10 colony stimulating factor 3 (granufocyte	1.00 0.75	117.00 2.20
	427983	M17706 AK002121	Hs.2233 Hs.184465	hypothetical protein FLI11259	0.76	2.25
	428467 428927	AA441837	Hs.90250	ESTs	0.01	3.62
35	429496	AA453800	Hs.192793	ESTs	1.00	138.00 132.00
	430468	NM_004673	Hs.241519	angiopoietin-like 1 membrane-spanning 4-domains, subfamily A	1.00 1.00	157.00
	431385 431728	BE178536 NM_007351	Hs.11090 Hs.268107	multimerin	1.00	157.00
	431848	A1378857	Hs.126758	ESTs, Highly similar to AF175283 1 zinc	0.34	2.24
40	432128	AA127221	Hs.117037	STE IN THE STATE OF THE STATE O	0.00 0.01	1.15 2.06
	432519 433043	AJ221311 W57554	Hs.130704 Hs.125019	ESTs, Weakly similar to BCHUIA S-100 pro lymphoid nuclear protein (LAF-4) mRNA	1.00	267.00
	433803	AI823593	Hs.27688	ESTs	1.00	105.00
	434730	AA644669	Hs.193042	ESTs	1.05	3.15 1.94
45	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid gb:nv54h12.r1 NCI_CGAP_Ew1 Homo sapiens	0.83 1.00	218.00
	436532 437119	AA721522 Al379921	Hs.177043	ESTs	1.00	133.00
	437140	AA312799	Hs.283689	activator of CREM in testis	0.67 1.00	122.67 142.00
50	437211	AA382207	Hs.5509 Hs.222194	ecotropic viral integration site 28 ESTs	1.00	147.00
30	437960 438202	A1669586 AW169287	Hs.22588	ESTs	1.00	141.00
	438873	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	0.71	3.66 370.00
	438875	AA827640	Hs.189059	ESTs ESTs	23.32 0.77	8.50
55	441048 441188	AA913488 AW292830	Hs.192102 Hs.255609	ESTs	3.43	16.36
-	441499	AW298235	Hs.101689	ESTs	1.00	167.00
	444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	1.00 46.47	151.00 153.00
	444527 444561	NM_005408 NM_004469	Hs.11383 Hs.11392	small inducible cylokine subfamily A (Cy c-fos induced growth factor (vascular en	0.01	3.08
60	445279	R41900	Hs.22245	ESTs	0.60	141.00
	446017	N98238	Hs.55185	ESTs	0.18	2.39 2.16
	446984	AB020722	Hs.16714	Rho guanine exchange factor (GEF) 15 Homo sapiens mRNA; cDNA DKFZp564B2062 (f	0.10 0.01	2.53
	446998 447357	N99013 Al375922	Hs.16762 Hs.159367	ESTs	0.46	2.64
65	448106	A1800470	Hs.171941	ESTs	18.05	296.00
	448253	H25899	Hs.201591	ESTs	1.00	141.00 1.38
	449275	AW450848	Hs.205457 Hs.279744	periaxin ESTs	0.56 0.88	4.33
	450400 450696	A1694722 A1654223	Hs.16026	hypothetical protein FLJ23191	0.52	2.08
70	450726	AW204600	Hs.250505	retinoic acid receptor, alpha	0.79	2.01
	451497	H83294	Hs.284122	Wnt inhibitory factor-1 serum deprivation response (phosphatidy)	0.35 0.13	2.03 2.25
	451533 453636	NM_004657 R67837	Hs.26530 Hs.169872	ESTs	1.00	116.00
	458332	AI000341	Hs.220491	ESTs	1.00	192.00
75	459580	AA022888	Hs.176065	ESTs	0.20	2.98
	400269			Eos Control NM 016369°:Homo sapiens claudin 18 (CLDN	0.40 0.53	2.40 1.77
	403421 407570	Z19002	Hs.37096	zinc finger protein 145 (Kruppel-like, e	0.01	3.18
	412295		Hs.117176	poly(A)-binding protein, nuclear 1	0.56	1.74
80	414517	M24461	Hs.76305	surfactant, pulmonary-associated protein	0.64 0.33	1.50 1.16
	417204	N81037 U70857	Hs.1074 Hs.83974	surfactant, pulmonary-associated protein solute carrier family 21 (prostaglandin	0.53	1.55
	418307 418935		Hs.89485	carbonic anhydrase IV	0.20	1.28
0.5	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospha	0.78	1.90 1.54
85	421798	N74880	Hs.29877	N-acylsphingosine amidohydrolase (acid c	0.59	127

		O 02/086			0.50	4.55
	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph ainway typsin-like prolease	0.59 10.14	1.55 51.00
	423738 425211	AB002134 M18667	Hs.132195 Hs.1867	progastricsin (pepsinogen C)	0.35	1.62
	425438	T62216	Hs.270840	ESTs	0.23	9.45
5	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	0.03	1.71
	427019	AA001732	Hs.173233	hypothetical protein FLJ 10970	0.01 0.42	1.49 1.26
	428043	T92248 AA361258	Hs.2240 Hs.237868	uteroglobin interleukin 7 receptor	0.46	2.43
	430280 431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	0.57	1.59
10	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DXFZp56482052 (f	0.29	1.60
	432985	T92363	Hs.178703	ESTs	0.32 0.31	2.27 1.51
	441835	AB036432	Hs.184	advanced glycosylation end product-speci ESTs	0.55	1.78
	442275 443709	AW449467 Al082692	Hs.54795 Hs.134662	ESTs	0.00	3.02
15	444325	AW152618	Hs.16757	ESTs	0.32	2.49
	450954	AJ904740	Hs.25591	receptor (calcitonin) activity modifying	0.46	1.74 1.87
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1 solute carrier family 6 (neurotransmitte	0.52 0.00	3.30
	453310 456855	X70697 AF035528	Hs.553 Hs.153863	MAD (mothers against decapentaplegic, Or	0.01	2.31
20	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	0.66	2.20
	400754			Target Exon	1.00	297.00 109.00
	401045			C11001883*;gi[6753278 ref[NP_033938.1] c	1.00 0.89	1.39
	401083			NM_016582*:Homo sapiens peptide transpor NM_004079:Homo sapiens cathepsin S (CTSS	1.45	4.47
25	402474 402808			ENSP00000235229:SEMB.	1.00	1.87
	403021			C21000030:gij9955960[ref]NP_063957.1] AT	1.00	149.00 2.96
	403438			NM_031419*:Homo sapiens motecule possess	1.06 0.04	4.89
	403687			NM_007037*:Homo sapiens a disintegrin-li NM_005463:Homo sapiens heterogeneous nuc	1.00	225.00
30	403764 404277			NM_019111°:Homo sapiens major histocompa	0.97	1.93
50	404288			NM_002944*:Homo sapiens v-ros avian UR2	1.00	68.00
	404518	AI815601		CD83 antigen (activated B lymphocytes, i	0.02	1.83 235.00
	405106			C11001637*:gij5032241 ref NP_005732.1 z	1.00 1.00	93.00
35	405381 406387			Target Exon Target Exon	1.37	6.02
33	406646	M33600		major histocompatibility complex, class	0.86	2.46
	406714	Al219304	Hs.266959	hemoglobin, gamma G	0.01	3.19 147.00
	406753	AA505665	Hs.217493	annexin A2	1.00 1.03	2.04
40	406973	M34996	Hs.198253 Hs.94498	major histocompatibility complex, class teukocyte immunoglobulin-like receptor,	1.00	64.00
40	407248 407510	U82275 U96191	113.34430	gb:Human trophoblast hypoxia-regulated f	1.00	90.00
	407731	NM_000066	Hs.38069	complement component B, beta polypeptide	1.00	67.00
	407830	NM_001086	Hs.587	arylacetamide deacetylase (esterase)	1.00 1.00	102.00 70.00
45	408045	AW138959	Hs.245123	ESTs ESTs	1.00	112.00
43	408074 408374	R20723 AW025430	Hs.155591	forkhead box F1	0.07	10.17
	409064	AA062954	Hs.141883	ESTs	0.39	2.31
	409083	AF050083	Hs.673	interieukin 12A (natural killer cell sti	1.00 0.01	95.00 4.55
50	409153	W03754	Hs.50813 Hs.687	hypothetical protein FLJ20022 cytochrome P450, subfamily IVB, polypept	0.01	3.72
30	409203 409238	AA780473 AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr	1.00	79.00
	409389	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	0.14	27.35
	409718	D86640	Hs.56045	src homology three (SH3) and cysteine ri	1.00 0.64	113.00 2.47
55	410798	BE178622	Hs.16291	gb:PM3-HT0605-270200-001-a02 HT0605 Homo macrophage receptor with collagenous str	0.55	240
33	411020 411667	NM_006770 BE160198	Hs.67726	gb:QV1-HT0413-010200-059-h03 HT0413 Homo	1.00	111.00
	412000	AW576555	Hs.15780	ATP-binding cassette, sub-family A (ABC1	1.00	95.00
	412358	BEC47490	Hs.24172	ESTs	1.00	87.00 8.07
60	412420	AL035668	Hs.73853	bone morphogenetic protein 2 cardiac ankyrin repeat protein	1.43 0.02	3.07
OU	412564 412869	X83703 AA290712	Hs.31432 Hs.82407	CXC chemokine ligand 16	0.93	1.72
	412870	N22788	Hs.82407	CXC chemokine ligand 16	0.97	1.51
	413529	U11874	Hs.846	interleukin 8 receptor, beta	0.02	2.42 1.50
65	413533	BE146973	11- 00021	gb:QV4-HT0222-011199-019-e05 HT0222 Homo zinc finger protein, subfamily 1A, 5 (Pe	0.65 20.87	232.00
65	413689 413724	BE157286 AA131466	Hs.20631 Hs.23767	hypothetical protein FLJ12666	1.00	80.00
	413800	Al129238	Hs.192235	ESTs	1.00	85.00
	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	1.00	213.00
70	413829	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)	0.02 1.00	3.93 115.00
70	414376	BE393856 AI056548	Hs.66915 Hs.72116	ESTs, Weakly similar to 16.7Kd protein (hypothetical protein FLJ20992 similar to	0.49	1.94
	414577 414700	H63202	Hs.38163	ESTs	0.03	3.75
	415078	AA311223	Hs.283091	found in inflammatory zone 3	0.86	1.95
75	415120	N54464	Hs.34950	ESTs	1.00	120.00 2.48
75	415323	BE269352	Hs.949 Hs.111030	neutrophil cytosolic factor 2 (65kD, chr ESTs	0.60 1.00	95.00
	415335 415582	AA847758 W92445	Hs.165195	Homo sapiens cDNA FLJ14237 fis, clone NT	1.00	136.00
	416030		Hs.21948	ESTs	0.02	8.07
00	416427	BE244050	Hs.79307	Rac/Cdc42 guanine exchange factor (GEF)	1.00	73.00 3.36
80	416464		Hs.79345	coagulation factor VIII, procoagulant co leiomodin 1 (smooth muscle)	0.70 0.06	3.36 6.56
	416585 416847		Hs.79386 Hs.80261	enhancer of filamentation 1 (cas-like do	0.70	3.66
	417148		Hs.293885	hypothetical protein FLJ14902	1.00	114.00
0.5	417370	T28651	Hs.82030	tryptophanyi-IRNA synthetase	0.85	1.30 15.54
85	417673	T87281	Hs.16355	ESTs	0.15	13.34

	W	O 02/086	443			4.74
	418067	Al127958	Hs.83393	cystafin E/M	0.81 1.00	1.74 99.00
	418296 418643	C01566 J03798	Hs.86671 Hs.86948	ESTs small nuclear ribonucleoprotein D1 polyp	1.00	60.00
_	418832	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro	2.40	14.74
5	418945	BE245762	Hs.89499	arachidonata 5-lipoxygenase	0.57 1.00	73.16 73.00
	419261 419564	X07876 U08989	Hs.89791 Hs.91139	wingless-type MMTV integration site fami solute carrier family 1 (neuronal/epithe	1.00	192.00
	419574	AK001989	Hs.91165	hypothetical protein	1.00	94.00
••	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	61.16	500.00 1.70
10	420256	U84722	Hs.76205 Hs.293878	cadherin 5, type 2, VE-cadherin (vascula ESTs, Moderately similar to ZN91_HUMAN Z	0.52 1.00	172.00
•	420285 420577	AA258124 AA278436	Hs.186649	ESTs	1.00	97.00
	421262	AA286746	Hs.9343	Homo sapiens cDNA FL/14265 fis, clone PL	1.00	64.00
15	421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054868, mRNA annexin A3	0.88 0.05	1.51 11.26
15	421470 421478	R27496 A1683243	Hs.1378 Hs.97258	ESTs, Moderately similar to S29539 ribos	1.00	73.00
	421563	NM_006433	Hs. 105806	granutysin	0.82	2.42
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop ESTs, Moderately similar to ALU4_HUMAN A	5.50 1.00	31,57 129.00
20	421855 421913	F06504 A1934365	Hs.27384 Hs.109439	osteoglycin (osteoinductive factor, mime	1.00	101.00
	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	0.60	63.60
	422232	D43945	Hs.113274	transcription factor EC	1.00 1.40	148.00 3.98
	422386 423168	AF105374 R34385	Hs.115830 Hs.124940	heparan sulfate (glucosamine) 3-O-sulfot GTP-binding protein	0.34	3.59
25	423196	AK001866	Hs.125139	hypothetical protein FLJ11004	0.55	2.00
	423387	AJ012074	11: 400400	vasoactive intestinal peptide receptor 1	0.09 1.00	2.13 141.00
	423424 423456	AF150241 AL110151	Hs.128433 Hs.128797	prostaglandin D2 synthase, hematopoietic DKFZP586D0824 prolein	1.00	66.00
	423696	Z92546	1.5.125101	Sushi domain (SCR repeat) containing	0.73	1.27
30	424027	AW337575	Hs.201591	ESTS	0.54 0.77	2.58 2.47
	424212 425087	NM_005814 R62424	Hs.143131 Hs.126059	glycoprotein A33 (transmembrane) ESTs	1.00	74.00
	425175	AF020202	Hs.155001	UNC13 (C. elegans)-like	0.85	1.96
25	425771	BE561776	Hs.159494	Bruton agammagiobulinemia tyrosine kinas	1.18	2.56 76.00
35	426486	BE178285 AF240467	Hs.170056 Hs.179152	Homo sapiens mRNA; cDNA DKFZp58680220 (f toll-like receptor 7	1.00 1.00	63.00
	427507 427618	NM_000760	Hs.2175	colony stimulating factor 3 receptor (gr	0.60	2.19
	427732	NM_002980	Hs.2199	secretin receptor	0.97	1.42 105.00
40	427952	AA765368 BE268717	Hs.293941 Hs.104916	ESTs, Moderately similar to AS3959 throm hypothetical protein FLJ21940	1.00 1.00	80.00
40	428709 428769	AW207175	Hs.106771	ESTs	0.09	2.55
	428780	Al478578	Hs.50636	ESTs	1.00	98.00
	428833	Al928355	Hs.185805 Hs.2465	ESTs KIAA0001 gene product; putative G-protei	1.00 1.00	113.00 52.00
45	429657 430212	D13626 AA469153	113.2400	gb:nc67f04.s1 NCI_CGAP_Pr1 Homo sapiens	1.00	132.00
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	0.11	15.60 103.00
	430376	AW292053 AW365665	Hs.12532 Hs.120388	chromosome 1 open reading frame 21 ESTs	1.00 0.50	6.96
	430414 430656	AA482900	Hs.162080	ESTs	1.00	70.00
50	430843	AI734149	Hs.119514	ESTs	1.00	90.00 1.84
	430998 431217	AF128847 NM_013427	Hs.204038 Hs.250830	indolethylamine N-methyltransferase Rho GTPase activating protein 6	0.29 1.00	79.00
	431921	N46466	Hs.58879	ESTs	0.91	1.67
c e	432176	AW090386	Hs.112278	arrestin, bela 1	0.66	2.63 76.00
55	432203 432231	AA305746 AA339977	Hs.49 Hs.274127	macrophage scavenger receptor 1 CLST 11240 protein	1.00 0.46	1.46
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	0.79	2.25
	432522	D11466	Hs.51	phosphatidylinositol glycan, class A (pa	1.93	4.83 5.79
60	432596 432850	AJ224741 X87723	Hs.278461 Hs.3110	matrilin 3 angiotensin receptor 2	0.04 1.00	167.00
00	433138	AB029496	Hs.59729	semaphorin sem2	0.04	9.16
	433563	A1732637	Hs.277901	ESTs	1.00 120.16	91.00 315.00
	433588 434445	A1056872 A1349306	Hs.133386 Hs.11782	ESTs ESTs	0.60	1.84
65	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	1.00	128.00
	435974	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	1.00	108.00 91.00
	436061 437157	A1248584 BE048860	Hs.190745 Hs.120655	Homo sapiens cDNA: FLJ21326 fis, clone C ESTs	1.00 1.00	87.00
_	437207	T27503	Hs.15929	hypothetical protein FLJ12910	1.00	105.00
70	437311	AA370041	Hs.9456	SWI/SNF related, matrix associated, acti	1.00	71.00 115.00
	437439 438199	H29796 AW016531	Hs.269622 Hs.122147	ESTS ESTS	1.00 1.00	80.00
	439551	W72062	Hs.11112	ESTs	0.30	3.10
75	440515	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene famil	1.00	77.00 85.00
75	440887 441025	A1799488 AA913880	Hs.135905 Hs.176379	ESTs ESTs	1.00 1.00	82.00
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	0.79	1.89
	441735	AI738675	Hs.127346	ESTs	1.00	75.00 5.83
80	442200 442832	AW590572 AW206560	Hs.235768 Hs.253569	ESTs ESTs	0.78 0.03	10.88
00	442832 442957	AVV200300 AI949952	Hs.49397	ESTs	1.00	70.00
	443282	T47764	Hs.132917	ESTs	1.00	197.00 253.00
	443547 443951	AW271273 F13272	Hs.23767 Hs.111334	hypothetical protein FLJ12665 ferntin, light polypeptide	1.00 0.55	2.09
85	444330	AI597655	Hs.49265	ESTs ESTs	1.00	90.00

PCT/US02/12476 WO 02/086443 84.00 1.00 444515 AW204908 Hs.169979 **ESTs** 4.38 97.00 A!741471 Hs.23666 **ESTs** 445763 Homo sapiens done 24425 mRNA sequence 1.00 445908 446291 R13580 BE397753 Hs.13436 interferon, gamma-inducible protein 30 1.69 Hs.14623 106.00 1.00 5 446917 AI347863 Hs.156672 0.40 47.20 extracellular link domain-containing 1 447261 NM_006691 AW958473 Hs.17917 nudix (nucleoside diphosphate linked moi KIAA1233 protein 100.00 Hs.301957 447432 0.05 8.21 AB033059 Hs.18705 447482 0.02 ESTs, Wealty similar to 138022 hypotheti 5 42 447997 448299 Hs.29792 H00656 79.00 Hs.20887 hypothetical protein FLJ 10392 KIAA0758 protein 10 AA497044 0.42 1.56 448782 AL050295 Hs.22039 purine-rich element binding protein A 450575 450584 NM_005859 AA040403 Hs.29117 1.00 94.00 Hs.60371 91.00 AW450461 Hs.203965 **ESTs** 450693 152.00 ESTs, Wealthy similar to KIAA1324 protein 1.00 15 AJ266484 R52804 450715 Hs.31570 1.00 Hs.25956 DKFZP564D206 protein 451103 0.60 1.30 novel SH2-containing protein 3 Hs.26054 Hs.326444 AF124251 451220 1.91 cartilage acidic protein 1 451668 743948 1.00 67.00 AW023595 Hs.232048 452197 4.53 0.72 purine-rich element binding protein A 11.07 20 AA598509 Hs.29117 452331 2.24 epithelial membrane protein 2 452353 C18825 Hs.29191 1.00 68.00 BE537217 Hs.30343 453049 vanilloid receptor-like protein 1 0.83 1.70 Hs.279746 Hs.31412 NM_016113 453107 132.00 Homo sapiens cDNA FLJ11422 fis, clone HE 1.00 AW295374 453355 1.00 25 AA862496 Hs.28482 **ESTs** 453390 ESTs. Weakly similar to JC5795 CDEP prot 1.00 68.00 AA417940 2.89 gb:CM2-HT0342-091299-050-b05 HT0342 Homo 0.57 BF154396 454741 82.00 1.00 up-regulated by BCG-CWS AA287827 Hs.284205 456579 0.79 1 96 Homo sapiens, clone MGC:16327, mRNA, com AK002016 Hs.114727 3.25 1 03 30 cathepsin Z Hs.252549 457400 AF032906 ESTs, Weakly similar to ALU4_HUMAN ALU S gb:HSC1KA072 normalized infant brain cDN 113.00 1.00 Hs.22978 457718 F18572 1.00 544.00 F03027 459696 TABLE 10B 35 Unique Fos probeset identifier number Pkey: Unique Eos probeset CAT number: Gene cluster number Accession: Genbank accession numbers 40 CAT Number Pkey R20723 AA263003 AA333976 AA334725 AA334151 AW965490 AA310513 AIB10530 D31302 AW134897 AAB30127 AA046953 AI668930 408074 103684_1 R20723 AA263003 AA333976 AA334725 AA334715 AW95590 AA310515 AB10530 D31302 AW104534
BE160198 AW935898 T11520 AW935930 AW856073 AW861034
BE146973 BE146972 BE147042 BE147018 BE146763 BE147020 BE146761 BE146766 BE147021 BE146952 BE146767 BE146767
BE146797 BE146767 BE146859 BE146793 BE146768 BE146771 BE146954 BE146760 BE147048 BE147025 BE147030
AJ012074 U11087 L13288 X75299 L20295 AW630780 H14880 T28037 AI872991 R72136 AW449839 T81622 T79697 T29519 R94105 T83923
AJ012074 U11087 L13288 X75299 L20295 AW630780 H14880 T28037 AI872991 R72136 AW449839 T81622 T79697 T29519 R94105 T83923
AJ012074 U11087 L13288 X75299 L20295 AW630780 H14880 T28037 AI872991 R72136 AW449839 T81622 T79697 T29519 R94105 T83923
AJ012074 U11087 L13288 X75299 L20295 AW630780 H14880 T28037 AI872991 R72136 AW449839 T81622 T79697 T29519 R94105 T83923
AJ012074 U11087 L13288 X75299 L20295 AW630780 H14880 T28037 AI872991 R72136 AW449839 T81622 T79697 T29519 R94105 T83923
AJ012074 U11087 L13288 X75299 L20295 AW630780 H14880 T28037 AI872991 R72136 AW884084 AW872978 AW872985 AA569805 AA569805 AA469788 T87351 R94072 T15187 AA928785 AA569895 1253334_1 1375344_1 413533 45 423387 22779_1 AAS08805 AA418798 T83751 R94072 T16182 AA928785 AA903896 Z92546 AA330586 AI570568 AW341487 AI827050 AW298668 AI792189 AI015693 AI733599 AI572251 AI672488 AW193262 AI244716 AI864375 AI206100 AA912444 AI269365 AI640254 AW772466 AI867336 AA627604 H16914 AA358477 AA338009 50 423696 23112_1 AA469153 AI718503 AA469225 314437 1 430212 AA721522 AW975443 T93070 AA417940 AA036735 T07025 421802_1 436532 55 453531 97026 1 1232559_1 BE154396 AW817959 BE154393 454741 TABLE 10C 60 Unique number corresponding to an Eos probeset refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al. refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495. Indicates DNA strand from which exons were predicted. Ref: Strand: Indicates nucleofide positions of predicted exons. 65 Nt_position: Pkey 400754 Strand Nt position 144559-144684 7331445 Plus 90044-90184,91111-91345 401045 8117619 Plus 70 33192-33360 401083 3242744 Plus 7547175 402474 Minus

PCT/US02/12476 WO 02/086443 TABLE 11A: Genes Distinguishing Adenocarcinoma from Other Lung Diseases and Normal Lung

Table 11A shows about 84 genes upregulated in lung adenocarcinomas relative to other lung tumors, non-malignant lung disease, and normal lung. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 11B show the accession numbers for those Pixey's lacking Unigenetit's for lable 11A. For each probeset we have listed the gene cluster number from which the oligonucteolides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tooks (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 11C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in lable 11A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number Pkey: ExAcon: 15

UnigenelD: Unigene number

5

10

Unique gene title
Average of lung turnors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid lumors) divided by the Unigene Title: R1:

average of normal tung samples

Average of normal tung disease samples (including bronchitis, emphysema, fibrosis, at electasis, asthma) divided by the average of normal tung disease samples. 20 R2:

20	R2:	Averag	e of non-malig	nant rung cisease sampes (abduming diductions, emp	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	
	24	Fulana	Unine no ID	Unigene Title	R1	R2
	Pkey	ExAcca	UnigenelD	Target Exon	1.00	61.00
	403329			NM 003122*:Homo sapiens serine prolease	1.00	39.00
25	406399 406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	226.37	350.00
25	400090	AJ827976	Hs.24391	hypothelical protein FLI13612	0.77	1.18
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	1.00	10.00
	408908	BE296227	Hs.250822	serine/threonline kinase 15	7.76	1.00
	400303	AF251237	Hs.112208	XAGE-1 protein	80.44	40.00
30	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	1.00	1.00
50	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	1.00	1.00
	410076	T05387	Hs.7991	ESTs	1.12	1.50
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	9.89	1.00
	410399	8E068889		synuclein, gamma (breast cancer-specific	0.92	1.06
35	411908	L27943	Hs.72924	cytidine deaminase	1.00	1.00
33	412612	NM_000047	Hs.74131	arylsulfatase E (chondrodysplasia puncta	1.02	1.03
	414075	U11862	Hs.75741	amiloride binding protein 1 (amine oxida	0.84	1.07
	416208	AW291168	Hs.41295	ESTs. Weakly similar to MUC2_HUMAN MUCIN	3.67	1.00
	417542	J04129	Hs.82269	progestagen-associated endometrial prote	1.28	1.35
40	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	1.00	1.00
	419502	AU076704		fibrinogen, A alpha polypeptide	13.05	115.00
	419631	AW188117	Hs.303154	popeye protein 3	1.00	13.00
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	1.00	8.00
	421155	H87879	Hs.102267	lysyl oxidase	1.00	15.00 1.55
45	421190	U95031	Hs.102482	mucin 5, subtype B, tracheobronchial	1.17	1.76
	421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	1.46 1.00	3.00
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase), 1	1.23	1.00
	421582	Al910275		trefoil factor 1 (breast cancer, estroge	1,00	52.00
50	422026	U80736	Hs.110826	trinucleotide repeat containing 9	4.37	2.34
50	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	1.15	1.78
	422311	AF073515	Hs.114948	cytokine receptor-like factor 1	1.69	3.17
	422867	L32137	Hs.1584 Hs.129057	cartilage oligomeric matrix protein (pse breast carcinoma amplified sequence 1	48.13	72.00
	423472	AF041260	Hs. 1674	obtamine-fructose-6-phosphate transamin	1,00	50.00
55	423554 424502	M90516 AF242388	Hs.149585	lengsin	1.00	1.00
33	424544	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci	1.00	59.00
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	21.35	1.00
	424960	BE245380	Hs.153952	5 nucleotidase (CO73)	1.00	1.00
	425523	AB007948	Hs.158244	KIAA0479 protein	1.00	35.00
60	426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	1.00	83.00
oo	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	7.41	34.00
	428585	AB007863	Hs.185140	KIAA0403 protein	1.00	6.00
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	1.06	1.13
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	16.18	105.00
65	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	1.07	1.00
90	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.59	1.69
	430508	AI015435	Hs.104637	ESTs	4.75	7.27
	430985	AA490232	Hs.27323	ESTs, Weakly similar to 178885 serine/th	0.94	1.28
	431548	A1834273	Hs.9711	novel protein	5.66	15.00
70	431566	AF176012	Hs.260720	J domain containing protein 1	49.76	37.00
	431986	AA536130	Hs.149018	Novel human gene mapping to chomosome 20	1.19	1.47
	432375	BE536069	Hs.2962	S100 calcium-binding protein P	1.65	1.06 48.00
	432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.00	19.00
95	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	1.00 3.71	8.00
75	433819	AW511097	Hs.112765	ESTs	29,31	72.00
	434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	1.00	64.00
	434424	Al811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, done L	8.52	44.00
	434792	AA649253	Hs.132458	ESTs	57.97	31.00
QΛ	436217	T53925	Hs.107 Hs.5302	fibrinogen-like 1 lectin, galactoside-binding, soluble, 4	1.10	1.41
80	436749	AA584890	Hs.25640	daudin 3	1.59	1.46
	436972		12.23040	metallothionein 1E (functional)	3.62	101.00
	437866	AW939591	Hs.5940	mucin 13, epithelial transmembrane	1.60	1.39
	437935 438915		Hs.285681	Williams-Beuren syndrome chromosome regi	1.00	1.00
85	436915	AF086270	Hs.278554	heterochromatin-like protein 1	23.28	52.00
Ų,	703431	. 4 0002.0	. 1012.7 5507			

	w	O 02/086	443				PCT/US02/12476
5	441031 441377 443614	AL359055 Al110684 BE218239 AV655386 AA876372	Hs.67709 Hs.7645 Hs.202656 Hs.7645 Hs.93961	Homo sepiers mRNA full length insert cDN fibrinogen, 8 beta polypeptide ESTs fibrinogen, B beta polypeptida Homo sepiens mRNA; cDNA DKFZp667D095 (fr	1.00 1.41 22.03 1.00 1.20	21.00 99.00 1.00 15.00 1.99	
J	443991 444670 444931 446102	NM_002250 H58373 AV652056 AW168067	Hs.10082 Hs.332938 Hs.75113 Hs.317694	potassium intermediate/smail conductance hypothetical protein MGC5370 general transcription factor IIIA ESTs	5.71 1.98 1.00 1.00	6.87 38.00 54.00 1.00	
10	446163 446469 447383	AA026880 BE094848 AW630534 AK000614	Hs.25252 Hs.15113 Hs.76277 Hs.18791	Homo sapiens cDNA FLJ13603 fis, clone PL homogentisate 1,2-dioxygenase (homogenti Homo sapiens, clone MGC:9381, mRNA, comp hypothetical protein FLJ20607	1.00 1.00 1.24 1.23	36.00 11.00 1.16 1.63	
15	448243 448844 449444 451807	AW369771 AI581519 AW818436	Hs.52620 Hs.177164 Hs.23590	Integrin, beta 8 ESTs solute carrier family 16 (monocarboxylic hypothetical protein FLJ23293 similar to	15.84 1.00 1.00 1.55	1.00 31.00 83.00 35.00	
20	452689 453392 453464 453735	F33868	Hs.284176 Hs.32964 Hs.32989 Hs.125073	transferrin SRY (sex determining region Y)-box 11 receptor (calcitonin) activity modifying ESTs	1.54 - 1.00 1.55 1.01	1.44 16.00 2.45 1.30	
	TABLE 1	18					
25	Pkey: CAT nun Accessio	nber. Gene dus	ns probeset ide ter number accession num				
30	Pkey 410399	CAT Numb 11995_1	BE068 Al936	889 BE068882 AF044311 AF017256 NM_003087 A 527 AA804675 AA394097 A1139933 AA946606 BE1 527 L140348 AA486473 AA445004 AA335594 AA44	71313 AA72240 2624 AA <i>A</i> 43638	I/ AA293803 AI468 3 AW452137 AA421	1708 AW265211 AI493266 AA365132 AW966044
35	419502	18535_1	AU076 T6836 T6822 T7320	7/37 H39345 M74860 172098 173265 173873 T6916 7 T68401 T53959 T72360 172099 T60377 T58961 1 0 T74673 T71800 T68355 T61227 T62738 T69317 7 3 T70498 T61409 T58925 NM_000508 M64982 T68 6 T60477 T74863 T61109 T68329 T58850 T71857 7 6 T73787 T56035 T64425 T71870 T60476 T61376	10 174658 1587 171712 T72821 153850 T64692 301 T73729 T65	86 160385 173410 T64738 T74645 T7 T73768 T73962 T7 9445 T60424 T6792 T68607 T58898 T6	168781 167643 167353 173552 167635 167635 2037 168688 172063 173258 172826 164242 3382 168914 170975 173400 160631 173277 22 167736 168716 167755 174765 173819 168719 4309 172031 172079 164305 171908 168107
40			H4835 N3359 AA312 AW47	3 T71914 T53939 T64121 AA693996 T72525 16777 4 AA344542 AW805054 A1207457 T61743 AA02677 919 T40156 H66239 AV652989 H38728 R98521 A\ 0774 AV651256 N54417 AA812862 AW182929 A\ 256 T73982 T47789 B95746 H70620 AA701463 A\ 256 T73982 T47789 B95746 H70620 AA701463 A\	79 (68078 AAU) 37 H94389 AA3 7655200 R9579 11192 H61463 H 7827166 R9847	11465 AA345378 A 82695 AA918409 T 0 W03250 W00913 172060 AA344503 I 15 C20925 AV65728	705467 AV65427 AV6567 AV65767 AV6576
45			AA344 T7047 T7251	272 1735 1747 1745 1745 AV64563 AV653476 T7: 1726 T27854 T74485 T74101 T73868 T71518 T7236 5 T64751 AA344441 AA343657 AA345732 AA34437 7 R02292 T60599 T69206 T70452 T74677 R29386 8 T63258 T68258 AV650429 T73341 T61702 T7457 7 T72042 T62764 A1064899 AA343060 T67832 T72	14 AA343853 17 28 Al110639 AA 161277 T74914 28 T40095 K022	73909 168070 1720 ,344603 AF063513 , T60352 R29675 T 272 T40106 AA3430	05 7/2/149 173491 173495 AV043995 AV02395 T64696 T68516 T72223 T60507 T67633 R29500 74843 AV045792 AA344408 T69197 T72057 I45 AA341908 AA341907 AA342807 AA341964
50			AA345 AA344 AA693	:234 T67598 AA011414 T68036 H48262 A1207557 T 1583 T60362 H58121 T95711 T72803 T68055 T717 1592 A1248502 R29454 T64764 T57001 T73052 T71	T68219 W86031 15 R29036 T727 429 T51176 TS 174474 T56068	. 169081 164232 R 793 T69122 T64599 8866 AV655414 H9	1762888 T69139 T68291 T64652 T67971 T46862 1426 AA342489 T73666 T67848 T72512 T53835
55	421582	2041_1	AI910: AA56: BE074	275 X00474 X52003 X05030 NM_003225 AA314326 1312 AA614409 AA307578 A1925552 A19350155 A1 1045 A1907407 AN568034 BE074051 BE074068 AV	5 AA308400 AA: 310083 M12075 V009769 AW050 524242 A197083	0690 AA858276 R5 09 A1909751 BE076	5389 Al001051 AW050700 AW750216 AA614539 078 Al909749 R55292
60	437866	44433_2	AA156 AA837	5781 AW293839 U52054 AA024963 AA778446 BEO 7481 AW468444 BE165091 AW468002 AA687333 A 7489 AW874142 A1471883 W84421 AA156850	73977 AW44490	04 AW602574 BE 1	24040 RE 104017 RE 107215 DE 107214 DE 107225
60	451807	8865_1	METO	2493 AW 1416 AW 1630 BE208439 BE006339 BE006339 BE006339 BE006539 AA351618 AV	2291 AW95342 N449522 Al827	23 AA351619 BE18 626 AA904788 AA3	0548 BE140560 W60080 AA865478 N90291 180381 AA886045 AA774409 BE003229 Z41756
65	TABLE	11C					•
	Pkey: Ref:	Segmence	some The	onding to an Eos probeset 7 digit numbers in this column are Genbank Identifie ornosome 22.° Dunham I. et al., Nature (1999) 402-4	r (GI) numbers. 189-495	"Dunham I, et al."	refers to the publication entitled "The DNA
70	Strand: Nt_posit	Indicates	DNA strand fro	ompsome 22. Durinant. et al., Naturo (1999) 402. Inn which exons were predicted. Itions of predicted exons.	100		
75	Pkey 403329 406399	Ref 8516120 9256288	Strand Plus Minus	Nt_position 96450-96598 63448-63554			

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TABLE 12A: Genes Distinguishing Squamous Cell Carcinoma from Other Lung Diseases and Normal Lung

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Table 12A shows about 72 genes upregulated in squamous cell carcinomas of the lung relative to other lung tumors, non-matignant lung disease, and normal lung. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 128 show the accession numbers for those Pkey's lacking UnigenelD's for table 12A. For each probeset we have listed the gene cluster number from which the oligorucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oaldand Catifornia). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 12C show the genomic positioning for those Pkey's tacking Unigene ID's and accession numbers in table 12A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

15		
13	Pkey: ExAcon: UnigenelD:	Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number Unigene number

20 Unigene Title: R1: Unigene gene title Average of lung lumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granufomatous and carcinoid lumors) divided by the Average of lung lumos samples average and normal lumo samples

average of normal lung samples Average of non-malignant bung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal hung samples R2: UnigenalD Hs.2258 Unigene Tille matrix metalloproteinase 10 (stromelysin ExAcon 132.45 4.00 25 400289 X07820 3.22 NM_002425:Homo sapiens matrix metallopro 3.26 400666 26.47 10.50 NM_005557°:Homo sapiens keratin 16 (foca 401780 10.33 4.61 Target Exon 401781 2.70 4.13 NM_002275*:Homo sapiens keratin 15 (KRT1 401785 47.00 Target Exon 30 401994 ENSP00000251056*:Plasma membrane calcium 1.00 1.00 402075 1.00 1.00 Target Exon 404996 173.91 108.00 AA045144 Hs.161566 ESTs 407839 151.17 8.00 bullous pemphigoid antigen 1 (230/240kD) 408000 L11690 Hs.620 1.24 Small proline-rich protein SPRK [human, Homo sapiens cDNA: FLJ22044 fis, clone H 1.98 35 AI541214 Hs.46320 408522 10.04 1.00 BE540255 Hs.6994 410561 3-hydroxy-3-methylglutaryl-Coenzyme A sy 1.00 30.00 Hs.77910 415091 AL044872 24.30 1.00 U88967 Hs.78867 protein tyrosine phosphatase, receptor-t 415817 fibrillin 2 (congenital contractural ara 53.29 51.00 Hs.79432 Hs.80962 416658 U03272 1.00 1.00 40 neurotensin 417034 NM 006183 3.27 8.97 small proline-rich protein 1B (comilin) BE185289 Hs.1076 417366 112.17 19.00 AK001100 Hs.41690 desmocollin 3 418663 cancer/testis antigen 1.18 1.10 Hs.87225 418678 NM 001327 1.00 AA374372 parathyroid hormone-like hormone 1.00 Hs.89626 419121 1.25 1.14 3.04 45 lectin, galactoside-binding, soluble, 7 A1659838 Hs.99923 420783 Hs.112457 1.12 **ESTs** 421773 W69233 51.83 20.25 Hs.334309 keratin 6A L42583 421948 0.91 1.01 421978 AJ243662 Hs.110196 NICE-1 protein 1.10 protease inhibitor 3, skin-derived (SKAL 2.37 Hs.112341 L10343 422158 aldo-keto reductase family 1, member 810 47.53 50 NM_004812 Hs.116724 422440 heparin-binding growth factor binding pr hypothetical protein LOC57822 76.02 1.00 AW959908 AJ403108 423634 Hs 1690 1.00 Hs.132127 4.20 423725 10.14 AB002134 Hs.132195 airway trypsin-like protease tumor protein 63 kDa with strong homolog 423738 233.42 68.00 424012 424046 AW368377 Hs 137569 1.00 1.00 serine (or cysteine) proteinase inhibito 55 Hs.138202 AF027866 137.82 small proline-rich protein 3 Hs.139322 Hs.153408 424098 AF077374 Homo saciens cDNA FLJ10570 fis, clone NT 56.19 12.00 424834 AK001432 1.00 Hs.1925 desmoglein 3 (pemphigus vulgaris antigen 33.45 NM_001944 425650 17.00 4.24 odd Oz/ten-m homolog 2 (Drosophila, mous Hs.173560 427099 51.83 4.00 60 AA448542 Gantigen 7B 427335 Hs.251677 1.00 ESTs, Weakly similar to GGC1_HUMAN G ANT BE386042 Hs.293317 1.00 4281B2 1.00 16.00 ESTs, Weakly similar to 2017205A dihydro 428645 AA431400 Hs.98729 1.00 87 00 Ksp37 protein 428748 AW593206 Hs.98785 1.18 2.01 Hs.292911 ESTs, Highly similar to S60712 band-6-pr AA420450 429259 2.90 65 429538 BE182592 Hs.11261 small profine-rich protein 2A cyclin-dependent kinase 5, regulatory su 11.80 1.00 429903 AI 134197 Hs.93597 41.00 Hs.241551 chloride channel, calcium activated, fam 12.28 BE062109 430486 1.40 430890 X54232 Hs 2699 glypican 1 60.25 28.00 Hs.48956 gap junction protein, beta 6 (connexin 3 BE149762 431009 4.49 2.51 70 431846 Hs.271580 uroptakin 1B BE019924 lymphocyte antigen 6 complex, locus D ESTs 1.20 1.09 433091 Y12642 Hs.3185 AW015415 Hs.127780 40.98 27.00 434360 1.00 cytochrome P450, subfamily IVF, polypept interleukin-1 homolog 1 1.00 434880 U02388 Hs.101 1.00 38.00 AF200492 Hs.211238 435505 42.00 75 Hs.4993 KIAA1313 protein 23 68 AB037734 435793 14.00 16.76 436511 AA721252 Hs.291502 **ESTs** 1.00 438403 439285 AA806607 Hs.292206 **ESTs** 139.00 hypothetical protein FLJ20093 46.23 AL133916 33.61 1.00 W79123 Hs.58561 G protein-coupled receptor 87 ESTs, Weakly similar to AC004858 3 U1 sm 439606 80 1.00 1.00 439670 AF088076 Hs 59507 ESTs, Weakly similar to DAP1_HUMAN DEATH 88 SS 11.00 Hs.59761 AW872527 439708 62.88 147.00 440325 NM_003812 Hs.7164 a disintegrin and metalloproteinase doma 1.42 38.00 Hs 127728 ESTs 441525 AW241867 DKFZP434G032 protein 31.11 Hs.9029 T49951 443162 1.00 85 444378 R41339 Hs.12569 **ESTs** 1.00

	WO 02	/086443				PCT/US02/12476			
5	446292 AF081 447078 AW88 447342 A1999 449003 X7634 449101 AA209 450832 AW91 452240 A1991 453317 NM_0	497 Hs.279682 5727 Hs.9914 268 Hs.19322 12 Hs.389 5847 Hs.2309 6002 Hs.105421 147 Hs.61232 02277 Hs.41696	Rh type C glycoprotein ESTs Homo septens, Similar to RIKEN cDNA 2010 atcohol dehydrogenase 7 (dass IV), mir o G protein-coupled receptor ESTs ESTs keratin, hair, acidic, 1	1.55 47.24 28.63 1.00 2.58 25.17 13.42 1.19 24.92	1.26 24.00 1.00 1.00 27.00 36.00 1.00 1.27 25.00				
10	453830 AA534 454098 W279 455601 Al368	53 Hs.292911	ESTs ESTs, Hightly similar to S60712 band-6-pr SRY (sex determining region Y)-box 2	1.26 206.11	1.11 1.00				
	TABLE 128								
15	•								
20	Pkey CAT I 439285 47065	Number Accessi 5_1 AL1339 AA7759	ion 116 N79113 AF086101 N76721 AW950828 AA36401 552 N62351 N59253 AA626243 AI341407 BE175539	3 AW955684 Al34 AA456968 Al358	16341 A1867454 N5478 1918 AA457077	34 Al655270 Al421279 AW014882			
25	TABLE 12C								
25	Ref: Seq	pence source. The 7	nding to an Eos probeset digit numbers in this column are Genbank Identifier mosome 22." Dunham I., et al., Nature (1999) 402:4	(GI) numbers. *Da 39-495.	unham i. et al." refers t	o the publication entitled "The ONA			
30	Strand Indi	cates DNA strand from	m which exons were predicted. tions of predicted exons.						
35	401785 7249190 Minus 165776-165995, 16519-1650 14, 166405-16505, 16505,								
40	404996 600	07890 Plus	31333-30170,00002 30000,00121 300131 (1001)	•					

TABLE 13A: Genes Distinguishing Non-Malignant Lung Disease from Lung Tumors and Normal lung

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Table 13A shows about 23 genes upregulated in non-malignant lung disease relative to lung lumors and normal lung. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 138 show the accession numbers for those Pikey's tacking UniquenelD's for table 13A. For each probeset we have listed the gene duster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 13C show the genomic positioning for those Pikey's lacking Unigene ID's and accession numbers in table 13A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

							•
15	Pkey:	Union	e Ens probes	et identifier number			
13	ExAcon:	Exem	olar Accession	number, Genbank accession number			
	UnigenelD:		ne number				
	Unigene Tibe						A STATE OF THE STA
	R1:	Avera	ae of luna turi	nors (including squamous cell carcinomas, adenocarci	nomas, small cell	carcinomas, granutomatous and carcinom tumo	2) avideo by the
20	• • • • • • • • • • • • • • • • • • • •						
	R2:	Avera	ige of non-mal	ung samples ignant lung disease samples (including bronchitis, em	physema, tibrosis,	, atelectasis, astrima) divided by the average of t	unities must sembles
					04	R2	
		xAccn	UnigenelD	Unigene Title	R1 1.00	230.00	
0.5	408562 A		Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	1.00	128.00	
25	409031 A		Hs.76728	ESTs	1.00	173.00	
	412372 R		Hs.285243	hypothetical protein FLJ22029 chemokine (C-X3-C) receptor 1	1.00	145.00	
	415910 U		Hs.78913	chordin-like	1.00	179.00	
	417511 Al 418819 A		Hs.82223 Hs.191721	ESTs	1.00	140.00	
30	418619 A 422060 R	AZZD110 20002	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.00	156.00	
20	424585 A		Hs.131987	ESTs	1.00	167.00	
	424565 A		Hs.170278	ESTs	1.00	141.00	
	429496 A		Hs.192793	ESTs	1.00	138.00	
	430719 A		Hs.293796	ESTs	1.00	133.00	
35	431089 B			FSTs. Weakly similar to unknown protein	23.32	941.00	
50	431385 B		Hs.11090	membrane-spanning 4-domains, subfamily A	1.00	157.00	
			Hs.268107	multimeria	1.00	157.00	
	436532 A			gb:nv54h12.r1 NCI_CGAP_Ew1 Homo sapiens	1.00	218.00	
	437960 A		Hs.222194	ESTs	1.00	147.00 141.00	
40	438202 A		Hs.22588	ESTs	1.00	141,00	
	441499 A		Hs.101689	ESTs	1.00 1.00	151.00	
	444513 A		Hs.7117	glutamate receptor, ionotropic, AMPA 1	1.00	141.00	
	448253 H		Hs.201591	ESTs	1.00	116.00	
45	453636 R		Hs.169872	ESTs ESTs	1.00	192.00	
43	458332 A		Hs.220491	ob:zk15e04.s1 Soares_pregnant_uterus_NbH	1.00	154.00	
	459587 A	AU3 1930		guzkitaona i oozies_pregnancearas_non			
	TABLE 13B						
	INDLE ISB						
50	Pkev:	Unique E	os probeset in	tentifier number .			
			ster number				
	Accession:		accession nu	mbers			
	•						
	Pkey		nber Accessio				
55	431089	327825_		95 AA491826 AA621946 AA715980 AA666102			
	436532	421802_	1 AA7215	22 AW975443 T93070			
	TABLE 13C						
60	IABLE ISC						
00	Pkey:	Unique r	umber corres	ponding to an Eos probeset			
	Ref:	Sequenc	e source. The	7 digit numbers in this column are Genbank Identifie	r (GI) numbers. "I	Dunham I. et al." refers to the publication entitled	The DNA
		sequenc	e of human ch	romosome 22.* Dunham L et al., Nature (1999) 4024	189-495.	•	
	Strand:	Indicates	DNA strand f	rom which exons were predicted.			
65	Nt_position:			sitions of predicted exons.			
	7		·				
	Pkey	Ref	Strand	Nt_position			
	400077	04474		404007 400005 400004 400004 404040 40445	1 124455 124510	125672-126076	
70	402075	8117407	Plus	121907-122035,122804-122921,124019-12416	1,124433-124810,	120012-120010	

Table 14A shows the subcellular localization and preferred utility for the genes appearing in Tables 9A and 10A. mAb symbolizes monoclonal antibody, diag symbolizes diagnostic, s.m. symbolizes small molecule, and CTL symbolizes cytoloxic lymphocytic ligand. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 5 Genechip array.

Table 14B show the accession numbers for those Pkey's lacking UnigenelD's for table 14A. For each probeset we have listed the gene cluster number from which the oligonucleofides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column. 10

Table 14C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 14A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Unique Eos probeset identifier number Pkey:

rxey: unque tos proceses derimae number
Exécut: Exemplar Accession number, Genbank accession number
Unigene Ditte, Unigene gene title
Praf. Utility: Preferred Utility
Pred.Loc: Preficted subcellular localization

15

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	Pkay	ExAcon	UnigenelD	Unigene Title	Pref Utility	Pred. Loc
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	mAb & diag & s.m.	extracellular
25	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	mAb	plasma membrana
	402075			ENSP00000251056*:Plasma membrane calcium		secreted
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	diag	secreted
	408243	Y00787	Hs.624	interleukin 8	diag	secreted
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	mAb & s.m.	plasma membrane
30	408908	BE296227	Hs.250822	serine/threonine kinase 15	S.M.	cytoplasm secreted
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	CTL & diag CTL	nuclear
	409103	AF251237	Hs.112208	XAGE-1 protein taminin, gamma 2 (nicein (100kD), kalini	diag	secreted
	409420	Z15008	Hs.54451	serine (or cysteine) proteinase inhibito	diag	secreted
35	409632	W74001	Hs.55279 Hs.123114	cystatin SN	diag	extracellular
33	409757 409893	NM_001898 AW247090	Hs.57101	minichromosome maintenance deficient (S.	CTL	nuclear
	409956	AW103364	Hs.727	Inhibin, beta A (activin A, activin AB a	diag	extracellular
	410001	AB041036	Hs.57771	kallikrein 11	diag	extracellular
	410407	X66839	Hs.63287	carbonic anhydrase IX	mAb & s.m.	plasma membrane
40	410418	D31382	Hs.63325	transmembrane protease, serine 4	mAb & diag & s.m.	plasma membrane
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	s.m.	
	412719	AW016610	Hs.816	ESTs	s.m.	nuclear
	414774	X02419	Hs.77274	plasminogen activator, urokinase	diag	extracellular
	414883	AA926960		CDC28 protein kinase 1	s.m.	
45	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	CTL & diag	extracellular
	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	mAb & diag & s.m.	secreted
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	mAb & s.m.	plasma membrane
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	diag	extracellular
	417034	NM_006183	Hs.80962	neurotensin	diag	extracellular
50	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	diag	extracellular mitochondrial
	417308	H60720	Hs.81892	KIAA0101 gene product	s.m. mAb & diag	secreted
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	mAb	plasma membrane
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein thymidylate synthetase	s.m.	endoplasmic reliculum
55	417933 418478	X02308 U38945	Hs.82962 Hs.1174	cyclin-dependent kinase inhibitor 2A (me	s.m.	cytoplasm
55	418506	AA084248	Hs.85339	G protein-coupled receptor 39	mAb & s.m.	plasma membrane
	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	CTL	cytoplasmic
	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	diag	secreted
	419171	NM_002846	Hs.89655	protein tyrosine phosphatase, receptor t	mAb & s.m.	plasma membrane
60	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	CTL & s.m.	mitochondrial
••	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	diag	secreted
	419235	AW470411	Hs.288433	neurotrimin	mAb & diag	plasma membrane
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	mAb & s.m.	plasma membrane
	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	mAb & diag	extracellular*
65	420610	AI683183	Hs.99348	distal-less homeo box 5	CTL	nuclear
	421110	AJ250717	Hs.1355	cathepsin E	sm & diag	extracellular
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	diag	secreted
	421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	mAb & s.m.	plasma membrana
70	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	diag	secreted plasma membrane
70	421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	mAb & s.m. mAb & s.m.	plasma membrane
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	diag	secreted
	422109	S73265 L10343	Hs.1473 Hs.112341	gastrin-releasing peptide protease inhibitor 3, skin-derived (SKAL	diag	secreted
	422158 422282	AF019225	Hs.114309	apolipoprotein L	diag	secreted
75	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	s.m.	nuclear
15	422424	A1186431	Hs.296638	prostate differentiation factor	diag	extracellular
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	s.m.	cytoplasm
	422809	AK001379	Hs.121028	hypothetical protein FLJ 10549	s.m.	nuclear
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	diag	extracellular
80	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	CTL & s.m.	
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	diag	
	423573	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	mAb & diag & s.m.	secreted
	423961	D13666	Hs.136348	periostin (OSF-2os)	mAb & diag	extracellular
0.5	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	diag	secreted
85	424381	AA285249	Hs.146329	protein kinase Chk2	s.m.	nuclear

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	424502	AF242388	Hs.149585	lengsin	s.m.	cytoplasmic
	424503	NM_002205	Hs.149609	integrin, alpha 5 (Ebronectin receptor,	mAb&s.m. diag	piasma membrane extracellular
	424687 425247	J05070 NM_005940	Hs.151738 Hs.155324	matrix metalloproteinase 9 (gelafinase B matrix metalloproteinase 11 (stromelysin	mAb & diag & s.m.	secreted
5	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	s.m.	cytoplasmic
	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	mAb s.m.	plasma membrane
	425734 425776	AF055209 U25128	Hs.159395 Hs.159499	peptidylglycine alpha-amidating monooxyg parathyroid hormone receptor 2	mAb & diag	plasma membrane
. 0	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	mAb & s.m.	plasma membrane
10	426215	AW963419	Hs.155223	stanniocalcin 2	mAb & diag CTL & s.m.	secreted nuclear
	426427	M86699 BE616633	Hs.169840 Hs.170195	TTK protein kinase bone morphogenetic protein 7 (osteogenic	mAb & diag	secreted
	426514 427335	AA448542	Hs.251677	Gantigen 7B	CTL	cytoplasmic
	427747	AW411425	Hs.180655	serine/threonine kinase 12	S.M.	cytoplasmic
15	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic matrix metalloprotainase 7 (matrilysin,	dlag mAb & diag & s.m.	extracellular
	428330 428450	L22524 NM_014791	Hs.2256 Hs.184339	KIAAD175 gene product	s.m.	nuclear
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	s.m.	nuclear
00	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	mAb & s.m. CTL & s.m.	plasma membrane nuclear
20	428654 428698	AK001666 AA852773	Hs.189095 Hs.334838	similar to SALL1 (sal (Drosophila)-like KIAA1866 protein	mAb	Hudou
	428748	AW593206	Hs.98785	Ksp37 protein	diag	extracellular
	428758	AA433988	Hs.98502	CA125 antigen; mucin 16	diag	mitochodria* extracellular
25	428969	AF120274	Hs.194689 Hs.198249	artemin gap junction protein, beta 5 (connexin 3	diag mAb & s.m.	plasma membrane
23	429211 429263	AF052693 AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	mAb & s.m.	plasma membrane
	429547	AW009166	Hs.99376	ESTs	diag	secreted
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	mAb & diag s.m.	secreted
30	429903 430485	AL134197 BE062109	Hs.93597 Hs.241551	cyclin-dependent kinase 5, regulatory su chloride channel, calcium activated, fam	mAb & s.m.	plasma membrane
50	431462	AW583672	Hs.256311	granin-like neuroandocrine peptide precu	dlag	extracellular
	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	mAb & s.m.	plasma membrane plasma membrane
	431846 431958	BE019924 X63629	Hs.271580 Hs.2877	uroplakin 1B cadherin 3, type 1, P-cadherin (placenta	mAb & diag mAb & diag	plasma membrane
35	432201	Al538613 -	Hs.298241	Transmembrane protease, serine 3	mAb & diag & s.m.	plasma membrane
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	s.m.	nuclear
	435505	AF200492	Hs.211238	interleukin-1 homolog 1 HSPC150 protein similar to ubiquitin-con	diag s.m.	secreted
	436481° 437016	AA379597 AU076916	Hs.5199 Hs.5398	quanine monphosphate synthetase	s.m.	cytoplasm
40	437044	AL035B64	Hs.69517	differentially expressed in Fanconi's an	CTL	ER
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	CTL mAb & s.m.	nuclear plasma membrane
	437852 439223	BE001836 AW238299	Hs.256897 Hs.250618	ESTs, Weakly similar to dJ365012.1 [H.sa UL16 binding protein 2	mAb	plasma membrane
	439477	W69813	Hs.58042	ESTs, Moderately similar to GFR3_HUMAN G	mAb & s.m.	-l
45	439606	W79123	Hs.58561	G protein-coupled receptor 87	mAb & s.m. mAb & s.m.	plasma membrane plasma membrane
	439738 440006	BE246502 AK000517	Hs.9598 Hs.6844	sema domain, immunoglobulin domain (lg), NALP2 protein; PYRIN-Containing APAF1-li	S.M.	nuclear
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	s.m.	
50	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	mAb & s.m. CTL	plasma membrane extracellular*
50	443247 443426	BE614387 AF098158	Hs.333893 Hs.9329	c-Myc target JPO1 chromosome 20 open reading frame 1	CTL	CAUGUCIICO
	443859	NM_013409	Hs.9914	follistatin	diag	extracellular
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	mAb	plasma membrane nuclear
55	444371 444381	BE540274 BE387335	Hs.239 Hs.283713	forkhead box M1 ESTs, Weakly similar to S64054 hypotheti	s.m. diag	secreted
33	444781	NM_014406	Hs.11950	GPI-anchored metastasis-associated prote	mAb & diag	plasma membrane
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	mAb & diag	secreted secreted
	446619	AU076643	Hs.313 Hs.16530	secreted phosphoprotein 1 (osteopontin, small inducible cytokine subfamily A (Cy	diag diag	extracellular
60	446921 _. 447033	AB012113 Al357412	Hs.157601	ESTs	CTL & diag	secreted
- •	447342	Al199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	CTL	nlaema mamhenna
	448243	AW369771	Hs.52620 Hs.177164	integrin, beta 8 ESTs	mAb & s.m mAb & s.m.	plasma membrane
	448844 449048	AI581519 Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	mAb	plasma membrane
65	449722	BE280074	Hs.23960	cyclin B1	s.m.	cytoplasm
	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte a disintegrin and metalloproleinase doma	mAb & s.m. mAb & diag & s.m.	plasma membrane plasma membrane
	450375 450701	AA009647 H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	mAb & diag	plasma membrane
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	diag	secreted
70	451668	Z43948	Hs.326444	cartilage acidic protein 1	mAb & diag diag	plasma membrane
	452281 452401	T93500 NM_007115	Hs.28792 Hs.29352	Homo sapiens cDNA FLJ11041 fis, clone PL tumor necrosis factor, atpha-induced pro	diag diag	extracellular
	452747	BE153855	Hs.61460	lg superfamily receptor LNIR	mAb	plasma membrane
76	452838	U65011	Hs.30743	preferentially expressed antigen in mela	CTL CTL	nuclear
75	453968 457489	AA847843 Al693815	Hs.62711 Hs.127179	High mobility group (nonhistone chromoso cryptic gene	CTL & s.m. diag	nuclear secreted
			100121113	arthra Bour		
	TABLE 1	148				
80	Pkey:	Unione F	os probeset iden	ntifier number		
50		nber: Gene dus		- Marian		
	Accessi	on: Genbank	accession numb	bers		

CAT Number Accession

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		02/086443 15024_1	AA926960 AA082436	PCT/US02/12476 AA926959 W76521 W24270 W21526 AA037172 BE267636 H83186 AA469909 N86396 AA001349 BE35736 AA081745 BE566245 H72525 H77575 M49786 W80665 H78746 BE559085 W04339 R98177 T55938 BE279271 AW960304 T29812 AA476873 BE297387 AA177049 NU_001826 X54941 BE314366 AA908783 A719075 BE270172 BE269819 AA889955 AI204630 W25243 A1935150						
5			AA872039 R75953 A AW61300	W72395 T99630 Al422691 H98430 N31428 BE255916 H03265 A157576 AA776920 AA910644 AA459522 AA293140 AW514667 W662396 AA662522 AI865147 A423153 AW262230 AA584410 AA583187 AW024595 AW009734 A1826996 AA282997 AA876046 A262396 AA662522 AI865147 A423153 AW262230 AA584410 AA583187 AW024595 AW009734 A1826996 AA282997 AA876046 AA772418 AA594628 A1034592 V950096 A0034317 AA398727 AW865031 A269427 AW26343 A1041437 AA938724 AA695763 A409459 A1041437 AA938727 AW865031 AA94597 A4276 A1041437 AA935729 AA677684 AA935829 A004687 AW26513 A1094597 H42079 R56703 A1630359 AA617681 AA978045 AV891888 AL537692 AW802662 AA740817 A312104 AU911822 AA416871 A185408 AA129788 AA701623 AW75239						
10			Al139549 Al494230 Al494211	AA633648 A133996 A1336880 AA399239 AUT8TOB A108331 A1362835 A1346518 A1145955 A1389380 A1348243 N92892 AA765850 A1278887 AA962996 A1336880 AA399239 AUT8TOB A108331 A1362835 A1346518 A1145955 A1389380 A1348243 N92892 AA037114 AA129785 AN065801 AN388710 P82750 N59755 A1361128 AN589407 HA7725 H97534 H48076 H48450 T99631 AN300758 H03431 R76789 I H77576 R96823 A4457100 N52845 N49682 H42038 BE220698 BE220715 H99552 AA701624 N74173 R54704 H79520 H72923 E261919 AA759633 AA480310 AA507454 AA910586 A1203723 AW104725 W25611 W25071 T88980 H03513 T77589 R99156						
15	450375	83327_1	W95095 F	E2013-103702275 777551 AA911982 H82956 N83873 AA283872 PAA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532 BH03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067						
20	TABLE 14C									
20	Pkey: Ref:	Securence sour	per corresponding to an Eos probeset urce. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA							
25	Strand: Nt_position:	Indicates DNA:	equence of human chromosome 22.° Dunham L et al., Nature (1999) 402:489-495. ndicates DNA strand from which exons were predicted. ndicates nucleotide positions of predicted exons.							
	Pkey	Ref S	Strand	Nt_position						
30	402075	8117407 F	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076						

TABLE 15A: Information for all sequences in Table 16

Table 15A shows the Seq ID No., Pkey, ExAcon, UnigeneID, and Unigene Title for all of the sequences in Table 16.

Table 159 show the accession numbers for those Pkey's lacking UnigeneID's for table 15A. For each probeset we have listed the gene cluster number from which the digonucleotides were designed. Gene clusters were conciled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (Oouthet wist, Oaktand Catifornia). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 15C show the genomic positioning for those Pixey's tacking Unigene ID's and accession numbers in table 15A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Seq ID No: Sequence ID number

Pkey: Unique Eos probeset identifier number

ExAcon: Exemplar Accession number, Genbank accession number

UnigenelD: Unigene number

Unigene Title: Unigene gene title

20	Seq ID No:	Pkey	ExAcon	UnigenelD	Unigene Title
	Seq ID No: 1 & 2	410407	X66839	Hs.63287	carbonic anhydrase IX
	Seq ID No: 3 & 4	412719	AW016610	Hs.816	ESTs
	Seq ID No: 5 & 6	417034	NM_006183	Hs.80962	neurotensin
25	Seq ID No: 7 & 8	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam
	Seq ID No: 9 & 10	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
	Seq ID No: 11 & 12	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
	Seq ID No: 13 & 14	407788	BE514982	Hs.38991	\$100 calcium-binding protein A2
20	Seq ID No: 15 & 16	407788	BE514982	Hs.38991	S100 calcium-binding protein A2 hypothetical protein FLJ20093
30	Seq ID No: 17 & 18	439285	AL133916	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin
	Seq ID No: 19 & 20	413753	U17760 AW368377	Hs.137569	turnor protein 63 kDa with strong homolog
	Seq ID No: 21 & 22	120486 425650 1		Hs.1925	desmogleln 3 (pemphigus vulgaris antigen
	Seq ID No: 23 & 24 Seq ID No: 25 & 26	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines
35	Seq ID No: 27 & 28	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage
55	Seq ID No: 29 & 30	452838	U65011	Hs.30743	preferentially expressed antigen in mela
	Seq ID No: 31 & 32	418663	AK001100	Hs.41690	desmocollin 3
	Seq ID No: 33 & 34	418663	AK001100	Hs.41690	desmocollin 3
	Seq ID No: 35 & 36	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito
40	Seq ID No: 37 & 38	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas
	Seq ID No: 39 & 40	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad
	Seq ID No: 41 & 42	431846	BE019924	Hs.271580	uroplakin 1B
	Seq ID No: 43 & 44	418830	BE513731	Hs.88959	hypothetical protein MGC4816
15	Seq ID No: 45 & 46	424098	AF077374	Hs.139322	small proline-rich protein 3
45	Seq ID No: 47 & 48	443648	AI085377	Hs.143610	ESTs ESTs, Highly similar to NKGD_HUMAN NKG2-
	Seq ID No: 49	311034	BE567130	Hs.311389 Hs.46320	Small proline-rich protein SPRK (human,
	Seq ID No: 50 & 51	408522	Al541214 L10343	Hs.112341	protease inhibitor 3, skin-derived (SXAL
	Seq ID No: 52 & 53	422158 435505	AF200492	Hs.211238	interleukin-1 homolog 1
50	Seq ID No: 54 & 55 Sea ID No: 56 & 57	417366	BE185289	Hs.1076	small proline-rich protein 18 (comifin)
50	Seq ID No: 58 & 59	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta
	Seq ID No: 60 & 61	441020	W79283	Hs.35962	ESTs
	Seq ID No: 62 & 63	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys
	Seq ID No: 64 & 65	429538	BE182592	Hs.11261	small proline-rich protein 2A
55	Seq ID No: 66 & 67	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte
	Seq ID No: 68 & 69	444371	BE540274	Hs.239	forthead box M1
	Seq ID No: 70 & 71	444371	BE540274	Hs.239	forkhead box M1
	Seq ID No: 72 & 73	444371	BE540274	Hs.239	forkhead box M1
~	Seq ID No: 74 & 75	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias
60	Seq ID No: 76 & 77	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias
	Seq ID No: 78 & 79	429259	AA420450	Hs.292911	Plakophilin solute carrier family 2 (facilitated glu
	Seq ID No: 80 & 81	426440	BE382756	Hs.169902 Hs.69517	differentially expressed in Fanconi's an
	Seq ID No: 82 & 83	437044 423662	AL035864 AK001035	Hs.130881	B-cell CLL/tymphoma 11A (zinc finger pro
65	Seq ID No: 84 & 85 Seq ID No: 86 & 87	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino
05	Seq ID No: 88 & 89	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3
	Seq ID No: 90 & 91	417389	BE260964	Hs.82045	midkine (neurile growth-promoting factor
	Seq ID No: 92 & 93	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr
	Seq ID No: 94 & 95	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated
70	Seq ID No: 96 & 97	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re
	Seq ID No: 98 & 99	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic
	Seq ID No: 100 & 101	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o
	Seq ID No: 102 & 103	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3
96	Seq ID No: 104 & 105	409103	AF251237	Hs.112208	XAGE-1 protein
75	Seq ID No: 106 & 107	417542	J04129	Hs.82269	progestagen-associated endometrial prote
	Seq ID No: 108 & 109	428471	X57348	Hs.184510	stratifin aldehyde dehydrogenase 3 family, member
	Seq ID No: 110 & 111	418004	U37519	Hs.87539 Hs.77256	enhancer of zeste (Drosophila) homolog 2
	Seq ID Not 112 & 113	414761 418203	AU077228 X54942	Hs.83758	CDC28 protein kinase 2
80	Seq ID No: 114 & 115 Seq ID No: 116	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m
50	Seq ID No: 117 & 118	437016	AU076916	Hs.5398	guanine monphosphate synthetase
	Seq ID No: 119 & 120	449230	BE613348	Hs.211579	melanoma cell adhesion molecule
	Seq ID No: 121 & 122	446989	AK001898	Hs.16740	hypothetical protein FLJ11036
	Seq ID No: 123 & 124	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein
85	Seq ID No: 125 & 126	424687	J05070	Hs.151738	matrix metafloproteinase 9 (gelatinase 8

	WO 02/086	113			
	Seq ID No: 127 & 128	414430	Al346201	Hs.76118	ubiquifin carboxyl-terminal esterase L1
	Seq ID No: 129 & 130	418462	BE001596	Hs.85266	integrin, beta 4 CD44 antigen (homing function and Indian
	Seq ID No: 131 & 132	100668 458933	L05424 A1638429	Hs.169610 Hs.24763	RAN binding protein 1
5	Seq ID No: 133 & 134 Seq ID No: 135 & 136	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
,	Seq ID No: 137 & 138	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
	Seq ID No: 139 & 140	418478	U38945	Hs.1174 Hs.1174	cyclin-dependent kinase inhibitor 2A (me cyclin-dependent kinase inhibitor 2A (me
	Seq ID No: 141 & 142 Seq ID No: 143 & 144	418478 446269	U38945 AW263155	Hs.14559	hypothetical protein FLJ 10540
10	Seq ID No: 145 & 146	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur
	Seq ID No: 147 & 148	436481	AA379597	Hs.5199	HSPC150 protein similar to utiquitin-con a disintegrin and metalloprotelnase doma
	Seq ID No: 149 & 150	440325 439606	NIM_003812 W79123	Hs.7164 Hs.58561	G protein-coupled receptor 87
	Seq ID No: 151 & 152 Seq ID No: 153 & 154	453884	AA355925	Hs.36232	KIAAD186 gene product
15	Seq ID No: 155 & 156	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 157 & 158	453884	AA355925	Hs.36232 Hs.36232	KIAAD185 gene product KIAAD186 gene product
	Seq ID No: 159 & 160	453884 404877	AA355925	113.002.02	NM_005365:Homo sapiens melanoma antigen,
	Seq ID No: 161 & 162 Seq ID No: 163 & 164	413129	AF292100	Hs.104613	RP42 homolog
20	Seq ID No: 165 & 166	413281	AA851271	Hs.222024	transcription factor BMAL2 GPI-anchored metastasts-associated prote
	Seq ID No: 167 & 168	444781	NM_014400 U77735	Hs.11950 Hs.80205	pim-2 oncogene
	Seq ID No: 169 & 170 Seq ID No: 171 & 172	416819 451320	AW118072	12.002.00	diacylglycerol kinase, zeta (104kD)
	Seq ID No. 173 & 174	418543	NM_005329	Hs.85962	hyahronan synthase 3
25	Seq ID No: 175 & 176	454034	NM_000691	Hs.575 Hs.156346	aldehyde dehydrogenase 3 family, member topoisomerase (DNA) li alpha (170kD)
	Seq ID No: 177 & 178 Seq ID No: 179 & 180	425397 415817	J04088 U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 181 & 182	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
••	Seq ID No: 183 & 184	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t protein tyrosine phosphatase, receptor-t
30	Seq ID No: 185 & 186	415817	U88967 U88967	Hs.78867 Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 187 & 188 Seq ID No: 189 & 190	415817 419121	AA374372	Hs.89626	parathyroid hormone-like hormone
•	Seq ID No: 191 & 192	448993	Al471630	Hs.8127	KIAA0144 gene product
	Seq ID No: 193 & 194	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR estrogen-responsive B box protein
35	Seq ID No: 195 & 196	430393 425057	BE185030 AA826434	Hs.241305 Hs.1619	achaete-scute complex (Drosophila) homol
	Seq ID No: 197 & 198 Seq ID No: 199 & 200	420462	AF050147	Hs.97932	chondromodulin I precursor
	Seq ID No: 201 & 202	102963	X02404	Hs.274534	catcitonin-retated polypeptide, beta
40	Seq ID No: 203 & 204	100576	X00356	Hs.37058 Hs.36980	catcitonin/calcitonin-related polypeptid metanoma antigen, family A, 2
40	Seq ID No: 205 & 206 Seq ID No: 207 & 208	101175 429038	U82671 AL023513	Hs.194766	seizure related gene 6 (mouse)-like
	Seq ID No: 209 & 210	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
	Seq ID No: 211 & 212	418678	NM_001327	Hs.167379	cancertestis antigen (NY-ESO-1) doublecortex; lissencephaty, X-linked (d
45	Seq ID No: 213 & 214	131927 428182	AJ003112 BE386042	Hs.34780 Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT
43	Seq ID No: 215 & 216 Seq ID No: 217 & 218	427335	AA448542	Hs.251677	G antigen 78
	Seq ID No: 219 & 220	409420	. Z15008	Hs.54451	taminin, gamma 2 (nicein (100k0), kalini ATPase, aminophospholipid transporter-li
	Seq ID No: 221 & 222	114346 438956	AL137256 W00847	Hs.130489 Hs.135056	Human DNA sequence from clone RP5-850E9
50	Seq ID No: 223 & 224 Seq ID No: 225 & 226	404440	1100011	1101100000	NM_021048:Homo sapiens melanoma antigen,
-	Seq ID No: 227 & 228	415569	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito
	Seq ID No: 229 & 230	103312	Y12642 BE069288	Hs.3185 Hs.34744	lysosomal Homo sapiens mRNA; cDNA DKFZp547C136 (fr
	Seq ID No: 231 & 232 Seq ID No: 233	320843 429065	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT
55	Seq ID No: 234 & 235	446102	AW168067	Hs.317694	ESTs
	Seq ID No: 236 & 237	330495	U47924	Hs.71642	guanine nucleotide binding protein (G pr ESTs
	Seq ID No: 238 Seq ID No: 239 & 240	413573 428479	AI733859 Y00272	Hs.149089 Hs.334562	cell division cycle 2, G1 to S and G2 to
	Seq ID No: 241 & 242	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to
60	Seq ID No: 243 & 244	332180	AF134160	Hs.7327	claudin 1 Homo sapiens clone N11 NTera2D1 teratoca
	Seq ID No: 245	437915	A1637993 AA281219	Hs.202312 Hs.121296	ESTs
	Seq ID No: 246 & 247 Seq ID No: 248 & 249	441553 331692	A1683487	Hs.152213	wingless-type MMTV integration site fami
	Seq ID No: 250 & 251	429413	NM_014058	Hs.201877	DESC1 protein
65	Seq ID No: 252 & 253	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis RAB38, member RAS oncogene family
	Seq ID No: 254 & 255 Seq ID No: 256 & 257	448357 446292	N20169 AF081497	Hs.108923 Hs.279682	Rh type C glycoprotein
	Seq ID No: 258 & 259	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h
70	Seq ID No: 260 & 261	453922	AF053306	Hs.36708	budding unInhibited by benzimidazoles 1 serine (or cysteine) proteinase inhibito
70	Seq ID No: 262 & 263	424046 439223	AF027866 AW238299	Hs.138202 Hs.250618	UL16 binding protein 2
	Seq ID No: 264 & 265 Seq ID No: 266 & 267	429228	AI553633	Hs.326447	ESTs
	Seq ID No: 268 & 269	409757	NM_001898	Hs.123114	cystatin SN
75	Seq ID No: 270 & 271	411089	AA456454 AA721252	Hs.214291 Hs.291502	cell division cycle 2-like 1 (PITSLRE pr ESTs
75	Seq ID No: 272 & 273 Seq ID No: 274 & 275	436511 428969	AF120274	Hs.194689	artemin
	Seq ID No: 276 & 277	428969	AF120274	Hs.194689	artemin
	Seq ID No: 278 & 279	428969	AF120274	Hs.194689	artemin artemin
80	Seq ID No: 280 & 281	428969 407137	AF120274 T97307	Hs.194689	artemin gb:ye53h05.s1 Soares fetal liver spleen
JU	Seq ID No: 282 Seq ID No: 283 & 284	412723	AA648459	Hs.335951	hypothetical protein AF301222
	Seq ID No: 285 & 286	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
	Seq ID No: 287 & 288	405770	DE364074	Hs.6566	NM_002362:Homo sapiens melanoma antigen, thyroid hormone receptor interactor 13
85	Seq ID No: 289 & 290 Seq ID No: 291 & 292	439453 414774	BE264974 X02419	Hs.77274	plasminogen activator, urokinase
95	ord 10 1.00 E01 @ E0E				

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	Seq ID No: 293 & 294	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub
	Seq ID No: 295 & 296	437789 437789	AI581344 AI581344	Hs.127812 Hs.127812	ESTs, Wealthy similar to T17330 hypotheti ESTs, Wealthy similar to T17330 hypotheti
	Seq ID No: 297 & 293 Seq ID No: 299 & 300	437769	AI581344	Hs.127812	ESTs, Wealthy similar to T17330 hypotheti
5	Seq ID No: 301 & 302	437789	Al581344	Hs.127812	ESTs, Wealdy similar to T17330 hypotheti
	Seq ID No: 303 & 304	437789	AI581344 AA847843	Hs.127812 Hs.62711	ESTs, Wealdy similar to T17330 hypotheti High mobility group (nonhistone chromoso
	Seq ID No: 305 & 306 Seq ID No: 307 & 303	453968 403478	701011043	1502111	NIM_022342Homo sapiens kinesin protain 9
• •	Seq ID No: 309	441525	AW241867	Hs.127728	ESTs
10	Seq ID No: 310 & 311	434105 428810	AW952124 AF068236	Hs.13094 Hs.193788	presenilins associated rhomboid-like pro nitric oxide synthase 2A (inducible, hep
	Seq ID No: 312 & 313 Seq ID No: 314 & 315	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B
	Seq ID No: 316 & 317	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription f
15	Seq ID No: 318 & 319	409228	R16811 AF056209	Hs.22010 Hs.159396	ESTs, Wealdy similar to 2109260A B cell peptidylgtycine alpha-amldaling monooxyg
15	Seq ID No: 320 & 321 Seq ID No: 322 & 323	425734 413582	AW295647	Hs.71331	hypothetical prolein MGC5350
	Seq ID No: 324 & 325	438403	AA806607	Hs.292206	ESTs unnamed protein product (Homo sapiens)
	Seq ID No: 326 & 327 Seq ID No: 328 & 329	403329 409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.
20	Seq ID No: 320 & 321	119073	BE245360	Hs.279477	v-ets erythroblastosis virus E26 oncogen
	Seq ID No: 332 & 333	113195	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom guanine nucleotide binding protein 11
	Seq ID No: 334 & 335 Seq ID No: 336 & 337	102283 101345	AW161552 NM_005795	Hs.83381 Hs.152175	calcitonin receptor-like
	Seq ID No: 338 & 339	103280	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula
25	Seq ID No: 340 & 341	102012	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas Homo sapiens HSPC285 mRNA, partial cds
	Seq ID No: 342 & 343 Seq ID No: 344 & 345	105729 134299	H46612 AW580939	Hs.293815 Hs.97199	complement component C1q receptor
	Seq ID No: 346 & 347	412719	AW016610	Hs.816	ESTs
20	Seq ID No: 348 & 349	422158	L10343	Hs.112341 Hs.26557	protease inhibitor 3, skin-derived (SKAL plakophliin 3
30	Seq ID No: 350 & 351 Seq ID No: 352 & 353	128924 100485	BE279383 T19006	Hs.10842	RAN, member RAS oncogene family
	Seq ID No: 354 & 355	419121	AA374372	Hs.89626	parathyroid hormone-like hormone
	Seq ID No: 356 & 357	409459	D86407	Hs.54481	low density lipoprotein receptor-related endogenous retroviral protease
35	Seq ID No: 358 & 359 Seq ID No: 360 & 361	330493 417866	M27826 AW067903	Hs.82772	collagen, type XI, alpha 1
-	Seq ID No: 362 & 363	418113	Al272141	Hs.83484	SRY (sex determining region Y)-box 4
	Seq ID No: 364 & 365	437016 429612	AU076916 AF062649	Hs.5398 Hs.252587	guanine monphosphate synthetase pitultary tumor-transforming 1
	Seq ID No: 366 & 367 Seq ID No: 368 & 369	440704	M69241	Hs.162	insulin-like growth factor binding prote
40	Seq ID No: 370 & 371	431221	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye
	Seq 1D No: 372 & 373 Seq 1D No: 374 & 375	431565 431565	AF161470 AF161470	Hs.260622 Hs.260622	butyrate-induced transcript 1 butyrate-induced transcript 1
	Seq ID No: 376 & 377	132354	BE185289	Hs.1076	small profine-rich protein 18 (comifin)
45	Seq ID No: 378 & 379	424441	X14850 AF086009	Hs.147097 Hs.296398	H2A histone family, member X gb:Homo sapiens full length insert cDNA
45	Seq ID No: 380 & 381 Seq ID No: 382 & 383	103768 417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb
	Seq ID No: 384 & 385	425266	J00077	Hs.155421	alpha-fetoprotein
	Seq ID No: 386 & 387 Seq ID No: 388 & 389	424503 400289	NM_002205 X07820	Hs.149609 Hs.2258	Integrin, alpha 5 (fibronectin receptor, matrix metalloproteinase 10 (stromelysin
50	Seq ID No: 390 & 391	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
	Seq ID No: 392 & 393	418007	M13509	Hs.83169	matrix metalloproteinase 1 (Interstitial
	Seq ID No: 394 & 395 Seq ID No: 396 & 397	418738 415138	AW388633 C18356	Hs.6682 Hs.295944	solute carrier family 7, (cationic amino tissue factor pathway inhibitor 2
	Seq ID No: 398 & 399	418506	AA084248	Hs.85339	G protein-coupled receptor 39
55	Seq ID No: 400 & 401	423961	D13666	Hs.136348 Hs.77367	periostin (OSF-2os) monokine induced by gamma interferon
	Seq ID No: 402 & 403 Seq ID No: 404 & 405	414812 417433	X72755 BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprolein
	Seq ID No: 406 & 407	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein
60	Seq ID No: 408 & 409 Seq ID No: 410 & 411	422867 428227	L32137 AA321649	Hs.1584 Hs.2248	cartilage oligomeric matrix protein (pse small inducible cytokine subfamily B (Cy
oo	Seq ID No: 412 & 413	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti
	Seq ID No: 414 & 415	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated
	Seq ID No: 416 & 417 Seq ID No: 418 & 419	411789 428698	AF245505 AA852773	Hs.72157 Hs.334838	Adlican KIAA1866 protein
65	Seq ID No: 420 & 421	450098	W27249	Hs.8109	hypothetical protein FLJ21080
	Seq ID No: 422 & 423	421552	AF026692	Hs.105700	secreted frizzled-related protein 4 lg superfamily receptor LNIR
	Seq ID No: 424 & 425 Seq ID No: 426 & 427	452747 450375	BE153855 AA009647	Hs.61450	a disintegrin and metalloproteinase doma
70	Seq ID No: 428 & 429	426215	AW953419	Hs.155223	stanniocalcin 2
70	Seq ID No: 430 & 431	425247 432201	NM_005940 Al538613	Hs.155324 Hs.298241	matrix metalloproteinase 11 (stromelysin Transmembrane protease, serine 3
	Seq ID No: 432 & 433 Seq ID No: 434 & 435	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph
	Seq ID No: 436 & 437	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447
75	Seq ID No: 438 & 439 Seq ID No: 440 & 441	431211 447033	M86849 Al357412	Hs.323733 Hs.157601	gap junction protein, beta 2, 26kD (conn ESTs
,,,	Seq ID No: 442 & 443	447033	Al357412	Hs.157601	ESTs
	Seq ID No: 444 & 445	447033	Al357412	Hs.157601	ESTs • Man tomat IBO1
	Seq ID No: 446 & 447 Seq ID No: 448 & 449	115522 410418	BE614387 D31382	Hs.333893 Hs.63325	c-Myc target JPO1 transmembrane protease, serine 4
80	Seq ID No: 450 & 451	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119
	Seq ID No: 452 & 453	409041 452461	AB033025 N78223	Hs.50081 Hs.108106	Hypothetical protein, XP_051860 (KIAA119 transcription factor
	Seq ID No: 454 & 455 Seq ID No: 456 & 457	412420	AL035668	Hs.73853	bone morphogenetic protein 2
95	Seq ID No: 458 & 459	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara
85	Seq ID No: 460 & 461	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon

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	Seq ID No: 452 & 453	437852	BE001836	Hs.256897	ESTs, Weakly similar to d.1365O12.1 [H.sa
	Seq ID No: 464 & 465	402075	4 4050747	Hs.1355	ENSP00000251056":Plasma membrane calcium calhepsin E
	Seq ID No: 466 & 467	421110 451668	AJ250717 Z43948	Hs.326444	cartilage acidic protein 1
5	Seq ID No: 468 & 469 Seq ID No: 470 & 471	4516E8	Z43948	Hs.326444	cartilage acidic protein 1
•	Seq ID No: 472 & 473	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 474 & 475	422282	AF019225	Hs.114309	apolipoprotein L death receptor 6, TNF superfamily member
	Seq ID No: 476 & 477	425852	AK001504	Hs.159651 Hs.9598	sema domain, immunoglobulin domain (lg),
10	Seq ID No: 478 & 479 Seq ID No: 480 & 481	439738 427747	BE246502 AW411425	Hs.180655	serine/threonine kinase 12
10	Seq ID No: 482 & 483	420281	AI623693	Hs.323494	Predicted cation efflux pump
	Seq ID No: 484 & 485	405932			C15000305:gij3806122[gb]AAC69198.1] (AF0
	Seq ID No: 486 & 487	405932			C15000305:gij3806122gbjAAC69198.1] (AFO
1.5	Seq ID No: 488 & 489	444342	NM_014398	Hs.10887	similar to hysosome-associated membrane small inducible cytokine subfamily B (Cy
15	Seq ID No: 490 & 491	421379	Y15221 U65590	Hs.103982 Hs.81134	interleukin 1 receptor antagonist
	Seq ID No: 492 & 493 Seq ID No: 494 & 495	417079 430890	X54232	Hs.2699	glypican 1
	Seg ID No: 496 & 497	419721	NM_001650	Hs.288650	aquaporin 4
	Seq ID No: 493 & 499	444471	AB020684	Hs.11217	KIAA0877 protein
20	Seq ID No: 500 & 501	413053	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote lung type-I cell membrane-associated gly
	Seq ID No: 502 & 503	433800	A1034361 NM_007115	Hs.135150 Hs.29352	tumor necrosis factor, alpha-induced pro
	Seq ID No: 504 & 505 Seq ID No: 506 & 507	452401 452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro
	Seq ID No: 508 & 509	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte
25	Seq ID No: 510 & 511	410407	X65839	Hs.63287	carbonic anhydrase IX
	Seq ID No: 512 & 513	309931	AW341683	U- 04C	gb:hd13d01.x1 Soares_NFL_T_GBC_S1 Homo s
	Seq ID No: 514 & 515	412719	AW016610	Hs.816 Hs.80962	ESTs neurotensin
	Seq ID No: 516 & 517 Seq ID No: 518 & 519	417034 430486	NM_006183 BE062109	Hs.241551	chloride channel, calcium activated, fam
30	Seq ID No: 520 & 521	413753	U17760	Hs.75517	łaminin, beta 3 (nicein (125kD), kalinin
50	Seq ID No: 522 & 523	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen
	Seq ID No: 524 & 525	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage
	Seq ID No: 526 & 527	418663	AK001100	Hs.41690 Hs.41690	desmocollin 3 desmocollin 3
35	Seq ID No: 528 & 529	418663 429610	AK001100 AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas
55	Seq ID No: 530 & 531 Seq ID No: 532 & 533	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad
	Seq ID No: 534 & 535	431846	BE019924	Hs.271580	uroplakin 1B
	Seq ID No: 536 & 537	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL cadherin 3, type 1, P-cadherin (placenta
40	Seq ID No: 538 & 539	431958	X63629	Hs.2877 Hs.69517	differentially expressed in Fanconi's an
40	Seq ID No: 540 & 541 Seq ID No: 542 & 543	437044 428484	AL035864 AF104032	Hs.184601	solute carrier family 7 (cationic amino
	Seq ID No: 544 & 545	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3
	Seq ID No: 546 & 547	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor
4.5	Seq ID No: 548 & 549	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3
45	Seq ID No: 550 & 551	417542	J04129	Hs.82269 Hs.211579	progestagen-associated endometrial prote melanoma cell adhesion molecule
	Seq ID No: 552 & 553 Seq ID No: 554 & 555	449230 410555	BE613348 U92649	Hs.64311	a disintegrin and metalloproteinase doma
	Seq ID No: 556 & 557	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma
	Seq ID No: 558 & 559	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B
50	Seq ID No: 560 & 561	418462	BE001596	Hs.85266	integrin, beta 4
	Seq ID No: 562 & 563	410274	AA381807	Hs.61762	hypoxia-inducible protein 2 · G protein-coupled receptor 87
	Seq ID No: 564 & 565 Seq ID No: 566 & 567	439606 404877	W79123	Hs.58561	NM_005365:Homo sapiens melanoma antigen,
	Seq ID No: 568 & 569	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote
55	Seq ID No: 570 & 571	418543	NM_005329	Hs.85962	hyaluronan synthase 3
	Seq ID No: 572 & 573	415817	U88967	Hs.78867	protein tyrosine phosphalase, receptor-t
	Seq ID No: 574 & 575	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t protein tyrosine phosphatase, receptor-t
	Seq ID No: 576 & 577	415817 415817	U88957 U88967	Hs.78867 Hs.78867	protein tyrosine phosphalase, receptor-t
60	Seq ID No: 578 & 579 Seq ID No: 580 & 581	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
00	Seq ID No: 582 & 583	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 584 & 585	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR
	Seq ID No: 586 & 587	418578	NM_001327	Hs.167379	canceritestis antigen (NY-ESO-1) canceritestis antigen (NY-ESO-1)
65	Seq ID No: 588 & 589	418578 409420	NM_001327 Z15008	Hs.167379 Hs.54451	laminin, gamma 2 (nicein (100kD), kalini
03	Seq ID No: 590 & 591 Seq ID No: 592 & 593	332180	AF134160	Hs.7327	claudin 1
	Seq ID No: 594 & 595	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,
	Seq ID No: 596 & 597	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,
70	Seq ID No: 598 & 599	439223	AW238299	Hs.250618	UL16 binding protein 2
70	Seq ID No: 600 & 601	409757	NM_001898	Hs.123114	cystatin SN artemin
	Seq ID No: 602 & 603 Seq ID No: 604 & 605	428969 428969	AF120274 AF120274	Hs.194689 Hs.194689	artemin
	Seq ID No: 606 & 607	428969	AF120274	Hs.194689	artemin
	Seq ID No: 608 & 609	428969	AF120274	Hs.194689	artemin
75	Seq ID No: 610 & 611	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
	Seq ID No: 612 & 613	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine- plasminogen activator, wokinase
	Seq ID No: 614 & 615	414774 407944	X02419 R34008	Hs.77274 Hs.239727	desmocollin 2
	Seq ID No: 616 & 617 Seq ID No: 618 & 619	407944	R34008	Hs.239727	desmocolin 2
80	Seq ID No: 620 & 621	457489	Al693815	Hs.127179	cryptic gene
	Seq ID No: 622 & 623	429547	AW009166	Hs.99376	ESTs
	Seq ID No: 624 & 625	407242	M18728		gb:Human nonspecific crossreacting antig gb:Human nonspecific crossreacting antig
	Seq ID No: 626 & 627	407242	M18728 M18728		gb:Human nonspecific crossreacting antig gb:Human nonspecific crossreacting antig
85	Seq ID No: 628 & 629 Seq ID No: 630 & 631	407242 444005	BE395085	Hs.10086	type I transmembrane protein Fn14
03	~~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~				•

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	110	02/0004	143			101/000412111
	Seq ID No: 6	32 & 633	429597	NM_003816	Hs.2442	a disintegrin and metafloproteinase doma
	Seq ID No. 6		422109	\$73265	Hs.1473	gastrin-releasing peptide
	Seq ID Nox 6		419235	AW470411	Hs.283433	neurotrinin
_	Seq ID Nox 6		449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc
5	Seq ID No: 6		419216	AU076718	Hs.164021	small inducible cytoline subfamily B (Cy
	Seq ID No: 6		431462	AW583672	Hs.256311	granin-like neuroendoorine pepäde precu
	Seq ID No: 6		448243	AW369771	Hs.52620	integrin, beta 8
	Seq ID No: 6		426427	M86699	Hs.169840 Hs.12844	TTK protein kinase EGF-Bke-domain, multiple 6
10	Seq ID No: 6		445537	AJ245671	Hs.114218	frizzled (Drosophila) homolog 6
10	Seq ID No: 6		422278	AF072873	Hs.184339	KIAA0175 gene product
	Seq ID No: 6		428450 446619	NM_014791 AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,
	Seq ID No: 6		453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11
	Seq ID No: 6		426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic
15	Seq ID No: 6 Seq ID No: 6		425776	U25128	Hs.159499	parathyroid hormone receptor 2
13	Seq ID No. 6		425776	U25128	Hs.159499	parathyroid hormone receptor 2
	Seq ID No: 6		431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha
	Seq ID No. 6		419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7
	Seq ID No: 6		432653	N62096	Hs.293185	ESTs, Wealthy similar to JC7328 amino aci
20	Seq ID No: 6		432653	N62096	Hs.293185	ESTs, Wealty similar to JC7328 amino aci
	Seq ID No: 6		432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci
	Seq ID No: 6		432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci
	Seq ID No:		410001	AB041036	Hs.57771	kallikrein 11
	Seg ID No: (426501	AW043782	Hs.293616	ESTs
25	Seq ID No: (408369	R38438	Hs.182575	solute carrier family 15 (H???? transport
	Seq ID Not 1		445413	AA151342	Hs.12677	CGI-147 protein
	Seq ID No: 6	684 & 685	422424	AI186431	Hs.295638	prostate differentiation factor
	Seq ID No: 6	586 & 687	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,
••	Seq ID No: (688 & 689	420610	A1683183	Hs.99348	distal-less homeo box 5
30						
	TABLE 15B					
	Pkey:			dentifier number		
25		r: Gene dust				
35	Accession:	Genbank a	ccession nu	imbers		
	Dt	CAT Numb	٨٠٠٠	ession		
	Pkey 309931	CAT Numb AW341683		2221011		
	330493	33264_5	1127	926 978416 443	07645 AW957879	AW957800 AA633529 H03662
40	439285	47065_1	ΔI 15	2301E N79113 AF	086101 N76721 A	W950828 AA364013 AW955684 AJ346341 AJ867454 N54784 AJ655270 AJ421279 AW014882
40	403263	41000_1	847	75559 NB2351 N	19253 AA626243 A	A1341407 RF 175639 AA456968 A1358918 AA457077
	450375	83327_1	ΔΑΝ	19647 AA131254	AA374293 AW954	1405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532
	400010		ΔΔ10	anaga H83231 H	9605 H01642 AA8	RS2R76 AA11375R AA626915 AA746952 AI161014 AA099554 R69U67
	451320	86576_1	Δ\ <i>N</i> 1	18072 41631982	T15734 AA224199	5 A1701458 W20198 F26326 AA890570 N90552 AW0/190/ A16/1352 A13/5892 103517 100205
45	101020	000.0	Al12	4088 AA224388	AJ084316 AJ35468	6 T33652 Al140719 Al720211 T03490 Al372637 T15415 AW205836 AA630384 T03515 T33230
			AA0	17131 AA443303	T33623 AI222556	T33511 T33785 AI419606 D55612
	TABLE 15C					
50						•
	Pkey:	Unique nut	nber corres	ponding to an Eo:	s probeset	
	Ref:	Sequence	source. The	e 7 digit numbers	in this column are	Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
		sequence	of human ch	romosome 22."	Dunham I. et al., N	ature (1999) 402:489-495.
	Strand:			from which exons		
55	Nt_position:	Indicates n	ucleotide po	ositions of predict	ed exons.	
	Pkey	Ref	Strand	Nt_position		24 - 24 - 24 - 24 - 24 - 24 - 24 - 24 -
	402075	8117407	Pius			21,124019-124161,124455-124610,125672-126076
60	403329	8516120	Plus	96450-9659		
60	403478	9958258	Plus	116458-116		
	404440	7528051	Plus	80430-815	51	
	404877	1519284	Plus	1095-2107	15	·
	405770	2735037	Plus	61057-6207		
65	405932	7767812	Minus	123525-123	0/13	
O)						

Table 16

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        Coding sequence: 43..1422
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        CTGTCACTGC TGCTTCTGAT GCCTGTCCAT CCCCAGAGGT TGCCCCGGAT GCAGGAGGAT
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        TCCCCCTTGG GAGGAGGCTC TTCTGGGGAA GATGACCCAC TGGGCGAGGA GGATCTGCCC
        AGTGAAGAGG ATTCACCCAG AGAGGAGGAT CCACCCGGAG AGGAGGATCT ACCTGGAGAG
                                                                                         300
        GAGGATCTAC CTGGAGAGGA GGATCTACCT GAAGTTAAGC CTAAATCAGA AGAAGAGGGC
                                                                                         360
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        TCCCTGAAGT TAGAGGATCT ACCTACTGTT GAGGCTCCTG GAGATCCTCA AGAACCCCAG
        ACTARTICC ACAGGACAA AGAAGGGAT GACCAGAGTC ATTGGCGCTA TGGAGGCCAC
CCCCCTTGGC CCCGGGTGTC CCCAGCCTGC GCGGGCCCCT TCCAGTCCCC GGTGGATATC
                                                                                         480
                                                                                         540
        OGCCCCAGC TOGCCGCCTT CTGCCCGGCC CTGCGCCCCC TGGAACTCCT GGGCTTCCAG
        CTCCGGCGG TCCCAGAACT GGGCCTGGGC AACAATGGGC ACAGTGTGCA ACTGACCCTG
CCTCCTGGGC TAGAGATGGC TCTGGGTCCC GGGGGGGAGT ACCGGGCTCT GCAGCTGCAT
                                                                                         660
20
        CTGCACTGGG GGGCTGCAGG TCGTCCGGGC TCGGAGCACA CTGTGGAAGG CCACCGTTTC
                                                                                         780
        CCTGCCGAGA TCCACGTGGT TCACCTCAGC ACCGCCTTTG CCAGAGTTGA CGAGGCCTTG
GGGCGCCCGG GAGGCCTGGC CGTGTTGGCC GCCTTTCTGG AGGAGGCCCC GGAAGAAAAC
        AGTGCCTATG AGCAGTTGCT GTCTCGCTTG GAAGAAATCG CTGAGGAAGG CTCAGAGACT
                                                                                         960
        CAGGTCCCAG GACTGGACAT ATCTGCACTC CTGCCCTCTG ACTTCAGCCG CTACTTCCAA
25
        TATGAGGGGT CTCTGACTAC ACCGCCCTGT GCCCAGGGTG TCATCTGGAC TGTGTTTAAC
                                                                                       1080
        CAGACAGTGA TGCTGAGTGC TAAGCAGCTC CACACCCTCT CTGACACCCT GTGGGGACCT
                                                                                       1140
        GGTGACTCTC GGCTACAGCT GAACTTCCGA GCGACGCAGC CTTTGAATGG GCGAGTGATT
        GAGGCCTCCT TCCCTGCTGG AGTGGACAGC AGTCCTCGGG CTGCTGAGCC AGTCCAGCTG
                                                                                       1260
        AATTCCTGCC TGGCTGCTGG TGACATCCTA GCCCTGGTTT TTGGCCTCCT TTTTGCTGTC
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                                                                                       1320
        ACCAGCGTCG CGTTCCTTGT GCAGATGAGA AGGCAGCACA GAAGGGGAAC CAAAGGGGGT
                                                                                        1380
        GTGAGCTACC GCCCAGCAGA GGTAGCCGAG ACTGGAGCCT AGAGGCTGGA TCTTGGAGAA
                                                                                       1440
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ATGCCACTTC CTTTTAACTG CCAAGAAATT TTTTAAAATA AATATTTATA AT
                                                                                       1500
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        Seq ID NO: 2 Protein sequence:
        Protein Accession #: NP_001207
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        GEEDLPSEED SPREEDPPGE EDLPGEEDLP GEEDLPEVKP KSEEEGSLKL EDLPTVEAPG
                                                                                         120
        DPQEPQNNAH RDKEGDDQSH WRYGGDPPWP RVSPACAGRF QSPVDIRPQL AAFCPALRPL
                                                                                         180
        ELLGFOLPPI, PELRLRNNGH SVOLTLPPGL EMALGPGREY RALQLHLHWG AAGRPGSEHT
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        VECHRFPAEI HVVHLSTAFA RVDEALGRPG GLAVLAAFLE EGPEENSAYE QLLSRLEEIA
                                                                                         300
        EEGSETQVPG LDISALLPSD FSRYFQYEGS LTTPPCAQGV IWTVFNQTVM LSAKQLHTLS
                                                                                         360
        DTLWGPGDSR LQLNFRATQP LNGRVIEASF PAGVDSSPRA AEFVQLNSCL AAGDILALVF
        GLLFAVTSVA FLVQMRRQHR RGTKGGVSYR PAEVAETGA
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        Nucleic Acid Accession #: BC013923
        Coding sequence: 438-1391
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55
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AGAGGAGAGA GAAAGAAAGG GAGAGAAGTT TGAGCCCCAG GCTTAAGCCT TTCCAAAAAA
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        TARTARTARC ARTCATCGGC GGCGGCAGGA TCGGCCAGAG GAGGAGGGAA GCGCTTTTTT
TGATCCTGAT TCCAGTTTGC CTCTCTCTTT TTTTCCCCCA AATTATTCTT CGCCTGATTT
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                                                                                         420
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        AGCAAACTTC GGGGGGGGGC GGCGGCAACT CCACCGCGGC GGCGGCCGGC GGCAACCAGA
AAAACAGCCC GGACCGCGTC AAGCGGCCCA TGAATGCCTT CATGGTGTGG TCCCGCGGGG
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                                                                                         600
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                                                                                         660
        TGGGGGCCGA GTGGAAACTT TTGTCGGAGA CGGAGAAGCG GCCGTTCATC GACGAGGCTA
AGCGGCTGCG AGCGCTGCAC ATGAAGGAGC ACCCGGATTA TAAATACCGG CCCCGGCGGA
                                                                                         720
        AAACCAAGAC GCTCATGAAG AAGGATAAGT ACACGCTGCC CGGCGGGCTG CTGGCCCCCG
                                                                                         840
70
        GOGGCAATAG CATGGCGAGC GGGGTCGGGG TGGGCGCCGG CCTGGGCGCG GGCGTGAACC
                                                                                         900
        AGCGCATGGA CAGTTACGCG CACATGAACG GCTGGAGCAA CGGCAGCTAC AGCATGATGC
        AGGACCAGCT GGGCTACCCG CAGCACCCGG GCCTCAATGC GCACGGCGCA GCGCAGATGC
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CCTACATGAA CGCTCGCCC ACCTACAGCA TGTCCTACTC GCAGCAGGGC ACCCTGGCA
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                                                                                       1140
75
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                                                                                       1200
        TTACCTCTTC CTCCCACTCC AGGGCGCCCT GCCAGGCCGG GGACCTCCGG GACATGATCA
        GCATGTATCT CCCCGGCGCC GAGGTGCCGG AACCCGCCGC CCCCAGCAGA CTTCACATGT
                                                                                       1320
        CCCAGCACTA CCAGAGCGGC CCGGTGCCCG GCACGGCCAT TAACGGCACA CTGCCCCTCT
                                                                                       1380
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80
        GGAAATGGGA GGGTGCAAA AGAGGAGGAT AAGAAACAGC ATGGAGAAAA CCCGGTACGC
TCAAAAAAAA AAAAAAAAA AAAATCCCAT CACCCACAGC AAATGACAGC TGCAAAAGAG
                                                                                       1500
                                                                                       1560
        AACACCAATC CCATCCACAC TCACGCAAAA ACCGCGATGC CGACAAGAAA ACTTTTATGA
                                                                                       1620
        GAGAGATCCT GGACTTCTTT TKGGGGGACT ATTTTTGTAC AGAGAAAACC TGGGGAGGGT
GGGGAGGGCG GGGGAATGGA CCTTGTATAG ATCTGGAGGA AAGAAACCTA CGAAAAACTT
                                                                                       1680
                                                                                       1740
85
        TTTAAAAGTT CTAGTGGTAC GGTAGGAGCT TTGCAGGAAG TTTGCAAAAG TCTTTACCAA
                                                                                       1800
        TAATATTTAG AGCTAGTCTC CAAGCGACGA AAAAAATGTT TTAATATTTG CAAGCAACTT
                                                                                       1860
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             TARARATTGT ACARAAGGAA ARAATTAGAA TAAGTACTGG CGAACCATCT CTGTGGTCTT
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                                                                                                                                                  2160
             GITTAAAAAG GGCAAAAGTT TTAGACTGTA CTAAATTTTA TAACTTACTG TTAAAAAGCAA
              AAATGGCCAT GCAGGTTGAC ACCGTTGGTA ATTTATAATA GCTTTTGTTC GATCCCAACT
  5
              TTOCATTITG TICAGATAAA AAAAACCATG AAATTACTGT GTTTGAAATA TTTTCTTATG
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GTAGTTGTAT TITAAAAGAT TCGGCTCTGT ATTATTGAA TCAGTCTGCC GAGAATCCAT
                                                                                                                                                  2400
             GTATATATTT GAACTAATAT CATCCTTATA ACAGGTACAT TITCAACTTA AGTTTTACT
CCATTATGCA CAGTITGAGA TAAATAAATT TITGAAATAT GGACACTGAA AAAAAAAAA
AAAAAACAA AACAAAAAAA CAAAAAACAA AAACAGAAAA AACCAAAAAAA AAAACAAAAC
                                                                                                                                                  2460
10
                                                                                                                                                  2580
              CCACAACACA AACAACAACA CACAGAGGG
              Seq ID NO: 4 Protein sequence:
15
              Protein Accession #: CAA83435.1
                                                                               31
                                                                                                     41
              MYNIMETELK PPGPQQTSGG GGGNSTAAAA GGNQKNSPDR VKRPMNAFMV WSRGQRRKMA
20
              QENPKMENSE ISKRLGAEWK LISETEKRPF IDEAKRIRAL HMKEHPDYKY RPRKTKTIM
KKDKYTLPGG LLAPGGNSMA SGYGVGAGLG AGVNQRMDSY AHRNGWSNGS YSMMQDQLGY
                                                                                                                                                     120
                                                                                                                                                     180
              POHPGINAEG AAQMQPMHRY DVSALQYNSM TSSQTYMNGS PTYSMSYSQQ GTPGMALGSM
              GSVVKSEASS SPPVVTSSSH SRAPCQAGDL RDMISMYLPG AEVPEPAAPS RLHMSQHYQS
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              Nucleic Acid Accession #: U91618
              Coding sequence: 29-541
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TGCTTTAGAT GGCTTTAGCT TGGAAGCAAT GTTGACAATA TACCAGCTCC ACAAAATCTG
                                                                                                                                                     360
              TCACAGCAGG GCTTTCAAC ACTGGGAGT AATCCAGGAA GATATTCTTG ATACTGGAAA
TCACAAAAAT GGAAAGGAAG AAGTCATAAA GAGAAAAATT CCTTATATTC TGAAACGGCA
                                                                                                                                                     420
                                                                                                                                                     480
40
              GCTGTATGAG AATAAACCCA GAAGACCCTA CATACTCAAA AGAGATTCTT ACTATTACTG
                                                                                                                                                     540
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              ATTATATTTG TGTGAAAATG TGACAAACAC ACTTATCTGT CTCTTCTACA ATTGTGGTTT
                                                                                                                                                     660
                                                                                                                                                     720
              ATTGAATGTG TTTTTCTGCA CTAATAGAAA TTAGACTAAG TGTTTTCAAA TAAATCTAAA
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               TCTTCAAAAA AAAAAAAAAA AAATGGGGCC GCAATT
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              Protein Accession #: AAB50564
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LIQEDILDTG NDKNGKEEVI KRKIPYILKR QLYENKPRRP YILKRDSYYY
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              Nucleic Acid Accession #: NM 006536.2
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              Coding sequence: 109-2940
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                                                                                                                                                       60
              ACCTAMANCE
ATGENTICAS
TOTAL
TO
 65
                                                                                                                                                      120
                                                                                                                                                      240
                                                                                                                                                      300
              ATTGCAATTA ATCCTCAGGT ACCTGAGAAT CAGAACCTCA TCTCAAACAT TAAGGAAATG
              ATAACTGAAG CTTCATTTTA CCTATTTAAT GCTACCAAGA GAAGAGTATT TTTCAGAAAT
ATAAAGATTT TAATACCTGC CACATGGAAA GCTAATAATA ACAGCAAAAT AAAACAAGAA
 70
                                                                                                                                                      420
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GGATGCACCT TTATCTACAA TAGCACCCAA AATGCAACTG CATCAATAAT GTTCATGCAA
                                                                                                                                                      780
                                                                                                                                                      840
               AGTITATOTT CTGTGGTTGA ATTTTGTAAT GCAAGTACCC ACAACCAAGA AGCACCAAAC
                                                                                                                                                      900
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 80
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                                                                                                                                                   1200
                                                                                                                                                    1260
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                                                                                                                                                    1320
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10	GCCACTGTGG	AAGCCTTTGT	GGAAAGAGAC ATTTTATCCC	AGCCTCCATT	TTCCTCATCC	TGTGATGATT	1980 2040
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	TCACCATGCA	COCCACAACA	CTTTGATCAG	GGCCAGGCTA	CAAGCTATGA	AATAAGAATG	2520
	TOGACAGCAC	TACACAATAT	CCAAGATGAC	TTTAACAATG	CTATTTTAGT	AAATACATCA	2580
20	AGIAMAGIC	CTCAGCCAACC	TGGCATCAGG	GAGATATTTA	CGTTCTCACC	CCAGATTTCC	2640
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	TTTCTAAGTT	TATTGCCTTG	GGTTATTATG	GAATGATAGT	TATAGCCCCN	TATAATGCCT	3660
	TACCTAGGAA	A					
40							
40		8 Protein					
	Protein Ac	cession #: 1	NP 006527.1				
			_				
	1	11	21	31	41	51	
15	1	11	21 	1	1	1	60
45	1 MTORSIAGPI	11 CNLKFVTLLV	21 ALSSELPFLG	AGVQLQDNGY	 NGLLIAINPQ	 VPENQNLISN	60 120
45	1 MTQRSIAGPI IKEMITEASF	11 CNLKFVTLLV YLFNATKRRV	21 ALSSELPFLG FFRNIKILIP	AGVQLQDNGY ATWKANNNSK	 NGLLIAINPQ IKQESYEKAN	 VPENQNLISN VIVTDWYGAH	120
45	1 MTQRSIAGPI IKEMITEASF GDDPYTLQYR	11 CNLKFVTLLV YLFNATKRRV GCGKEGKYIH	21 ALSSELPFLG FFRNIKILIP FTPNFLLNDN	AGVQLQDNGY ATWKANNNSK LTAGYGSRGR	 NGLLIAINPQ IKQESYEKAN VFVHEWAHLR	VPENQNLISN VIVTDWYGAH WGVFDEYNND	120 180
45	1 MTQRSIAGPI IKEMITEASF GDDPYTLQYR	11 CNLKFVTLLV YLFNATKRRV GOGKEGKYIH IKVTRCSSDI	21 ALSSELPFLG FFRNIKILIP FTPNFLLNDN TGIPVCEKGP	AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPOENCLISK	 NGLLIAINPQ IKQESYEKAN VFVHEWAHLR LFKEGCTFIY	VPENQNLISM VIVTDWYGAH WGVFDEYNND NSTQNATASI	120 180 240
	1 MTQRSIAGPI IKEMITEASP GDDPYTLQYR RPPYINGQNQ MFMOSLSSVV	11 CNLKFVTLLV YLFNATKRRV GCGKEGKYIH IKVTRCSSDI EFCNASTHNQ	21 ALSSELPFLG FFRNIKILIP FTPNFLLNDN TGIFVCEKGP EAPNLQNQMC	AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPQENCIISK SLRSAWDVIT	 NGLLIAINPQ IKQESYEKAN VFVHEWAHLR LFKEGCTFIY DSADFHHSFP	VPENQNLISN VIVTDWYGAH WGVFDEYNND NSTQNATASI MNGTELPPPP	120 180 240 300
45 50	1 MTQRSIAGPI IKEMITEASF GDDPYTLQYR KPFYINGQNQ MFMQSLSSVV TFSLVOAGDK	11 CNLKFVTLLV YLFNATKRRV GCGKEGKYIH IKVTRCSSDI EFCNASTHNQ VVCLVLDVSS	21 ALSSELPFLG PFRNIKILIP FTPNFLLNDN TGIFVCEKGP EAPNLQNQMC KMAEADRLLQ	AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPQENCIISK SLRSAWDVIT LQQAAEFYLM	 NGLLIAINPQ IKQESYEKAN VFVHEWAHLR LFKEGCTFIY DSADFHHSPP QIVEIHTFVG	VPENQNLISN VIVTDWYGAH WGVFDEYNND NSTQNATASI MNGTELPPPP IASFDSKGEI	120 180 240 300 360
	1 MTQRSIAGPI IKEMITEASF GDDPYTLQYR KPFYINGQNQ MFMQSLSSVV MFMQSLSSVV TFSLVQAGDK RAOLHQINSN	11 CNLKFVTLLV YLFNATKRRV GCGKEGKYIH IKVTRCSSDI EFCNASTHIQ VVCLVLDVSS DDRKLLVSYL	21 ALSSELPFLG PFRNIKILIP FTPNFLLNDN TGIFVCEKGP EAPNLQNQMC KMAEADRLLQ PTTVSAKTDI	AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPQENCIISK SLRSAWDVIT LQQAAEFYLM SICSGLRKGF	NGLLIAINPQ IKQESYEKAN VFVHEWAHLR LFKEGCTFIY DSADFHHSPP QIVEIHTFVG EVVEKLNGKA	VPENQNLISM VIVTDWYGAH WGVFDEYNND NSTQNATASI MNGTELPPPP IASFDSKGEI YGSVMILVTS	120 180 240 300
	1 MTQRSIAGPI IKEMITEASF GDDPYTLQYR KPFYINGQNQ MFMQSLSSVV TFSLVQAGDU TFSLVQAGDU GDDKLLGNCL	11 CNLKFVTLLV YLFNATKRRV GCGKEGKYIH IKVTRCSSDI EFCNASTHNQ VVCLVLDVSS DDRKLLVSYL PTVLSSGSTI	21 ALSSELPFLG FFRNIKILIP FTPNFLLNDN TG FVCEKGP EAPNLQNQMC KMAEADRLLQ PTTVSAKTDI HSIALGSSAA	AGVQLQDNGY ATWKANNINSK LTAGYGSRGR CPQENCIIS SLRSAWDVIT LQQAAEFYLM SICSGLKKGF PNLEELSRLT	I NGLLIAINPQ IKQESYEKAN VFVHEWAHLR LFKEGCTFIL DSADFHHSFP QIVEIHTFVG EVVEKLNGKA GGLKPFVPDI	VPENQNLISM VIVTDWYGAH WGVFDEYMND NSTQNATASI MNGTELPPPP IASFDSKGEI YGSVMILVTS SNSNSMIDAF	120 180 240 300 360 420
50	1 MTQRSIAGPI IKEMITEASF GDDPYTLQYR KPFYINGQNQ MFMQSLSSVV TFSLVQAGDK RAQLHQINSN GDDKLLGNCL SRISSGTGDI	11 CNLKFVTLLV YLFNATKRRV GCGKEGKYIH IKVTRCSSDI EFCNASTHNQ VVCLVLDVSS DDRKLLVSYL PTVLSSGSTI FQQHIQLEST	21 ALSSELPFLG FFRNIKILIP FTPNFLLNDN TGIFVCEKGP EAPNLQNQMC KMAEADRLLQ PTTVSAKTDI HSIALGSSAA GENVKPHEQL	AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPQENCIISK SLRSAWDVIT LQQAAEFYLM SICSGLKKGF PNLEELSRLT KNTVTVDNTV	 NGLLIAINPQ IKQESYEKAN VFVHEWAHLR LFKEGCTFIY DSADFHHSPP QIVEIHTFVG EVVEKLINGKA GGLKFFVPDI GNDTMFLVTW	VPENQNLISM VPENQNLISM VIVTDWYGAH MGVFDEYNND NSTQNATASI MNGTELPPPP IASFDSKGEI YGSVMILUTS SNSNSMIDAF QASGPPEIIL	120 180 240 300 360 420 480
50	1 MTQRSIAGPI IKEMITEASF GDDPYTLOYR KPPYINGQNQ MFMQSLSSVV TFSLVQAGDK RAQLHQINSN GDDKLLGNCL SRISSGTGDI FDPDGRKYYT	11 CNLKFVTLLV YLFNATKRRV GCGKEGKYIH IKVTRCSSDI EFCNASTHNQ VVCLVLDVSS DDRKLLVSYL FTVLSSGSTI FQOHIQLEST NNFITNLTFR	21 ALSSELPFIG PFRNIKILIP FTPNFILNDN TGIPVCEKGP EAPNLQNQMC KMAEADRILQ PTTVSAKTDI HSIALGSSAA GENVKPHEQL TASLWIPGTA	AGVQLQDNGY ATWKANTNSK LTAGYGSRGR CPQENCIISK SLRSAWDVIT LQQAAEFYLM SICSGLKKGF PNLEELSRLT KNTVTVDNTV KPGHWTYTLN	NGLLIAINPQ IKQESYEKAN VFVHEWAHLR LFKEGCTFIY DSADFHHSFP QIVEIHTFVG EVVEKLNGKA GGLKFFVPDI GNDTMFLVTW NTHHSLQALK	VPENQNLISM VIVTDWYGAH MGVFDEYNND NSTQNATASI MNGTELPPPP IASFDSKGEI YGSVMILVTS SNNNSMIDAF QASGPPEIIL VTVTSRASNS	120 180 240 300 360 420 480 540
	1 MTQRSIAGPI KEMITEASF GDDPYTLQYR RPFYINGONQ MFMQSLSSVV TFSLVQAGDK RAQLHQINSN GDDKLLGNCL SRISSGTGDI FDPDGRKYYT AVPPATVEAF	11 CNLKFVTLLV YLFMATKRRV GCGKEGKYIH IKVTRCSSDI EFCNASTINQ VVCLVLDVSS DDRLLLVSYL PTVLSSGSTI FOORIQLEST NNFITNLTFR VERDSLHPPH	21 ALSSELPFLG FFRNIKILIP FTPNFLIMDN TGIFVCEKGP EAPNLONGMC KMAEADRLLQ FTTVSAKTDI HSIALGSSAA GENVKPHKOL TASLWIPGTA TASLWIPGTA	AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPQENCIISK SLRSAWDVIT LQQAAEFYLM SICSGLKKGF PNLEELSRLT KNTVTVDNTV KPGHWTYTLN GFYPILNATV	NGLLIAINPQ IKQESYEKAN VPVHEWAHLR LFKEGCTFIY DSADFHHSFP QIVEIHTFVG EVVEKLNGKA GGLKPFVPDI GNDTMFLVTW NTHHSLQALK TATVEPETGD	VPENONLISM VIVTDWYGAH WGVFDEYNND NSTQNATASI MNGTELPPPP IASFDSKGEI YGSVMILVTS SNSNSMIDAF QASGPPEILL VTVTSRASNS PVTLRLLDDG	120 180 240 300 360 420 480 540
50	1 MTQRSIAGPI IKEMITEASF GDDPYTLOYR KPFYINGONQ MFMQSLSSVV TFSLVQAGDK RAQLHQINSN GDDKLLGNCL SRISSGTGDI FDPDGRKYYT AVPATVEAF AGADVIKNDG	11 CNLKFVTLLV CNLKFVTLLV COKEGKYIH IKVTRCSSDI EFCNASTHNQ WYCLVLDVSS DDRKLLVSYL PTVLSSGSTI FQQHIQLEST NNFITNLTFR VERDSLHFPH VERDSLHFPH VSRYFFSFA	21 ALSSELPFLG FFRNIKILIP FTPNFLIMDN TGIPVCEKGP EAPNLQNOMC KMAEADRLLQ PTTVSAKTDI HSIALGSSAA GENVKPHEQL TASLMIPGTA PVMIYANVKQ ANGRYSLKVH	AGVQLQDNGY AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPQENCIISK SLRSAMDVIT LQQAAEFYLM SICSGLKRGF PNLEELSRLT KNTTYVDNTV KPCHWTYTLN KPGHWTYTLN VNRSPSISTP	NGLLIAINPQ IKQESYEKAN VFVHEWAHLR LFKEGCTFIY DSADFHESPP QIVEIHTFVG EVVEKLNGKA GGLKFFVPDI GNDTMFLVTW NTHESLQALK TATVEPETGD AHSIPGSHAM	VPENQNLISM VIVTDWYGAH WGVFDEYNND NSTQNATASI MNGTELPPP IASFDSKGEI YGSVMILUTS SNNNSMIDAF QASGPPEIIL VTVTSRASMS PVTLRLLDDG YVPGYTANGN	120 180 240 300 360 420 480 540 600 660
50	1 MTQRSIAGPI KEMITEASF GDDPYTLOYR KFFYINGONQ KFMSLSSVV TFSLVQAGDK RAQLHQINSN GDDKLLGNCL SRISSGTGDI FDPDGRKYYT AVPPATVEAF AGADVIKNDG	11 CMLKPYTLLV YLFNATKRRV GCGKEGKYIH IKVTRCSSDI EFCNASTHINQ VVCLVLDVSS DDRKLLVSYL PTVLSSGSTI FQQHIQLEST NNFITNLTFR VERDSLHPPH IYSRYFFSFA GRMEEERKWG	21 ALSSELPFLG PFRNIKILIP FTPNFLIMDN TGIPVCEKGP EAPNLQNGMC KMAEADRLLQ PTTVSAKTDI HSIALGSSAA GENVKPHKQL TASLWIPGTA PVMIYANVKQ ANGRYSLKVH FSRVSSGGSF	AGVQLQDNGY AGVQLQDNGY AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPQENCIISK SLRSAMDVIT LQQAAEFYLM SICSGLKKGF PNLEELSRLT KNTTYUDNTV KPGHWTYTLN GFYPILMATV VNHSPSISTP SVLGVPAGPH	NGLLIAINPQ IKQESYEKAN VFVHEWARLR LFKEGCTFIY DSADFHHSPP GIVEINTFVG GVVEKLNGKA GGLKFFVPDI GNDTMFLVTW NTHHSLQALK TATVEPETGD AHSIPGSHAM PDVPPPCKII	VPENONLISM VPENONLISM VIVTDWYGAH WGVFDEYMND NSTONATASI MNGTELPPPP IASFDSKGEI YGSVMILVTS SNSNSMIDAF QASGPPEIIL VTVTSRASNS FVTLRLLDDG YVPGYTANGN DLEAVKVEEE	120 180 240 300 360 420 480 540 600 660 720
50	1 MTQRSIAGPI IKEMITEASF RDPYTLQYR RPPYINGONQ MFMQSLSSVV TFSLVQAGDK RAQLHQINSN GDDKLLGNCL SRISSGTGDI FDPDGRKYYT AVPPATVEAF AGADVIKNDG IQMNAPRKSV	11 CNLKFVTLLV YLFMATKRRV YLFMATKRRV GCGKEGKYIH IKVTRCSSDI EFCNASTHNQ VVCLVLDVSS DDRRLLVSYL PTVLSSGSTI FQQRIQLEST MNFITNLTFR VERDSLHPPH IYSRYFFSFA GRNEEERKWG DFDDGGOATSY	21 ALSSELPFLG FFRNIKILIP FTPNFLIMDN TGIFVCEKGP EAPNLONGMC KMAEADRLLQ PTTVSAKTDI HSIALGSSAA GENVKPHEQL TASLWIFATA FVMIYANVKO ANGRYSLKVH FSRVSSGGSF EIRMSKSLQN	AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPQENCIISK SLRSAMDVIT LQQAAEFYLM SICSGLKKGF PNLEELSRLT KNTYTVDNTV KPGHWTYTLN VMRSPSISTP SVLGVPAGPH IQDDFNNAIL	I NGLLIAINPQ IKQESYEKAN VFVHEWAKLR LFKEGCTFIY DSADFHESPP QIVEIHTFVG EVVEKLNGKA GGLKFFVPDI GNITMFLVTW NTHISLQALK TATVEPETGD AHSIPGSHAM PDVPPCKII VNTSKRIPQQ	VPENQNLISM VPENQNLISM VIVTDWYGAH WGVFDEYNND NSTQNATASI MNGTELPPPP IASFDSKGEI YGSVMILVTS SNSNSMIDAF QASGPPEIIL VTVTSRASNS PVTLRLLDDG YVPGYTANCM DLEAVKVEEE AGIREIFFTS	120 180 240 300 360 420 480 540 600 660 720 780
50	1 MTQRSIAGPI IKEMITEASF GDDPYTLOYR REFYINGONQ MFMQSLSSVV TFSLVQAGDK RAQLHQINSN GDDKLLGNCL GDDKLLGNCL TOPDGRKYYT AVPPATVEAF AGADVIKNDG IQMIAPRRSV LTLSWTAPGE	11 CNLKFVTLLV CNLKFVTLLV CGCKEGKYIH IKVTRCSSDI EFCNASTHNQ VCLVLDVSS DDRKLLVSYL PTVLSSGSTI FQGHIQLEST NNFITNLIFF VERDSLHFPH VERDSLHFPH GRNEEERKWG DFDQGQATSY QPNGETHESH	21 ALSSELPFIG PFRNIKILIP FTPNFLIMDN TGIFVCEKGP EAPNLQNQMC KMAEADRILQ PTTVSAKTDI HSIALGSSAA GENVKPHEQL TASLMIPGTA PVMIYANVKQ ANGRYSLKVH FSRVSSGGSF EIRMSKSLQN RIYVAIRAMD	AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPQENCIISK SLRSAMDVIT LQQAAEFYLM SICSGLKRGF PNLEELSRLT KNTVTVDNTV KPCHWTYTLN VNHSPSISTP SVLGYPACPH IQDDFNNAIL RNSLQSAVSN	NGLLIAINPQ IKQESYEKAN VFVHEWAHLR LFKEGCTFIY DSADFHISPP QIVEIHTFVG EVVEKLNGKA GGLKFFVDI GNDTMFLVTW NTHEIGALK TATVEPETGD AHSIPGSHAM PDVPPCKII VNTSKRNPQQ LAQAPLEIPP	VPENQNLISM VPENQNLISM VIVTDWYGAH WGVFDEYNND NSTQNATASI MNGTELPPPP IASFDSKGEI YGSVMILVTS SNSNSMIDAF QASGPPEIIL VTVTSRASNS PVTLRLLDDG YVPGYTANCM DLEAVKVEEE AGIREIFFTS	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55	1 MTQRSIAGPI IKEMITEASF GDDPYTLOYR REFYINGONQ MFMQSLSSVV TFSLVQAGDK RAQLHQINSN GDDKLLGNCL GDDKLLGNCL TOPDGRKYYT AVPPATVEAF AGADVIKNDG IQMIAPRRSV LTLSWTAPGE	11 CNLKFVTLLV CNLKFVTLLV CGCKEGKYIH IKVTRCSSDI EFCNASTHNQ VCLVLDVSS DDRKLLVSYL PTVLSSGSTI FQGHIQLEST NNFITNLIFF VERDSLHFPH VERDSLHFPH GRNEEERKWG DFDQGQATSY QPNGETHESH	21 ALSSELPFLG FFRNIKILIP FTPNFLIMDN TGIFVCEKGP EAPNLONGMC KMAEADRLLQ PTTVSAKTDI HSIALGSSAA GENVKPHEQL TASLWIFATA FVMIYANVKO ANGRYSLKVH FSRVSSGGSF EIRMSKSLQN	AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPQENCIISK SLRSAMDVIT LQQAAEFYLM SICSGLKRGF PNLEELSRLT KNTVTVDNTV KPCHWTYTLN VNHSPSISTP SVLGYPACPH IQDDFNNAIL RNSLQSAVSN	NGLLIAINPQ IKQESYEKAN VFVHEWAHLR LFKEGCTFIY DSADFHISPP QIVEIHTFVG EVVEKLNGKA GGLKFFVDI GNDTMFLVTW NTHEIGALK TATVEPETGD AHSIPGSHAM PDVPPCKII VNTSKRNPQQ LAQAPLEIPP	VPENQNLISM VPENQNLISM VIVTDWYGAH WGVFDEYNND NSTQNATASI MNGTELPPPP IASFDSKGEI YGSVMILVTS SNSNSMIDAF QASGPPEIIL VTVTSRASNS PVTLRLLDDG YVPGYTANCM DLEAVKVEEE AGIREIFFTS	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55	1 MTQRSIAGPI IKEMITEASF GDDPYTLOYR REFYINGONQ MFMQSLSSVV TFSLVQAGDK RAQLHQINSN GDDKLLGNCL GDDKLLGNCL TOPDGRKYYT AVPPATVEAF AGADVIKNDG IQMIAPRRSV LTLSWTAPGE	11 CNLKFVTLLV CNLKFVTLLV CGCKEGKYIH IKVTRCSSDI EFCNASTHNQ VCLVLDVSS DDRKLLVSYL PTVLSSGSTI FQGHIQLEST NNFITNLIFF VERDSLHFPH VERDSLHFPH GRNEEERKWG DFDQGQATSY QPNGETHESH	21 ALSSELPFIG PFRNIKILIP FTPNFLIMDN TGIFVCEKGP EAPNLQNQMC KMAEADRILQ PTTVSAKTDI HSIALGSSAA GENVKPHEQL TASLMIPGTA PVMIYANVKQ ANGRYSLKVH FSRVSSGGSF EIRMSKSLQN RIYVAIRAMD	AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPQENCIISK SLRSAMDVIT LQQAAEFYLM SICSGLKRGF PNLEELSRLT KNTVTVDNTV KPCHWTYTLN VNRSPSISTP SVLGYPACPH IQDDFNNAIL RNSLQSAVSN	NGLLIAINPQ IKQESYEKAN VFVHEWAHLR LFKEGCTFIY DSADFHISPP QIVEIHTFVG EVVEKLNGKA GGLKFFVDI GNDTMFLVTW NTHEIGALK TATVEPETGD AHSIPGSHAM PDVPPCKII VNTSKRNPQQ LAQAPLEIPP	VPENQNLISM VPENQNLISM VIVTDWYGAH WGVFDEYNND NSTQNATASI MNGTELPPPP IASFDSKGEI YGSVMILVTS SNSNSMIDAF QASGPPEIIL VTVTSRASNS PVTLRLLDDG YVPGYTANCM DLEAVKVEEE AGIREIFFTS	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55	1 MTQRSIAGPI KEMITEASF GDDPYTLOYR KPPYINGONO MFMQSLSSVV TFSLVQAGDK RAQLHQINSN GDDKLLGNCL RAGLHQINSN GDDKLLGNCL FDPDGRKYYT AVPPATVEAF AGADVIKNDG IQMNAPRKSV LTLSWTAPGE PQISTINGPEH LILKGVLTAM Seq ID NO:	11 CNLKPVTLLV YLFNATKRRV GCGKEGKYIH IKVTRCSSDI EFCNASTHNQ VVCLVLDVSS DDRKLLVSYL PTVLSSGSTI FOORIGLEST NNFITNLTFR VERDSLHFPH LYSRYFFSFA GRNEEERXWG DFDQQATSY QPNGETHESH 9 DNA seque	21 ALSSELPFLG PFRNIKILIP FTPNFLIMDN TGIFVCERGP EAPNLQNOMC KMAEADRILQ PTTVSAKTDI HSIALGSSAA GENVKPHKQL TASLWIPGTA PVMIYANNKQ ANGRYSLKVH FSRVSSGGSF EIRMSKSLQN RIYVAIRAMO VVTHHTLSRK	AGVQLQDNGY AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPQENCIISK SLRSAWDVIT LQQAAEFYLM SICSGLKKGF PNLEELSRLT KNTOTVONTV KPGHWTYTLN GFYPILNATV VNRSPSISTP SVLGVPAGPH IQDDFNNAIL RNSLQSAVSN KRADKKENGT	NGLLIAINPQ IKQESYEKAN VFVHEWAHLR LFKEGCTFIY DSADFHISPP QIVEIHTFVG EVVEKLNGKA GGLKFFVDI GNDTMFLVTW NTHEIGALK TATVEPETGD AHSIPGSHAM PDVPPCKII VNTSKRNPQQ LAQAPLEIPP	VPENQNLISM VPENQNLISM VIVTDWYGAH WGVFDEYNND NSTQNATASI MNGTELPPPP IASFDSKGEI YGSVMILVTS SNSNSMIDAF QASGPPEIIL VTVTSRASNS PVTLRLLDDG YVPGYTANCM DLEAVKVEEE AGIREIFFTS	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55 60	1 MTQRSIAGPI KEMITEASF GDDPYTLOYR KPFYINGONQ KPFYINGONQ KFFYINGONQ KFMCSLSSVV TSLVQAGDK RAQLHQINSN GDDKLLGNCL SRISSGTGDI FDPDGRKYYT AVPPATVEAF AGADVIKNDG GDNORPRESV LTLSWTAPGE PQISTNGPEH LILKGVLTAM Seq ID NO: Nucleic Ac.	11 CNLKPVTLLV YLFNATKRIV YLFNATKRIV YLFNATKRIV YLFNATKRIV IKVTRCSSDI EFCNASTHINQ VVCLVLDVSS DDRKLLVSYL PTVLSSGSTI FQQHIQLEST NNFITNLTFR VERDSLHPPH 1YSRYFFSFA GRNEEERKWG DFDQGQATSY QPNGETHESH GLIGIICLII 9 DNA seque id Accession	21 ALSSELPFLG PFRNIKILIP FTPNFLIMDN TGIPVCEKGP EAPNIQNOMC KMAEADRILQ PTTVSAKTDI HSIALGSSAA GENVKPHKQL TASLWIPGTA PVMIYANVKQ ANGRYSLKVH FSRVSSGSF EIRMSKSLQN RIYVAIRAMD VVTHHTLSRK ENCE ##: Eos see	AGVQLQDNGY AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPQENCIISK SLRSAWDVIT LQQAAEFYLM SICSGLKKGF PNLEELSRLT KNTOTVONTV KPGHWTYTLN GFYPILNATV VNRSPSISTP SVLGVPAGPH IQDDFNNAIL RNSLQSAVSN KRADKKENGT	NGLLIAINPQ IKQESYEKAN VFVHEWAHLR LFKEGCTFIY DSADFHISPP QIVEIHTFVG EVVEKLNGKA GGLKFFVDI GNDTMFLVTW NTHEIGALK TATVEPETGD AHSIPGSHAM PDVPPCKII VNTSKRNPQQ LAQAPLEIPP	VPENQNLISM VPENQNLISM VIVTDWYGAH WGVFDEYNND NSTQNATASI MNGTELPPPP IASFDSKGEI YGSVMILVTS SNSNSMIDAF QASGPPEIIL VTVTSRASNS PVTLRLLDDG YVPGYTANCM DLEAVKVEEE AGIREIFFTS	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55	1 MTQRSIAGPI KEMITEASF GDDPYTLOYR KPFYINGONQ KPFYINGONQ KFFYINGONQ KFMCSLSSVV TSLVQAGDK RAQLHQINSN GDDKLLGNCL SRISSGTGDI FDPDGRKYYT AVPPATVEAF AGADVIKNDG GDNORPRESV LTLSWTAPGE PQISTNGPEH LILKGVLTAM Seq ID NO: Nucleic Ac.	11 CNLKPVTLLV YLFNATKRRV GCGKEGKYIH IKVTRCSSDI EFCNASTHNQ VVCLVLDVSS DDRKLLVSYL PTVLSSGSTI FOORIGLEST NNFITNLTFR VERDSLHFPH LYSRYFFSFA GRNEEERXWG DFDQQATSY QPNGETHESH 9 DNA seque	21 ALSSELPFLG PFRNIKILIP FTPNFLIMDN TGIPVCEKGP EAPNIQNOMC KMAEADRILQ PTTVSAKTDI HSIALGSSAA GENVKPHKQL TASLWIPGTA PVMIYANVKQ ANGRYSLKVH FSRVSSGSF EIRMSKSLQN RIYVAIRAMD VVTHHTLSRK ENCE ##: Eos see	AGVQLQDNGY AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPQENCIISK SLRSAWDVIT LQQAAEFYLM SICSGLKKGF PNLEELSRLT KNTOTVONTV KPGHWTYTLN GFYPILNATV VNRSPSISTP SVLGVPAGPH IQDDFNNAIL RNSLQSAVSN KRADKKENGT	NGLLIAINPQ IKQESYEKAN VFVHEWAHLR LFKEGCTFIY DSADFHISPP QIVEIHTFVG EVVEKLNGKA GGLKFFVDI GNDTMFLVTW NTHEIGALK TATVEPETGD AHSIPGSHAM PDVPPCKII VNTSKRNPQQ LAQAPLEIPP	VPENQNLISM VPENQNLISM VIVTDWYGAH WGVFDEYNND NSTQNATASI MNGTELPPPP IASFDSKGEI YGSVMILVTS SNSNSMIDAF QASGPPEIIL VTVTSRASNS PVTLRLLDDG YVPGYTANCM DLEAVKVEEE AGIREIFFTS	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55 60	1 MTQRSIAGPI KEMITEASF GDDPYTLOYR KPFYINGONQ KPFYINGONQ KFFYINGONQ KFMCSLSSVV TSLVQAGDK RAQLHQINSN GDDKLLGNCL SRISSGTGDI FDPDGRKYYT AVPPATVEAF AGADVIKNDG GDNORPRESV LTLSWTAPGE PQISTNGPEH LILKGVLTAM Seq ID NO: Nucleic Ac.	11 CNLKPVTLLV YLFNATKRIV YLFNATKRIV YLFNATKRIV YLFNATKRIV IKVTRCSSDI EFCNASTHINQ VVCLVLDVSS DDRKLLVSYL PTVLSSGSTI FQQHIQLEST NNFITNLTFR VERDSLHPPH 1YSRYFFSFA GRNEEERKWG DFDQGQATSY QPNGETHESH GLIGIICLII 9 DNA seque id Accession	21 ALSSELPFIG PFRNIKILIP FTPNFLIMDN TGIPVCERGP EAPNLQNOMC KMAEADRILQ PTTVSAKTDI HSIALGSSAA GENVKPHEQL TASLMIPGTA FVMIYANVKO ANGRYSLKVH FSRVSSGGSF EIRWSKIQN VVTHHTLSRK CICCE 1 #: Eos sec	AGVQLQDNGY AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPQENCIISK SLRSAMDVIT LQQAAEFYLM SICSGLKKGF PNLEELSRLT KNTVTVDNTV KPCHWTYTLN GFYPILMATV VNRSPSISTP SVLGYPACPH IQDDFNNAIL KNSLGYPACPH KNSLGSAVSN KRADKKENGT	NGLLIAINPQ IKQESYEKAN VFVHEWAHLR LFKEGCTFIY DSADFHISPP QIVEIHTFVG EVVEKLNGKA GGLKFFVPDI GNDTMFLVTW NTHISLQALK TATVEPETGD AHSIPGSHAM PDVPPCKII VNTSKRNPQQ LAQAPLFIPP KLL	VPENQNLISM VIVTDWYGAH WGVFDEYNND NSTQNATASI MNGTELPPP IASFDSKGEI YGSVMILUTS SNNNSMIDAF QASGPPEIIL VTVTSRASNS PVTLRLLDDG YVPGYTANCN DLEAVKVEEE AGIREIFTFS NSDPVPARDY	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55 60	1 MTQRSIAGPI KEMITEASF GDDPYTLOYR KPFYINGONQ KPFYINGONQ KFFYINGONQ KFMCSLSSVV TSLVQAGDK RAQLHQINSN GDDKLLGNCL SRISSGTGDI FDPDGRKYYT AVPPATVEAF AGADVIKNDG GDNORPRESV LTLSWTAPGE PQISTNGPEH LILKGVLTAM Seq ID NO: Nucleic Ac.	11 CNLKPVTLLV YLFNATKRIV YLFNATKRIV YLFNATKRIV YLFNATKRIV IKVTRCSSDI EFCNASTHINQ VVCLVLDVSS DDRKLLVSYL PTVLSSGSTI FQQHIQLEST NNFITNLTFR VERDSLHPPH 1YSRYFFSFA GRNEEERKWG DFDQGQATSY QPNGETHESH GLIGIICLII 9 DNA seque id Accession	21 ALSSELPFLG PFRNIKILIP FTPNFLIMON TGIPVCENGP EAPPLQNEG EAPPLQNEG EAPPLQNEG EAPPLQNEG EAPPLQNEG EAPPLQNEG EAPPLQNEG EAPPLQNEG HSIAGSSAA ANGRYSLEVH FSRVSSGSF EIRWSKSLQN RIYVAIRAMD VVTHHTLSRK PCCC 1 #: EOS Sec 32 21	AGVQLQDNGY AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPQENCIISK SLRSAWDVIT LQQAAEFYLM SICSGLKRGF PNLEELSRLT KNTTYTVDNTV KPGHWTYTLN GFYPILMATV VMRSPSISTP SVLGVPAGPH IQDDFNNAIL RNSLQSAVSN KRADKKENGT Quence	NGLLIAINPQ IKQESYEKAN VFVHEWAHLR LFKEGCTFIY DSADFHISPP QIVEIHTFVG EVVEKLNGKA GGLKFFVDI GNDTMFLVTW NTHEIGALK TATVEPETGD AHSIPGSHAM PDVPPCKII VNTSKRNPQQ LAQAPLEIPP	VPENQNLISM VPENQNLISM VIVTDWYGAH WGVFDEYNND NSTQNATASI MNGTELPPPP IASFDSKGEI YGSVMILVTS SNSNSMIDAF QASGPPEIIL VTVTSRASNS PVTLRLLDDG YVPGYTANCM DLEAVKVEEE AGIREIFFTS	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55 60	THE PROPERTY OF THE PROPERTY O	11 CNLKFVTLLV CNLKFVTLLV COKEGKYIH IKVTRCSSDI EFONASTHNQ VCLVLDVSS DDRALLVSYL PTVLSSGSTI FQGRIQLEST NNFITNLTFR VERDSLHFPH CYRDSLHFPH CYRDSLHFPH GRIEEERKWG DFDQGQATSY GPNGETIESH GLIGIICLII O DNA sequence: 336-6	21 ALSSELPFIG PFRNIKILIP FTPNFLIXON TGIPVCEKGP EAPNLQNQMC EAPNLQNGMC EAPNLQNGMC ANGENVEPHEQL TASLMIPGTA PVMIYANVX O ANGRYSLKVH FSRVSSGGSF EIRMSKSLQN RIYVAIRAMD VVTHHTLSRK ence 1 #: Eos sec 32 21	AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPQENCIISK SLRSAMDVIT LQQAAEFYLM SICSGLKKGF PNLEELSRLT KNTUTVDNIV KPGHWTYTLN VNHSPSISTP SVLGUPACPH LQDDFNNLI RNSLQSAVSN KRADKKENGT QUEENCE 31	NGLLIAINPQ IKQESYEKAN VFVHEWAHLR LFKEGCTFIY DSADFHISPP QIVEIHTFVG EVVEKLNGKA GGLKFFVPDI GNDTMFLVTW NTHHSLQALK TATVEPETGD AHSIPGSHAM PDVPPCKII VNTSKRIPGU LAQAPLFIPP KLL 41	VPENQNLISM VPENQNLISM VIVTDWYGAH WGVFDEYNND NSTQNATASI MNGTELPPPP IASPDSKGEI YGSVMILUTS SNNNSMIDAF QASGPPEIIL VTVTSRASNS PVTLRLLDDG YVPGYTANGN DLEAVKVEES NSDPVPARDY	120 180 240 300 360 420 480 600 660 720 780 840 900
50556065	TOTAL COLORS OF	11 CNLKPVTLLV YLFNATKRRV GCGKEGKYIH IKVTRCSSDI EFCNASTHNQ VVCLVLDVSS DDRKLLVSYL PTVLSSSTI FOORIQLEST NNFITNLTFR VERDSLHFPH LYSRYFFSFA GRNEEERXWG DFDQQATSY QPNGETHESH GLIGIICLII 9 DNA seque id Accession idence: 336-6	21 ALSSELPFLG PFRNIKILIP FTPNFLLMDN TGIFVCERGP EAPNLQNQMC KMAEADRILQ PTTVSAKTDI HSIALGSSAA GENVKPHHQL TASLWIPGTA PVMIYANVKQ ANGRYSLKVH FSRVSSGGSF EIRWSKSLQN RIYVAIRAMO VVTHHTLSRK CENCE 1 #: Eos sec 532 21 GATGCCCAGT	AGVQLQDNGY AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPQENCIISK SLRSAMDVIT LQQAAEFYLM SICSGLKKGF PNLEELSRLT KNTUTUDNTV KPGHWTYTLN GFYPILNATV VNRSPSISTP SVLGYPAGPH IQDDFNNAIL RNSLQSAVSN KRADKKENGT Quence 31 CCCCACGACACA	NGLLIAINPQ IKQESYEKAN VFVHEWAHLR LFKEGCTFIY DSADFHESPP QIVEIHTFVG EVVEKLNGKA GGLKFPVPDI GNDTMFLVTW NTHISLQALK TATVEPETGD AHSIPGSHAM PDVPPCKII VNTSKRNPQQ LAQAPLFIPP KLL 41 CCTCCCACTT	VPENQNLISM VPENQNLISM VIVTDWYGAH WGVFDEYNND NSTQNATASI MNGTELPPPP IASFDSKGEI YGSVMILUTS SNNNSMIDAF QASGPPEIIL VTVTSRASNS PVTLRLLDDG YVPGYTANCN DLEAVKVEEE AGIREIFTFS NSDPVPARDY	120 180 240 300 360 420 540 600 720 780 840 900
50 55 60	1 MTORSIAGPI KEMITEASF GDDPYTLOYR KPFYINGONO MFMGSLSSVV TFSLVQAGDK RAQLHQINSN GDDRLLGNCL SRISSGTGOI FDPDGRKYYT AVPPATVEAF AGADVIKNDG IQMNAPRESV LTLSWTAPGE PQISTNOPEH LILKGVLTAM Seq ID NO: Nucleic Ac. Coding sequence 1 CTCCCCTCAC CTCCCCTCAC CTCCGGTGGG	11 CMLKPVTLLV YLFNATKRRV GCGKEGKYIH IKVTRCSSDI EFCNASTHINQ VVCLVLDVSS DDRKLLVSYL PTVLSSGSTI FQQBIQLEST NNFITNLTFR VERDSLHPPH IYSRYFFSFA GRNEEERKWG DFDQQATSY QPNGETHESH 9 DNA seque id Accession ience: 336-6	21 ALSSELPFLG PFRNIKILIP FTPNFLIMDN TGIPVCEKGP EAPNIQNOMC KMAEADRILQ PTTVSAKTDI HSIALGSSAA AGREYATDI HSIALGSSAA ANGRYSLKVH FSRVSSGSF EIRWSKSLQN RIYVAIRAMD VVTHHTLSRK PCC 1 #: Eos sec 32 21 GATGCCCAGT GATGCCCAGT GCCTTGACC	AGVQLQDMGY AGVQLQDMGY ATWKANNNSK LTAGYGSRGR CPQENCIISK SLRSAMDVIT LQQAAEFYLM SICSGLKKGF PNLEELSRLT KNTVTVDNTV KPGHWTYTLN KPGHWTYTLN RYSLQSAVSN KRADKKENGT QUENCE 31 CCCCCACGACA TGGCCTAGAG	NGLLIAINPQ NGLLIAINPQ NGLLIAINPQ NGLIAINPQ NGLESYEKAN VFVHEWAKLR LFKEGCTFIY DSADFHESPP QIVEINTFVG EVVEKLNGKA GGLKFFVPDI GNDTMFLVTW NTHHSLQALK TATVEPETGD AHSIPGSHAM PDVPPPCKII VNTSKRIPQQ IAQAPLFIPP KLL 41 CCTCCCCCCT	VPENQNLISM VPENQNLISM VIVTDWYGAH WGVFDEYNND NSTQNATASI MNGTELPPPP IASFDSKGEI YGSVMILUTS QASGPPEIIL VTVTSRASNS PVTLRLLDDG YVPGYTANCN DLEAVKVEEE AGIREIFTFS NSDPVPARDY 51 CCCCACTGTGG GCTGGTGGT	120 180 240 360 420 540 600 660 720 780 840 900
50556065	THE PROPERTY OF THE PROPERTY O	11 CNLKFVTLLV CNLKFVTLLV COKEGKYIH IKVTRCSSDI EFCNASTHNQ WCLVLDVSS DDRALLVSYL PTVLSSGSTI FQGHIQLEST NNFITNLTFR VERDSLHFPH USSRYFSFA GRNEEERKWG DFDQGQATSY QPNCETHESH GLIGIICLII ONA sequence: 336-6 11 CCCGGTCCAG CTCAGGGGCT TCTCTGGGAG	21 ALSSELPFIG PFRNIKILIP FTPNFLIMDN TGIFVCEKGP EAPNLQNOMC KMAEADRILQ PTTVSAKTDI HSIALGSSAA GENVKPHEQL TASLMIPGTA PVMIYANVKQ ANGRYSLKVH FSRVSSGGSF EIRMSKSIQN VVTHHTLSRK PRICE 1 #: Eos sec 32 1 GATGCCCAGT GCCCTTGACC GGAGGGGGGT	AGVQLQDNGY AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPQENCIISK SLRSAMDVIT LQQAAEFYLM SICSGLKKGF PNLEELSKIT KNTUTVDNTV KPGHWTYTLN GFYPILATUL RNSLQSAVSN KRADKKENGT QUENCE 31 CCCCACGACA TGGCCTAGACA TGGCCTAGACA TGGCCTAGACA	NGLLIAINPQ NKQESYEKAN VFVHEWAHLR LFKEGCTFIY DSADFHISPP QIVEIHTFVG EVVEKLNGKA GGLKFFVDI GNDTMFLVTW NTHRISQALK ATTATVEPETG AHSIPGSHAM PDVPPCKII VNTSKRIPG LIAQAPLFIPP KLL 41 CCTCCCACTT CCCTCCCCCA GAGTGGGAT	VPENQNLISM VPENQNLISM VIVTDWYGAH WGVFDEYNND NSTQNATASI MNGTELPPP IASFDSKGEI YGSVMILUTS SNNSNMIDAF QASGPPEIIL VTVTSRASNS PVTLRLLDDG YVPGYTANGN DLEAVKVEEE AGIREIFTES NSDPVPARDY	120 180 240 300 360 420 600 720 780 900
50556065	TOTAL CONTROL OF CONTR	11 CNLKFVTLLV YLFNATKRRV GCGKEGKYIH IKVTRCSSDI EFCNASTHNQ VVCLVLDVSS DDRKLLVSYL PTVLSSGSTI FOORIQLEST NNFITNLTFR VERDSLHFPH LYSRYFFSFA GRNEEERKWG DFDQGATSY QPNGETHESH GLIGIICLII 9 DNA seque id Accession dence: 336-6 11 CCCGGTCCAG CTCAGGGGCT TCTCTGGGAG TGGGATCAGG	21 ALSSELPFIG PFRNIKILIP FTPNFLIMIN TGIPVCERGP EAPNLQNOMC KMAEADRILQ PTTVSAKTDI HSIALGSSAA GENVEPHEQL TASLWIPGTA PVMIYANVKO ANGRYSLKVH FSRVSSGGSF EIRWSKSLQN RIYVAIRAMO VVTHHTLSRK ence 1 #: Eos sec 532 21 GATGCCCAGT GCCCTTGACC GGAGGGGGCT TTGAGGCAGC TTGAGGCAGC	AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPQENCIISK LTAGYGSRGR CPQENCIISK SLRSAMDVIT LQQAAEFYLM SICSGLKKGF PNLEELSRLT KNTVTVDNTV KPCHWTYTLN GFYPILNATV VNRSPSISTP SVLGVPAGPH IQDDFNNAIL RNSLQSAVSN KRADKKENGT QUENCE 31 CCCCACGACA TGGCCTAGAG GGGAGGGAAT TTTGGTTTCC	NGLLIAINPQ IKQESYEKAN VFVHEWAHLR LFKEGCTFIY DSADFHISPP QIVEIHTFVG EVVEKLNGKA GGLKFFVPDI GNDTMFLVTW NTHISLQALK TATVEPETGD AHSIPGSHAM PDVPPCKII VNTSKRNPQQ LAQAPLFIPP KLL 41 CCTCCCCACTT CCCTCCCCAC GAGTGGGAAT TTARAAATGCC	VPENQNLISM VPENQNLISM VIVTDWYGAH WGVFDEYNND NSTQNATASI MNGTELPPP IASFDSKGEI YGSVMILUTS SNNNSMIDAF QASGPPEIIL VTVTSRASNS PVTLRLLDDG YVPGYTANCN DLEAVKVEEE AGIREIFTFS NSDPVPARDY 51 CCCCACTGTGG GCCAAGAGGC AAGTTGGGGG	120 180 340 360 420 480 540 660 720 780 900
50556065	1 MTQRSIAGPI IKEMITEASF GDDPYTLOYR RPFYINGONO MFMQSLSSVV TFSLVQAGDK RAQLHQINSN GDDKLLGNCL SRISSGTGDI FDPDGRKYYT AVPPATVEAF AGADVIKNDG IQMNAPRSSV LTLSWTAPGE PQISTNGPEH LILKGVLTAM Seq ID NO: Nucleic AcCoding sequence of the company	11 CNLKFVTLLV CNLKFVTLLV COKEGKYIH IKVTRCSSDI IKVTRCSSDI DEFCNASTHNQ VVCLVLDVSS DDRALLVSYL FQHIQLEST NNFITNLTFR GRNEBERKWG DFDQGQATSY QPNGETHESH GLIGIICLII CCCGGTCCAG CTCAGGGGCT CCCACATATAA	21 ALSSELPFLG PFRNIKILIP FTPNFLLNDN TGIFVCEKGP EAPNLQNGMC KMAEADRLLQ PTTVSAKTDI HSIALGSSIA GENVKPHEQL TASLMIPGTA PVMIYANVKO ANGRYSLKVH PSRVSSGSF EIRMSKSLOR RIYVAIRAMD VVTHHTLSRK COCC 21 GATGCCCAGT GACGGGGGGT TTGAGGGGGGGT TTGAGGGGGGGGT ATGCTCACCC	AGVQLQDMGY AGVQLQDMGY ATWKANNNSK LTAGYGSRGR CPGENCIISK SLRSAMDVIT LQQAAEFYLM SICSGLKKGF PNLEELSRLT KNTYTVDNTV KPGHWTYTLN KPGHWTYTLN TV MRSPSISTP SVLGVPAGPH QDDFNNAIL RNSLQSAVSN KRADKKENGT QUENCE 31 CCCCCACGACA CGGAGGGAAT TTTGGTTTCC TGGCAGCCTTGGGCAGCCT	NGLLIAINPQ NGLLIAINPQ NGLLIAINPQ NGLIAINPQ NGLESYEKAN VFVHEWAHLR LFKEGCTFIY DSADFHESPP QIVEHTFVG EVVEKINGKA GGLKFFVPDI GNITMFLVTW NTHHSLQALK TATVEPETGD AHSIPGSHAM PDVPPPCKII VNTSKRIPQQ LAQAPLFIPP KLL 41 CCTCCCCCA GGTGGGAAT TTAAAATGCC GCTCCCTTGC	VPENQNLISM VPENQNLISM VIVTDWYGAH WGVFDEYNND NSTQNATASI MNGTELPPP IASFDSKGEI YGSVMILVTS SNNSNMIDAF QASGPPEILL VTVTSRASNS PVTLRLLDDG YVPGYTANCN DLEAVKVEE AGIREIFFFS NSDPVPARDY 51 CCCACTGTGG GCTAGTGGGGCAAGAGGCC TCTCCTTCCT	120 180 340 480 540 480 660 720 720 730 840 900
5055606570	TOTAL	11 CNLKFVTLLV CNLKFVTLLV COKEGKYIH IKVTRCSSDI EFCNASTHNQ WCLVLDVSS DDRALLVSYL PTVLSSGSTI FQGHIQLEST NNFITNLTFR VERDSLHFPH USSAYFFSFA GRNEEERKWG DFDQGQATSY QPNCETHESH GLIGIICLII CCCGGTCCAG CTCAGGGGCT TCTCTGGGAG TGCGATCAGG CCACATATAA	21 ALSSELPFIG PFRNIKILIP FTPNFLIXDIN TGIFVCEKGP EAPNLQNOMC EAPNL	AGVQLQDNGY AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPQENCIISK SLRSAMDVIT LQQAAEFYLM SICSGLKKGF PNLEELSKIF KNTUTVDNTV KPGHWTYTLN GFYPILANT VNHSPSISTP SVLGVPACPH LQDDFNNLI RNSLQSAVSN KRADKKENGT JL CCCCACGACA TGGCATGAGA TGGCATGAGA TTGGTTTCC TGGGAGCATG GATCCATGAT	NGLLIAINPQ NKQESYEKAN VFVHEWAHLR LFKEGCTFIY DSADFHISPP QIVEIHTFVG EVVEKLNGKA GGLKFFVDI GNDTMFLVTW NTHRISQALK TATVEPETGD AHSIPGSHAM PDVPPCKII VNTSKRIPG LIAQAPLFIPP KLL 41 CCTCCCACTT CCCTCCCCA GAGTGGGAAT TTAAAATGCC GCTGCCTTGC GTGCAGTTCT	VPENQNLISM VPENQNLISM VIVTDWYGAH WGVFDEYNND NSTQNATASI MNGTELPPP IASFDSKGEI YGSVMILUTS SNNSNMIDAF QASGPPEIIL VTVTSRASNS PVTLRLLDDG YVPGYTANGN DLEAVKVEEF AGIREIFFE NSDPVPARDY S1 CCCACTGTGG GCTGGTGGTG GCGAAGAGGC AAGTTGGGGG TCTCCTTCCT TCGTGGGGG	120 180 360 420 480 540 660 720 780 900
50556065	TOTAL CONTROLL OF THE CONTROLL	11 CNLKFVTLLV YLFNATKRRV GCGEGGKYIH IKVTRCSSDI EFCNASTHNQ VVCLVLDVSS DDRKLLVSYL PTVLSSGSTI FOORIQLEST NNFITNLTFR VERDSLHFPH IYSRYFFSFA GRNEEERKWG DFDQGATSY QPNGETHESH GLIGIICLII 9 DNA seque id Accession ience: 336-6 11 CCCGGTCCAG CTCAGGGGCT TCTCTGGAGG CCACATATAA CTGCCACTG GCTGGTCACT GCTGCTCACT CTGCCACTG GCTGCTCACT CTGCCACTG GCTGCTCACT CTGCCACTG GCTGCTCACT	21 ALSSELPFIG PFRNIKILIP FTPNFLIMIN TGIPVCERGP EAPNLONOMC REMANDATION HSIALGSSAA HSIALGSSAA HOSANGHEN HSIALGSSAA HSIALGSSAA HOSANGHEN	AGVQLQDNGY AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPQENCIISK SLRSAMDVIT LQQAAEFYLM SICSGLKKGF PNLEELSRLT KNTVTVDNTV KPCHWTYTLN GFYPILNATV VNRSPSISTP SVLGVPAGPH IQDDFNNAIL RNSLQSAVSN KRADKKENGT QUENCE 31 CCCCACGACA TGGCCTAGAG GGGAGGCAT TTTGGTTTCC TGGGAGCCTG GATCCATGAT AGTACTCCTG	NGLLIAINPQ IKQESYEKAN VFVHEWAHLR LFKEGCTFIY DSADFHISPP QIVEIHTFVG EVVEKLNGKA GGLKFFVPDI GNDTMFLVTW NTHISLQALK TATVEPETGD AHSIPSHAM PDVPPCKII VNTSKRNPQQ LAQAPLFIPP KLL 41 CCTCCCACTT CCCTCCCCACT GAGTGGGATTCT TTARAATGCC GCTGCCTTGC GTGCAGTTCC CCAAGAGGGC	VPENQNLISM VPENQNLISM VIVTDWYGAH WGVFDEYNND NSTQNATASI MNGTELPPP IASFDSKGEI YGSVMILUTS SNNSNMIDAF QASGPPEIIL VTVTSRASNS PVTLRLLDDG YVPGYTANGN DLEAVKVEEE AGIREIFTFS NSDPVPARDY 51 CCCACTGTGG GCTAGTGGG GCTAGTGGGGC AGGTTGGGGG AGGTTGGGGG TCTCCTTCCT CTGGAGCAGG GACAAGTTCA	120 180 360 360 420 480 540 600 660 720 780 900
5055606570	TIME TO THE TENT OF THE TENT O	11 CNLKFVTLLV CNLKFVTLLV COKEGKYIH IKVTRCSSDI IKVTRCSSDI IKVTRCSSDI DRRALLVSYL PTVLSSST PQOHIQLEST NNFITNLTFR GRIBEERKWG DFDQGQATSY QPNGETHESH GLIGIICLII CCCGGTCCAG CTCAGGGGCT TCTCTGGGAG TGGGATCAGG CTCATGTCACT CTCATGTCACT CTCATGTCACT CTCATGTCACT CTCATGTCACT CTCATGTCACT CTCATGTCACT CTCATGTCACT CTGGTCACT CTGGGGGAAATGAA CTGCCACTG	21 ALSSELPFLG PFRNIKILIP FTPNFLLNDN TGIPVCEKGP EAPNLQNGMC KMAEADRLLQ PTTVSAKTDI HSIALGSSA GENVKPHEQL TASLWIPCTA PVMIYANVKO ANGRYSLKVH PSRVSSGSF EIRMSKSLON RIYVAIRAMD VVTHHTLSRK 21 GATGCCCAGT GGAGGGGGT TTGAGCCAGG GCCTTGACC GGAGGGGGCT TTGAGCCAGC GTCTCCCCACA ACCTTCCACA ACCTTCCACA ACCTTCCACA	AGVQLQDNGY AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPQENCIISK SLRSAMDVIT LQQAAEFYLM SICSGLKKGF PNLEELSRLT KNTYTVDNTV KPGHWTYTLN KPGHWTYTLN LQDDFNNIL RNSLQSAVSN KRADKKENGT CCCCACGACA TGGCCTAGAG GGGAGGAAT TTTGGTTTCC TGGCAGCCTTGGATCATCAT AGTCATCATT TGCCACGAGGA	NGLLIAINPQ NGLLIAINPQ NGLLIAINPQ NGLLIAINPQ NGLESYEKAN VFVHEWAHLR LFKEGCTFIY DSADFHESPP QIVEIHTFVG EVVEKLNGKA GGLKFFVPDI GNDTMFLVTW NTHESLQALK NTHESLQALK TATVEPETGD AHSIPGSHAM PDVPPCKII CCTCCCCA LAGAGAGGG GCTGCCCCAG GGTGGCAGTTCT CCCAAGAGGGG GCTGCCCCAG GCTGCCCAGG GCTGCCCCAG GCTGCCCAGG GCTGCCCAGG GCTGCCCCAGG GCTGCCCAGG GCTGCCCCAGG GCTGCCCCAGC GCTGCCCCAGG GCTGCCCCAGC GCTGCCCCCAGC GCTGCCCCAGC GCTGCCCCACC GCTGCCCCAGC GCTGCCCCAGC GCTGCCCCAGC GCTGCCCCAGC GCTGCCCCAGC GCCCCCCACC GCTCCCCCACC GCTCCCCCCCCCC	VPENQNLISN VPENQNLISN VIVTDWYGAH WGVFDEYNND NSTQNATASI MNGTELPPPP IASFDSKGEI YGSVMILVTS SNNSNMIDAF QASGPPEILL VTVTSRASNS PVTLRLLDDG YVPGYTANCN DLEAVKVEE AGIREIFFS NSDPVPARDY 51 CCCCACTGTGG GCCAAGAGGC CAGTTGGGGC AGTTGGGGG GACAAGTTCA TTTGTGGGGG	120 180 360 480 540 660 720 720 720 720 730 840 900
5055606570	TIME TO THE TOTAL TO THE TOTAL THE T	11 CNLKFVTLLV CNLKFVTLLV CNLKFVTLLV GCKEGKYIH IKVTRCSSDI EFCNASTHNQ WCLVLDVSS DDRALLVSYL PTVLSSGSTI FQGHIQLEST NNFITNLTFR VERDSLHFPH USSAYFFSFA GRIBEERKWG DFDQGATSY QPNGETHESH GLIGIICLII CCCGGTCCAG CTCAGGGGCT TCTCTGGGAG TGGGATCAGG CCACATATAA CTGCCACCTG GCTGGTCACT GCTGGTCACT GCGGGAAATG GGGGAAATG TGAGGAGGGG	21 ALSSELPFIG PFRNIKILIP FTPNFLIXDN TGIPVCEKGP EAPNLQNQMC KMAEADRILQ PTTVSAKTDI HSIALGSSAA GENVKPHEQL TASLMIPGTA PVMIYANVKO ANGRYSLKVH FSRVSSGGSF EIRMSKSLQN RIYVAIRAMD VVTHHTLSRK ence 1 #: Eos sec 32 21 GATGCCCAGT GCCCTTGACC GGAGGGGGCT TTGAGGCAGG ATCCTCACCA ACGTTCCACA ACGTTCCACA AAGGAACTTC CTGAAGGAAGC	AGVQLQDNGY AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPQENCIISK SLRSAMDVIT LQQAAEFYLM SICSGLKKGF PNLEELSELT KNTVTVDNTV KPGHWTYTLN VNHSPSISTP SVLGVPACPH LQDDFNNLI RNSLQSAVSN KRADKKENGT JUENCE 31 CCCCACGACA TGGCCTAGAG GGGAGGGAAT TTGGGTTCCT GATCCATGAT AGTACTCCTG TGCACAAGGA TGCATGAGC TGCACAGCA TGCACAGCA TGCACAGCA TGCACAGCA TGCACAGCA TGCACAGGGA TGCACAGGGA TGGACGCAGG	NGLLIAINPQ NGLLIAINPQ NGLLIAINPQ NGLLIAINPQ NGLESYEKAN VFVHEWAHLR LFKEGCTFIY DSADFHISPP QIVEIHTFVG EVVEKLNGKA GGLKFFVPDI GNDTMFLVTW NTHENSLQALK TATVEPETGD AHSIPGSHAM PDVPPCKII VNTSKRIPG LAQAPLFIPP KLL 41 CCTCCCCCC GAGTGGGAAT TTANAATGCC GCTGCCTTGC GCTGCCCTGC CCTGGATGAG CCTTGCATGC CCTGGATGAG	VPENQNLISM VPENQNLISM VIVTDWYGAH WGVFDEYNND NSTQNATASI MNGTELPPP IASPDSKGEI YGSVMILUTS SNNSNMIDAP QASGPPEIIL VTVTSRASNS PVTLRLLDDG YVPGYTANGN DLEAVKVEEE AGIREIFTES NSDPVPARDY S1 CCCACTGTGG GCCAGGGGGG GAGAGAGGC AAGTTGGGGG GTCTCCTTCCT TCCTTGCGTGG GACAAGTTCA TTTGTGGGGG AACAGTGACC	120 180 360 420 480 540 660 720 780 900 840 900 180 240 360 420 480 480 480 480 480 480 480 480 480 48
5055606570	TOTAL CONTROLL AND	11 CNLKFVTLLV YLFNATKRRV GCGEGGKYIH IKVTRCSSDI EFCNASTHNQ VVCLVLDVSS DDRALLVSYL PTVLSSGSTI FQOHIQLEST NNFITNLTFR VERDSLHFPH IYSRYFFSFA GRNEEERKWG DFDQGATSY QPNGETHESH GLIGIICLII 9 DNA SEQUE id Accession Lence: 336-6 CTCAGGGGCT TCTCTGGGAG CCACATATAA CTGCCACTG GCTGGTCACT GCGGGAAATG GCTGGTCACT GCGGGAAATG TGAGGAGCGC CTTCCAGGAG CTTCAGGAG CTTTCAGGAG	21 ALSSELPFIG PFRNIKILIP FTPNFLIMIN TGIPVCERGP EAPNLONOMC REPIT SAMPLE PTTVSAKTDI HSIALGSSAA GENVKPHEQL TASLMIPGTA PVMIYANVKO ANGRYSLKVH FSRVSSGGSF EIRMSKIQN VVTHHTLSRK PTT GATGCCCAGT GCCCTTGAGGCAGG ATCCTCACCA AAGGACTTC CTGAAGAAGT CTGAAGAAGT CTGAAGAAGAC CTGAAGAC CTTCAC CTGAAGAC CTTCAC CTGAAGAC CTTCAC CTGAAGAC CTTCAC CTGAAGAC CTTCAC	AGVQLQDNGY AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPQENCIISK SLRSAMDVIT LQQAAEFYLM SICSGLKKGF FNLEELSKIF KRTYTVDNTV KPCHWTYTLN GFYPILATATV VMRSPSISTP SVLGYPAGPH IQDDFNNAIL RNSLQSAVSN KRADKKENGT 31 CCCCACGACA TGGCCTAGAG GGGAGGCAT TTGGTTTCC TGGGAGCCTG GATCCATGAT TTGGTTCCTTG GATCCATGAT TGATGGCCAG TCCTGGCACT TCGTGGCACT	NGLLIAINPQ NGLLIAINPQ NGLLIAINPQ NGLEITPYG VEYPHEMAHLR LFKEGCTFIY DSADFHISPP QIVEIHTFVG EVVEKLNGKA GGLKPFVDI GNDTMFLVTW NTHISLQALK TATVEPETGD AMSIPPECKII VNTSKRNPQQ LAQAPLFIPP KLL 41 CCTCCCCACTT CCCTCCCCACT CAGGAGGGAT TTAAAATGCC GCTCCCTTGC CCAAGAGGCG GCTGCCAGGC CCTGGATGAG CATCACTGTC	VPENQNLISM VPENQNLISM VIVTDWYGAH WGVFDEYNND NSTQNATASI MNGTELPPP IASFDSKGEI YGSVMILUTS SSNNSNMIDAF QASGPPEIIL VTVTSRASMS PVTLRLLDDG YVFGYTANGN DLEAVKVEEE AGIREIFTFS NSDPVPARDY 51 CCCACTGTGG GCCAGAGGC AAGTTGGGGG TCTCCTTCCT TCTGAGGCAG GACAAGTTCA TTTGTGGGGC AACATGTCAATG	120 180 360 360 480 540 660 720 780 780 900
505560657075	TIME TO THE TOTAL OF THE TOTAL	11 CNLKFVTLLV CNLKFVTLLV CNLKFVTLLV GCKEGKYIH IKVTRCSDI IKVTRCSDI IKVTRCSDI EFCNASTHNQ VVCLVLDVSS DDRALLVSYL FQQHIQLEST NNFITNLTFR GRIBEERKWG DFDQGQATSY QPNGETHESH GLIGIICLII OCCGGTCCAG CTCAGGGGCT TCTCTGGGAG TGGATCAGG CTCAGGGGCT CTCAGGAGCCT CTCAGGAGCCT CTCAGGAGCCT CTCAGGAGCCT CTCAGGAGCCCT CTCAGGAGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	21 ALSSELPFIG PFRNIKILIP FTPNFLLNDN TGIPVCEKGP EAPNLQNGMC KMAEADRLIQ PTTVSAKTDI HSIALGSSA GENVKPHEQL TASLWIPCTA PVMIYANVKQ ANGRYSLKVH PSRVSSGSF EIRMSKSLON RIYVAIRAMD VVTHHTLSRK 21 GATGCCCAGT GGCCTTGACC GGAGGGGCT TTGAGCCAGG ATCCTCCACA ACCTTCCACA ACCTTCCACA ACCTTCCACA ACCTTCCACA ACCTTCCACA ACGTAGATCTC TAGGGAGGG TATGCTGTTT CTGAAGAAGC TATGCTGTTT CTGAAGAAGC TATGCTGTTT	AGVQLQDNGY AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPQENCIISK SLRSAMDVIT LQQAAEFYLM SICSGLKKGF PNLEELSRLT KNTVTVDNTV KPGHWTYTLN KPGHWTYTLN KPGHWTYTLN KRSLQSAVSN KRADKKENGT CCCCACGACA TGGCCTAGAG GGGAGGAAT TTTGGTTTCC TGGCAGCCT GATCCATGAT AGTACTCCTG GATCCATGAT AGTACTCCTG GATCCATGAT AGTACTCCTG GATCCATGAT AGTACTCCTG GATCCAGGAC TGCACGAAGGA TGATCGCAG TGCACGAAGGA TGATCGCAG TGAAGGAAGAAC	NGLLIAINPQ NGLLIAINPQ NGLLIAINPQ NGLLIAINPQ NGLEINPE NGAPHESPP QIVEHHTPVG EVVEKLNGKA GGLKPFVPDI GNDTMFLVTW NTHENSLQALK TATVEPETGD AHSIPGSHAM PDVPPCKII CCTCCCACTT CCCTCCCCA GATGGGAAT TTAAAATGCC GCTGCCTTGC GCTGCCTTGC GCTGCCTTGC GCTGCCTTGC CCTCCCAGC CCCCAGC CCCCCAGC CCTCCCCAGC CCTCCCCCAGC CCTCCCCAGC CCTCCCCACC CCTCCCCAGC CCTCCCCACC CCTCCCCACC CCTCCCCACC CCTCCCCCAC CCTCCCCCAC CCTCCCCAC CCTCCCCAC CCTCCCCAC CCTCCCCCAC CCTCCCCCAC CCTCCCCAC CCTCCCCAC CCTCCCCCAC CCTCCCCCAC CCTCCCCCAC CCTCCCCCAC CCTCCCCCAC CCTCCCCAC CCTCCCCCAC CCTCCCCCAC CCTCCCCCCAC CCTCCCCCAC CCTCCCCCAC CCTCCCCCAC CCTCCCCCAC CCTCCCCCAC CCTCCCCCCAC CCTCCCCCCCC	VPENQNLISN VPENQNLISN VIVTDWYGAH WGVFDEYNND NSTQNATASI MNGTELPPPP IASFDSKGEI YGSVMILVTS SNNSNMIDAF QASGPPEILL VTVTSRASNS PVTLRLLDDG YVPGYTANCN DLEAVKVEEL AGIREIFTFS NSDPVPARDY 51 CCCCACTGTGG GCCAAGAGGC CAGTTGGGGGAAGAGGC CAGTTGGGGGAACAGTTCA TTTGTGGGGG AACAGTGACC ATGTGCAATG CTGCCATGGA	120 180 360 480 540 660 660 720 720 720 730 180 240 360 420 360 420 480 540 660 660 660 660 660 660 660 660 660 6
5055606570	TIME TO THE TOTAL THE TOTAL TO THE TOTAL THE TOTAL TO THE TOTAL THE TO	11 CNLKFVTLLV CNLKFVTLLV CNLKFVTLLV GCGEGKYIH IKVTRCSSDI EFCNASTHNQ WCLVLDVSS DDRALLVSYL PTVLSSGSTI FQGHIQLEST NNFITNLIFR VERDSLHFPH USSYPTSFA GRIBEERKWG DFDQGQATSY QPNCETHESH GLIGIICLII ONA sequence: 336-6 11 CCCGGTCCAG CTCAGGGGCT TCTCTGGGAG TGGGATCAG CCACACTATAA CTGCCACCTG GCTGGTCACT GCTGGTCACT GCTGGTCACT GCTGGTCACT GCTGGGAATT TGAGGAGGGG CTTCCAGGAG CTCCAGGACTGCTCAGAGGCCT CCAGGACTGCTCAGAGGCCT CCAGGACTGTCACAGAGCGCCT CCAGGACTGTCACAGACCAGGACTGCTCACAGACTGTCACAGACTGCTCACAGACTGCTCACAGACTGCTCACAGACTGCTCACAGACTGTCACAGACTGTCACAATATAAA CCCCCACACACTGTCACACACACACACACACACACACACA	21 ALSSELPFIG PFRNIKILIP FTPNFLIKINDN TGIFVCEKGP EAPNLQNOMC EAPNLQNOMC EAPNLQNOMC EAPNLQNOMC TASLMIPGTA PVMIYANVKO ANGRYSLKVH FSRVSSGGSF EIRMSKSLQN RIYVAIRAMD VVTHHTLSRK PACE A #: Eos sec 32 21 GATGCCCAGT GGCCTTGACC GGAGGGGGT TTGAGGCAGG ATCCTCACCA ACGTTCCACA ACGAACTT CCTGAAGAGCT TAGATCCTTT GACCCCTT TGATCCCTTT GACCCTT TGATCCCTT TGATCCCTT TGATCCCTT TTGATCCCTT TTGATCCCT TTGATCCCT TTGATCCCT TTGATCCCT TTGATCCCT TTGATCCT TTGATCCCT TTGATCCT TTGATCCT TTGATCCT TTGATCCCT TTGATCCT TTGATCT TTGATCT TTGATCCT TTGATCCT TTGATCCT TTGATCT TTGA	AGVQLQDNGY AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPQENCIISK SLRSAMDVIT LQQAAEFYLM SICSGLKKGF PULEELSELT KNTUTVDNTV KPGHWTYTLN VNHSPSISTP SVLGVPACPH LQDFFNNLL RNSLQSAVSN KRADKKENGT J CCCCACGACA TGGCCTAGG GGGAGGGAAT TTGGTTTCC GATCCATGAT AGTACTCCTG TGCACCAGCAG TGGACTAGAT TGGATCAGCAG TGGACGCAG TCTGGCACT GAAGCAGAC GAGCTTTTTA	NGLLIAINPQ NGLLIAINPQ NGLLIAINPQ NGLLIAINPQ NGLESYEKAN VFVHEWAHLR LFKEGCTFIY DSADFHESPP QIVEIHTFVG EVVEKLNGKA GGLKFFVDI GNDTMFLVTW NTHESLQALK NTHESLQALK ANTHESLQALK ANTHESLQALK ANTHESLQALK UNTSKRIPQ LAQAPLFIPP KLL 41 CCTCCCCCCC GAGGGGAT TTAAAATGCC GCTGCAGTTCT CCAAGAGGGC CCTGGATGGC CCTCGCATGC CCTGCCCCAGC CCTGCATGC CCTGCATTCT CCAAGAGGGC CCTCGATGACTCT TCTCAATTAAAC TCTCAATTAAAC TCTCAATTAAAACTCC TCTCAATTAAAC TCTCAATTAAAACTCC CTTCGATTCT TCTCAATTAAAACTCC TCTCAATTAAAACTCC CTTCGATTCT TCTCAATTAAAACTCC TCTTCAATTAAAACTCC TCTTGAATTAC	VPENQNLISM VPENQNLISM VIVTDWYGAH WGVFDEYNND NSTQNATASI MNGTELPPP IASFDSKGEI YGSVMILUTS SINNSMIDAF QASGPPEIIL VTVTSRASMS PVTLRLLDIG YVPGYTANGN DLEAVKVEEE AGIREIFTES NSDPVPARDY 51 CCCACTGTGG GCTAGTGGGGC GAGAGAGGC AAGTTCA TTTGTGGGGG AACAGTTCA TTTGTGGGGG AACAGTGCATG CTGCCATGGATC CTGCCATGGATC CTGCCATGGATC CTGCCATGGATT TTTTTTTTTT	120 180 360 420 480 540 660 720 780 900 180 240 300 420 420 420 480 660 660 660 660 660 670 670 670 670 67
505560657075	TIME TO THE TOTAL THE TOT	11 CNLKFVTLLV YLFNATKRRV GCGEGGKYIH IKVTRCSSDI EFCNASTHNQ VCLVLDVSS DDRKLLVSYL PTVLSGSTI FOORIOLEST NNFITNLTFR VERDSLHFPH IYSRYFFSFA GRNEEERKWG DFDQGATSY QPNGETHESH GLIGIICLII 9 DNA seque id Accession idence: 336-6 CCACATATAA TCTCTGGGAG CCACATATAA TGGGATCACG GCGGGAAATG TGAGGAGCGG CTTCCAGGAG GGCTGCCCA CCTGCAGGAGGGG CTTCCAGGAG GGCTGCCCA CCAGGAGTGT CTTCAGGAG GGGCTGCCCA CCAGGACTGT CTTCCAGGAG GGCTGCCCA CCAGGACTGT ATTTTAATTG	21 ALSSELPFIG PFRNIKILIP FTPNFLIMIN TGIPVCERGP EAPNLONGMC KMAEADRILQ PTTVSAKTDI HSIALGSSAA MGRYSLKYH HSIALGSSAA MAGRYSLKYH FSRVSSGGSF EIRWSKSLON RIYVAIRMO VVTHHTLSRK CECCE 1 #: Eos sec 532 21 GATGCCCAGT GGCGTTGAGGCGT TTGAGGCAGG ATCCTCACC AAGGACTTC CTGAAGAAGC CTGAAGAAGC TTATGCTGTTT GACCACCT TGATGCCTTT GACCACCT TGATGCCTTT GATGCCTTT GATGCCTTT GATGCCTTT TGATGCCTTT TGATGCCTT TCTCATGTATG	AGVQLQDNGY AGVQLQDNGY AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPQENCIISK SLRSAMDVIT LQQAAEFYLM SICSGLKKGF PNLEELSRLT KNTVTVDNTV KPGHWTYTLN GFYPILNATV VNRSPSISTP SVLGVPAGPH IQDDFNNAIL RNSLQSAVSN KRADKKENGT CCCCACGACA GGGGGGAT TGGCTAGAG GTGGCAGG GATCCTGGATCCTG GATCCATGAT TGATGGGCAG TGATGGGCAG TGATGGGCAG TGATGGGCAG GAGTTTGTT TGATGGCACT GAGCAGAAC GAGTTTTGTA	NGLLIAINPQ IKQESYEKAN VFVHEWAHLR LFKEGCTFIY DSADFHISPP QIVEIHTFVG EVVEKLNGKA GGLKPFVPDI GNDTMFLVTW NTHISLQALK TATVEPETGD AHSIPSSHAM PDVPPCKII VNTSKRNPQQ LAQAPLFIPP KLL 41 CCTCCCACTT CCCTCCCCACT GAGTGGGATGAG GTGCAGTTCC CCAAGAGGGC GCTGCCAGC CCTCGCCAGC CCTCGCCAGC CCTCGCCAGC CCTCGCAGC CCTCGATGAC CCGCTGGATGAG CATCACTGTC TCTTGACTTC TTCAATAAAC CCGCTGGGCTC	VPENQNLISM VPENQNLISM VIVTDWYGAH WGVFDEYNND NSTQNATASI MNGTELPPP IASFDSKGEI YGSVMILUTS SSNSNSMIDAF QASGPPEIIL VTVTSRASNS PVTLRLLDDG YVPGYTANCN DLEAVKVEEE AGIREIFTFS NSDPVPARDY 51 CCCACTGTGG GCTAGTGGG GCTAGGGGGAAGAGGG AAGTTGAGGGG TCTCCTTCCT CTGGAGCAG GACAAGTTCA TTTGTGGGGC ATGTGCAATG CTGCCATGGA TTTTTTTTTC AGCTGGAGTG AGCTGGAGTG AGCTGGAGTG AGCTGGAGTG AGTTGCAATG CTGCCATGGA TTTTTTTTTT	120 180 360 420 480 540 600 660 720 780 900 601 120 180 300 360 480 540 600 660 720 720 780 780 780 780 780 780 780 780 780 78
505560657075	TIME TO THE TOTAL OF THE TOTAL	11 CNLKFVTLLV CNLKFVTLLV COKEGKYIH IKVTRCSSDI IKVTRCSSDI DERALLVSYL DORALLVSYL DORALLVSYL FQOHIQLEST NNFITNLTFR GRIBEERKWG DFDQGQATSY QPNGETHESH GLIGIICLII CCCGGTCCAG CTCAGGGGCT TCTCTGGGAG TGGGATCAGG CTCAGGAGGCT CTCAGGAGGCT CTCAGGAGGCT CTCCAGGAG CTTCCAGGAG	21 ALSSELPFIG PFRNIKILIP FTPNFLINDN TGIPVCEKGP EAPNLQNGMC KMAEADRLIQ PTTVSAKTDI HSIALGSAG GENVKPHEQL TASLMIPGTA PVMIYANVKO ANGRYSLKVH FSRVSSGSF EIRMSKSION RIYVAIRAMD VVTHHTLSRK 21 GATGCCCAGT GGAGGGGGT TTGAGCCAGG GCCCTTGACC GGAGGGGGCT TTGAGCAGG ATCCTCACCA ACCTTCACCA ACCTTCACCA ACCTTCACCA CTAGGGAGGGCT TATGCTGTTT GAGGAGGGCT TGATGCCTTT GATGCCTTT GATGCCTTT GATGCCTTT TGATGCACTT TGATGCACTT TGATGCACTT TGATGCACTT TGATGCACTT TCTCAGTGATG GGATCCTCTT TCTCAGTGATG GGATCCTCTT TCTCAGTGATG GGATCCTCTCT TCTCAGTGATG TCTCACTCT TCTCAGTGATG TCTCACTCT TCTCACCT TCTCACTC TCTCACTCT TCTCACTCT TCTCACTCT TCTCACTC TCTCT TCTCACTC TCTCACTC TCTCACTC TCTCACTC TCTCACTC TCTCT TCTCACTC TCTCT TCTCACTC TCTCACTC TCTCACTC TCTCT TCTCACTC TCTCACTC TCTCT TCTCACTC TCTCT TCTCACTC TCTCT TCTCACTC TCTCT TCTCT TCTCT TCTCT TCTCT TCTCT TCTCACTC TCTCT T	AGVQLQDMGY AGVQLQDMGY AGVQLQDMGY ATWKANNNSK LTAGYGSRGR CPGENCIISK SLRSAMDVIT LQQAAEFYLM SICSGLKKGF PNLEELSRLT KNTYTVDNTV KPGHWTYTLN YMRSPSISTP SVLGVPAGPH (QDDFNNAIL RNSLQSAVSN KRADKKENGT	NGLLIAINPQ NGLLIAINPQ NGLLIAINPQ NGLLIAINPQ NGLLIAINPQ LFKEGCTFIY DSADFHESPP QIVEIHTPVG EVVEKINGKA GGLKPFVPDI GNDTMFLVTW NTHESLQALK TATVEPETGD AHSIPGSHAM PDVPPCKII NTTKKRIPQQ LAQAPLFIPP KLL 1 CCTCCCCCA GAFIGGGAT TTAAAATGCC GCTGCCTTGC GTGCAGTTCT CCCAGAGAGGGC CCTGATAGA GCCC CCTGATAGA GCCC CCTGATAGA GCCC CCTCTGACTTC CCCTCTGATAGA GCCC CCTCTGATAGA GCCC CCTCTGACTCT CCTCTGACTCT CTCTGACTCT CTCTACTCT CTCTGACTCT CTCTACTCT CTCTACTT C	VPENQNLISN VPENQNLISN VIVTDWYGAH WGVFDEYNND NSTQNATASI MNGTELPPPP IASFDSKGEI YGSVMILVTS SNNSNMIDAF QASGPPEILL VTVTSRASNS PVTLRLLDDG YVPGYTANCN DLEAVKVEEE AGIREIFFFS NSDPVPARDY 51 CCCCACTGTGG GCCAAGAGGC CAGTTGGGGGAAAGTCC ATTGTGGAGCAGG GACAAGTTCA TTTGTGGGGG ACAGTGACC ATGTGCAATC CTGCCATGGAAATC	120 180 360 480 540 660 720 720 730 840 900
505560657075	TOTCCCAGGGGTTTGAGAGT	11 CNLKFVTLLV CNLKFVTLLV CNLKFVTLLV GCKEGKYIH IKVTRCSSDI EFCNASTHNQ WCLVLDVSS DDRALLVSYL PTVLSSGSTI FQGHIQLEST NNFITNLIFR VERDSLHFPH VERDSLHFPH USSAYFFSFA GRIBEERKWG DFDQGQATSY QPNCETHESH GLIGIICLII CCCGGTCCAG CTCAGGGGCT CTCTCTGGGAG TGGGATCAG CCACATATAA CTGCCACCTG GCTGGTCACT GCTGTCACT GCTGGTCACT GCTGCT GCTGTCACT GCTGTCACT GCTGCTCACT GCTGCTCACT GCTGCTCACT GCTGCTCACT GCTGCTCACT GCTGCTCACT GCTGCTCACT GCTGCTCACT GCTGCTCCT GCTGCTCACT GCTGCTCT GCTGTCACT GCTGTCACT GCTGTCACT GCTGCTCACT GCTGTCACT GCTGCTCACT GCTGTCACT GCTG	21 ALSSELPFIG PFRNIKILIP FTPNFLIXDIN TGIFYCERGP EAPNLQNOMC EAPNLQNOMC EAPNLQNOMC TGIFYCERGP EAPNLQNOMC EAPNLQNOMC TASLMIPGTA PVMIYANVKO ANGRYSLKVH FSRVSSGGSF EIRMSKSLQN RIYVAIRAMD VVTHHTLSRK 21 GATGCCCAGT GGCCTTGACC GGAGGGGGCT TTGAGGCAGG ATCCTCACCA ACGTTCACCA ACGAACTTC CTGAAGAGCT TGATGCTTT GACCAGT TGATGCCTTT TGATGATG GGATCCTCT CTTTAGGTCT TTTAGGTCT TTTAGGTCT TCTCATGATG GGATCCTCT CTTTAGGTCT TCTTTAGGTCT TCTTTAGGTCT TCTTTAGGTCT TCTTTAGGTCT TCTTTAGGTCT TCTTTAGGTCT TTTTAGGTCT TTTAGGTCT TTTTAGGTCT TTTAGGTCT TTTTAGGTCT TTTTAGGTCT TTTTAGGTCT TTTTAGGTCT TTTTAGGTCT TTTTAGGTCT TTTAGGTCT TTTAGGTCT TTTAGGTCT TTTTAGGTCT TTTAGGTCT TTTAGTCT TTTAGGTCT TTTAGGT	AGVQLQDNGY AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPQENCIISK SLRSAMDVIT LQQAAEFYLM SICSGLKKGF PNLEELSELT KNTVTVDNTV KPGHWTYTLN VNHSPSISTP SVLGVPACPH (QDDFNNL) RNSLQSAVSN KRADKKENGT 31 CCCCACGACA GGGAGGGAAT TTGGTTTCC GATCCATGAT GAATCACTG GAACCAGCAC GAAGCAGAC TGGAGGGAAT TTGGATCAC GAAGCAAGC GAAGCAAGC GAAGCAAGC GAAGCAAGC	NGLLIAINPQ NGLLIAINPQ NGLLIAINPQ NGLLIAINPQ NGLEITPYC EVVEKLNGKA VFVHEWAHLR LFKEGCTFIY QIVEIHTFVG EVVEKLNGKA QIVEIHTFVG GILKFYVEDI GNDTMFLVTW NTHENSLQALK TATVEPETGD AHSIPGSHAM PDVPPCKII VNTSKRIPG LIAQAPLFIPP KLL 41 CCTCCCACTT CCCTCCCCCA GAGGGGAT TTAAAATGCG GTGCAGTTCT CCAAGAGGGC CCTGGATGGC CCTGGATGGC CCTGGATGGC CCTGGATGGC CCTGGATGGC CCTCGACTT TTCAATAAAC CGGCTGGCTC CTCTGACTTC TCTCAATAAAC CGGCTGGCTC CCTCTGACTCT CTCTGACTCT ATTTCAAAAAA	VPENQNLISN VPENQNLISN VIVTDWYGAH MGVFDEYNND NSTQNATASI MNGTELPPP IASPDSKGEI YGSVMILUTS SNNSNMIDAF QASGPPEIIL VTVTSRASNS PVTLRLLDIG YVPGYTANGN DLEAVKVEES AGIREIFTES NSDPVPARDY 51 CCCACTGTGG GCTGGTGGTG GCGAAGAGGC AAGTTCA TTTGTGGGGG AACAGTTCA TTTGTGGGGG CTGCATGGATTC CTGCCATGGATTC CTGCCATGGATTC AGCTGGAGTG CCCACTGGAATC CCCGGAATAA CCCAGGAATAA	120 180 360 420 480 540 660 720 780 840 900 180 240 360 420 480 480 660 660 720 780 840 840 840 840 840 840 840 840 840 8
505560657075	TOTCCCAGGGGTTTGAGAGT	11 CNLKFVTLLV CNLKFVTLLV CNLKFVTLLV GCKEGKYIH IKVTRCSSDI EFCNASTHNQ WCLVLDVSS DDRALLVSYL PTVLSSGSTI FQGHIQLEST NNFITNLIFR VERDSLHFPH VERDSLHFPH USSAYFFSFA GRIBEERKWG DFDQGQATSY QPNCETHESH GLIGIICLII CCCGGTCCAG CTCAGGGGCT CTCTCTGGGAG TGGGATCAG CCACATATAA CTGCCACCTG GCTGGTCACT GCTGTCACT GCTGGTCACT GCTGCT GCTGTCACT GCTGTCACT GCTGCTCACT GCTGCTCACT GCTGCTCACT GCTGCTCACT GCTGCTCACT GCTGCTCACT GCTGCTCACT GCTGCTCACT GCTGCTCCT GCTGCTCACT GCTGCTCT GCTGTCACT GCTGTCACT GCTGTCACT GCTGCTCACT GCTGTCACT GCTGCTCACT GCTGTCACT GCTG	21 ALSSELPFIG PFRNIKILIP FTPNFLIXDIN TGIFYCERGP EAPNLQNOMC EAPNLQNOMC EAPNLQNOMC TGIFYCERGP EAPNLQNOMC EAPNLQNOMC TASLMIPGTA PVMIYANVKO ANGRYSLKVH FSRVSSGGSF EIRMSKSLQN RIYVAIRAMD VVTHHTLSRK 21 GATGCCCAGT GGCCTTGACC GGAGGGGGCT TTGAGGCAGG ATCCTCACCA ACGTTCACCA ACGAACTTC CTGAAGAGCT TGATGCTTT GACCAGT TGATGCCTTT TGATGATG GGATCCTCT CTTTAGGTCT TTTAGGTCT TTTAGGTCT TCTCATGATG GGATCCTCT CTTTAGGTCT TCTTTAGGTCT TCTTTAGGTCT TCTTTAGGTCT TCTTTAGGTCT TCTTTAGGTCT TCTTTAGGTCT TTTTAGGTCT TTTAGGTCT TTTTAGGTCT TTTAGGTCT TTTTAGGTCT TTTTAGGTCT TTTTAGGTCT TTTTAGGTCT TTTTAGGTCT TTTTAGGTCT TTTAGGTCT TTTAGGTCT TTTAGGTCT TTTTAGGTCT TTTAGGTCT TTTAGTCT TTTAGGTCT TTTAGGT	AGVQLQDNGY AGVQLQDNGY ATWKANNNSK LTAGYGSRGR CPQENCIISK SLRSAMDVIT LQQAAEFYLM SICSGLKKGF PNLEELSELT KNTVTVDNTV KPGHWTYTLN VNHSPSISTP SVLGVPACPH (QDDFNNL) RNSLQSAVSN KRADKKENGT 31 CCCCACGACA GGGAGGGAAT TTGGTTTCC GATCCATGAT GAATCACTG GAACCAGCAC GAAGCAGAC TGGAGGGAAT TTGGATCAC GAAGCAAGC GAAGCAAGC GAAGCAAGC GAAGCAAGC	NGLLIAINPQ NGLLIAINPQ NGLLIAINPQ NGLLIAINPQ NGLEITPYC EVVEKLNGKA VFVHEWAHLR LFKEGCTFIY QIVEIHTFVG EVVEKLNGKA QIVEIHTFVG GILKFYVEDI GNDTMFLVTW NTHENSLQALK TATVEPETGD AHSIPGSHAM PDVPPCKII VNTSKRIPG LIAQAPLFIPP KLL 41 CCTCCCACTT CCCTCCCCCA GAGGGGAT TTAAAATGCG GTGCAGTTCT CCAAGAGGGC CCTGGATGGC CCTGGATGGC CCTGGATGGC CCTGGATGGC CCTGGATGGC CCTCGACTT TTCAATAAAC CGGCTGGCTC CTCTGACTTC TCTCAATAAAC CGGCTGGCTC CCTCTGACTCT CTCTGACTCT ATTTCAAAAAA	VPENQNLISN VPENQNLISN VIVTDWYGAH WGVFDEYNND NSTQNATASI MNGTELPPPP IASFDSKGEI YGSVMILVTS SNNSNMIDAF QASGPPEILL VTVTSRASNS PVTLRLLDDG YVPGYTANCN DLEAVKVEEE AGIREIFFFS NSDPVPARDY 51 CCCCACTGTGG GCCAAGAGGC CAGTTGGGGGAAAGTCC ATTGTGGAGCAGG GACAAGTTCA TTTGTGGGGG ACAGTGACC ATGTGCAATC CTGCCATGGAAATC	120 180 360 420 480 540 660 720 780 840 900 180 240 360 420 480 480 660 660 720 780 840 840 840 840 840 840 840 840 840 8

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WO 02/086443

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PCT/US02/12476

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Protein Accession #: NP_001784.2

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10	CONCORDED CC	CALC & CO. A. CALCAL	CTTC A ATGCC	ACAGGCTGCT	TGAGGAACCT	GAGCTCCGCC	1500
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15	DOCCACA DEA	TCATCAACAA	CAACTATGAC	TGCCCCCTGC	CTGAGGAAGA	GACCAACCCC	1800
15	*********	CONTRACTOR A	プロスマヤアなごみで	GCCATCCGCA	CCTACCTGAA	CCTCATGGGC	1860
	******	AACATCCEAC	CCTCGAGGCC	TGTGCTGGTG	CCCTGCAGAA	CCTGACAGCC	1920 1980
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20	COCCACCTCA	CAN CICCARACLE	CACCAGCCAC	ACTGGCAATA	CCAGCAACTC	CGAAGACATC	2160
	THE PROPERTY OF THE PROPERTY O	CALCACTURE	TOTGAGGAAC	CTGATGGCCT	CGCAGCCACA	ACTUGUCAAG	2220 2280
	CAGTACTTCT	CCAGCAGCAT	CCCCCTTCTC	ATCATCAACC CTGTCTGACA	TGTGGTCCAG	CAAGGAACTG	2340
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	TGCAGGAAGA	TATGACCCAG	CTGAGAAGCC	CTCAGGCCTC AGAAACTGAG	BACARACCTA	BAARCTCTCC	2520 2580
	ATTACTOCA A A	CATTTTACA	January Property of the Proper	CCTTGGGGAA	ACTGGCAGGC	AATGGGGGTT	2640
30	ACCCACCTTC	CCCCCCCCCCC	GGCTTTCTTG	AGTTAAAGGG	GCTTATATGT	GATGTCAATA	2700
•	THE PROPERTY OF THE PROPERTY O	TEAGAAATGG	TATATATATG	TGTCTAATGT	AAGTGTGTGC	ATGCATGTGC	2760
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10	Nucleic Ac:	80 DNA sequid Accession lence: 180-1	#: NM_0065	516.1			
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65		81 Protein cession #: 1			•		
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75	CCTGAAGCCA CATCCAGTTT GGAAGGCAAG TACCTTTGCG GGTGTCCATC CCTTTTTTCA CAAGCCCAC CCTTTGAGGCC CCAGACCTGC AGTGGAGGAG GCTCAAGATC CAAGAGCTTC	GOGAAGTA GTCGAGTCCA GGAGAGCCG AAAAGGCCG ATGGAGCCCG CGGTCAAGT CTGGAGGCCG CGCAAGTGTC GCCAAGGCCG GCCAAGGCCG ATTGGAGCCC ATTGGAGCCC ATTGAGATTC ACCACCAATG	GGAGCGCCT GGGACAAA ACGCAGGGCT ACGTGCGCAA GGGAGACCCG CCGGCTTCCG CCGTGCTTGCT TTTGCATTGT AGAAGGAAA AGGATGAAGC AGATGAAGCAAA	GTTCGCGGGC GAACTCCAAC CCAGCTGGGG GTCCATTTC GGGAACAGC GGACGGGCC AGACCACCAG CCAGAGGACAC CCAGAGGCAC GGAGCTGCTG TGCAGAGCAC GGAGCTGTCA TGAGAAGTGG CCTGGAGCAG GCTCGGAGCAG	ANTEAGTGGG TACTTCAGCA GCTGCCAAGA TOGGAGTCCC TACCCCCGGG TGCGACTCCT TCCTTCTGGG CTGCTCGAGC CAGCTCTTCT AAGAATCATA CTGCAAAAGG CAGAAGGAGA AACTTCCGGG	GGGGACCCAT TGGACTCTAT AGCCACCGT GGAAGCCCAC CCGACACGGG GCATCGGCAA AGCTGCATC CCATCCGGGA GCCAGACCGA GCCAGACCGA AGCACGTGCA AGCACGTGCA AGGACCGCAT ACCTGGTGCA AGCAGGATGG	420 480 540 600 660 720 780 840 900 960 1020 1080
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75 80	CCTGAAGCCA CATCCAGTTT GGAAGGCAAG TACCTTTGCC GGTGTCCATC CAAGCAGAAG CAAGCCCCAC CCTTTTGAGCCC CAGACCTGC AGTGGAGGAG GCTCAAGATC GGACCTGGAGGAG ATTTGGTCACAA ATTTGGTCACAA ATTTGGTGCA CAGAGCTGC GGACAGCAG ATTTGGTGCA CAGAGCTGC GGACGAGGAG ATTTGGTGCA CAGAGCTGCAAGATC AGAGCTGCAAGATC AGACAGCAGCAG ATTTGGTGCA CAGAGCAGCAG ATTTGGTGCACAA ATTTGGTGCACAAA ATTTGGTGCACCAA	GGGAAGTA GTCGAGTCCG AGGTCGCG AAAAGGCCG ATGGAGCCCG GCGACCAAGT CTGGAGGCCG ATCGAGGCCG ATCGAGGCCG ATCGAGGCCG ATCGAGGCCG ATCGAGGCCG ATCGCTAACT ATCGCTACC ATCGCTACC ATCGAAGTCTA AGCAAAAGG ACCACCAATG AAGCAAAGC ATGAAGTTA AACCAGGAGC ACCACGGAGC ACCACGAGC ACCACGGAGC ACCACGAGC ACCACGGAGC ACCACGAGC ACCACGGAGC ACCACGGAGC ACCACGGAGC ACCACGAGC	GGAGGGCCCT GGGAGAGAA ACGCAGGGCA ACGCAGAGACCA CCGGCTCCGA CCGCCTCCGC CCGCCTCCGC TTTGCATGT AGAAGGAGAC AGAAGGAGAA AGAAGGCAT AGAAGTAGAA ACTAGATGC AGCTACTGC ACTAGATGCA ACTAGATCA AC	GTTGCGGGGC GAACTCCAAC CCAGCTGGGG GTCCATTTC GCGAACAGC GGAGGTGCTG GTGCCAGGCC AGACCACCAG GAAGCACGAG CCAGGAGGAC GCAGGAGGAC CCTGGAGGAG GCTGGCTG TCTGGATGAG GCTGGATGAC CCCCCACCC AGGCAACTC CCCCCACCC AGGCAACTC GCAGGAACTC CCCCCACCC	ANTEAGTIGGE TACTTCAGCA GCTGCCAAGA TCGGAGTCCC TACCCCCGGG TGGGACTCCT TCCTTCTGGG CTGCTTCTTCTG AAGAATCATA CTGCAAAAGG CAGAAGGAGA AACTTCCGGG AAGAGCAAGG ACAGCCAAGG CTGCTTTTCTGGG CAGAAGGAACA AACTTCCGGAAAGGAACA AACTTCCGGAAAGGAACA AACTTCCGGAAAGGAACA AACTTCCGGAAAGAACAACG AAGAAGAACAACG CTGCGCAACT AAGAAGAACAACG AGCCCTAAACT	GGGGACCCAT TGGACTCTAT AGCCACCGT GGAAGCCCAC CCGACACGGG GCATCGGCAA AGCTGCATC CCATCCGGGA GCAGACCGG GCACCGTGA AGCAGCTGCA AGGACCGCAT ACCTGGTGCA AGGACCGCAT ACCTGGTGCT TGCTGCACGA TTCTGCACGA ATCATGTCCT	420 480 540 660 720 780 840 900 900 1020 1140 1260 1320 1320 1440

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5	ACCOCCAC	CONCOUNT	GCTAAACACC	TCCCCGGAAG	GATGGAAGCT	CCTGAAGAAG	4140
,	CA COMMONOTA	ATACACACCT.	CATCAGAGTC	CTGGTGCAGA	CGCTGTGTGA	GCCCGCAAGC	4200
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10	as s amags as	CCACCACCCC	COMPARTMENT	CHETCHGCCT	GTAAACAGCT	TCACAGAGCT	4440
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PCT/US02/12476

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Protein Accession #: NP 004172

	WO 02/	1086143					
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	Immanace	ALI ILICEOU					
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00	であれたれででんぐれ	CCATHITITICA	CACAGTGCTG	ATGGCGCCCC	GCTCGGCCAA	GCCGGCCCTG	2820 2880
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		id Accession Lence: 104-4		1190.1			
	Course, mod						
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	COCA CTCCCCC	CACCACCACC	TECTCCACGG	CGCGGAGCCC	AACTGCGCCG	ACCCCCCCCAC	180
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	GCACCGGGCC	GGGGCGCGC CTGGGCCATC	TGGACGTGCG	ACGGTACCTG	CGCGCGGCTG	CGGGGGGCAC	360
	CACACCCACT	እ አ <i>ር</i> ር አጥርርርር	CCATAGATGC	CGCGGAAGGT	CCCTCAGACA	TUCCUGATIG	420
40	******	ACACCCTCTC	ACABACCTCG	GGAAACTTAG	ATCATCAGIC	ACCGAAGGTC	480 540
40	******	ACAACTGCCC TTAAAAATGT	CCTCCCTTTT	AACGTAGATA	TAAGCCTTCC	CCCACTACCG	600
	アススカサビサビであ	ምፈማ ው ልጥ ልጥተው	ATATAT-T-TTT	TTCTTATAAA	AATGTAAAAA	AGAAAAACAC	660
	CONTRACTOR OF THE PROPERTY OF	TTTTCACTGT GGCATTTCTT	GTTGGAGTTT	TCTGGAGTGA	GCACTCACGC	CCTAAGCGCA	720 780
45	AGCATTTTGT	GAACTAGGGA	AGCTCAGGGG	GGTTACTGGC	TTCTCTTGAG	TCACACTGCT	840
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	1	1			DAL THE REPORT	ARLDVRDAWG	60
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55							
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	ASSESSMENT TO A SECOND	LUNIUMUMMU	-M4 1 1 1 1 1 1 GA	AU-AU-OUAAU			
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OGEKOKOVID LLASAKKOLE VEROTITOLS FELSEFRRKY EETOKEVINL NQLLYSQRRA

DVOBILEDDRH KTEKIQKLRE ENDIARGKLE EEKKRSEELL SQVQSLYTSL LKQQEEQTRV
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          1020
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                                                                                                                1140
                                                                                                                1200
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65
                                                                                                       2820
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          CTGTCTCTTT TGGAAATAAT GTCAAAGAAC ACCTTTCACC ACCTGTCAGT AAACGGGGGA
          CCCCCCAAAA GACCATGCTA TAAAAAGAAC TGTTCCAGAA TCTTTTTTT TCCCTAATGG
                                                                                                       3000
          ACGAAGGAAC AACACACACA CAAAAATTAA ATGCAATAAA GGAATCATTA AAAA
70
          Seg ID NO: 150 Protein sequence:
          Protein Accession #: NP_003803
75
                                                                       41
          MKPPGSSSRQ PPLAGCSLAG ASCGPQRGPA GSVPASAPAR TPPCRLLLVL LLLPPLAASS
          RPRAWGAAAP SAPHWNETAE KNLGVLADED NTLQQNSSSN ISYSNAMQKE ITLPSRLIYY
          INQDSESPYH VLDTKARHQQ KHNKAVHLAQ ASFQIEAFGS KFILDLILNN GLLSSDYVEI
80
          HYENGKPQYS KGGEHCYYHG SIRGVKDSKV ALSTCNGLHG MFEDDTFVYM IEPLELVHDE
         KSTGRPHIIQ KTLAGQYSKQ MKNLTMERGD QWPFLSELQW LKRRKRAVNP SRGIFEEMKY
LELMIVNDHK TYKKRRSSHA HTNNFAKSVV NLVDSIYKEQ LNTRVVLVAV ETWTEKDQID
                                                                                                         300
          ITTNPVQMLH EFSKYRQRIK QHADAVHLIS RVTFHYKRSS LSYFGGVCSR TRGVGVNEYG
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          LPMAVAQVLS OSLAQNLGIQ WEPSSRKPKC DCTESWGGCI MEETGVSHSR KFSKCSILEY
RDFLORGGGA CLFRPTKLF EPTECGNGYV EAGEECDCGF HVECYGLCCK KCSLSNGAHC
                                                                                                         480
85
          SDGPCCNNTS CLFQPRGYEC RDAVNECDIT EYCTGDSGQC PPNLHKQDGY ACNQNQGRCY
          NGECKTRONQ CQYIWGTKAA GSDKFCYEKL NTEGTEKGNC GKOGDRWIQC SKHOVFCGFL
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25	CCTTTGGGGG	TCAAATGGCA	ATTETTACATA	CCCATATCCA	GGTACATCCA	CAAATCCAGC	960
	ACCCA ATTCA	TAACTCACTC	AAGCCGAAAG	CGAAAACATA	ACCAGAGCAT	CAGGGTTGTT	1020
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	TGTAGGTCAT	TTTCAAGAAG	GLIGITCAAA	GAAGTTCCCA	TATATTATGA	TTACACTGAT	1320
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	MGFNLTLAKL	RNKTSFIFYL	KNIVVADLIM	TLTFPFRIVE	DAGFGPWYFK	FILCRYTSVL	120
	THE STREET	PICITCIDAY	T.MARK DECING	PMYSTTPTKV	LSVCVWVIMA	VLSLPNIILT	180
45	MCCOPTEDNIE	DOSKI KSDIG	VKWHTAVTYV	NSCLEVAVLV	ILIGCYIAIS	RYIHKSSRQF	240 300
	ISQSSRKRKH	NQSIRVVVAV PIIYFFMCRS	PETCELPYHL PEDDI PVVCN	CRIPFTFSHL	LOSVERSEVE	IYYDYTDV	300
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55	GTTCGGCGCC CGAAAGGAGT AAGGCCGCGG	11 AAAGCGCGGA GAGGGGCCGA GAGTGGGAAG	21 GCGGAGGCCG GAGCCCAGAT CGTCCGCCAT AAGGGCAACT	AGGCGAGAGC ACCATTTTGG GTTCTGCGAA GCCTGCCTTC	CTGGCGCTGT CGTGAGAGCT AAAGCCATGG AACGAGGATG	AGGACTAGAA GGTGGTTGGC AACTGATCCG GACTCAGACA	120
	GTTCGGCGCC CGAAAGGAGT AAGGCCGCGG CGAGCTGCAT	11 AAAGCGCGGA GAGTGGAAG GGCGGCCCG GAGATGAAAG	21 GCGGAGGCCG GAGCCCAGAT CGTCCGCCAT AAGGGCAACT CTTTGTATGA	AGGCGAGAGC ACCATTTTGG GTTCTGCGAA GCCTGCCTTC ACAAAACCAG	CTGGCGCTGT CGTGAGAGCT AAAGCCATGG AACGAGGATG TCTGATGTGA	AGGACTAGAA GGTGGTTGGC AACTGATCCG GACTCAGACA ATGAAGCAAA	120 180 240 300
55 60	GTTCGGCGCC CGAAAGGAGT AAGGCCGCGG CGAGCTGCAT AGTTCTGGAG	11 AAAGCGCGGA GAGCGCCGA GAGTGGAAAG GAGATGAAAG CGAGATGAATG	21 GCGGAGGCCG GAGCCCAGAT CGTCCGCCAT AAGGGCAACT TCTTTGTATGA TGATACCAAC	AGGCGAGAGC ACCATTTTGG GTTCTGCGAA GCCTGCCTTC ACAAAACCAG TATCAAATTT	CTGGCGCTGT CGTGAGAGCT AAAGCCATGG AACGAGGATG TCTGATGTGA CGACACTGTT	AGGACTAGAA GGTGGTTGGC AACTGATCCG GACTCAGACA ATGAAGCAAA CTCTGTTAAG	120 180 240 300 360
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	GTTCGGCGCC CGAAAGGAGT AAGGCCGCGG CGAGCTGCAT AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT GGAGTGGTTT	11 AAAGCGCGGA GAGCGCCCG GACATGAAAG CGAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA	21 GCGGAGGCCG GAGCCCAGAT CGTCCGCCAT AAGGCCAACT CTTTGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC AAAGATCTCT AGGATATGAA	AGGCGAGAGC ACCATTTTGG GTTCTGCGAA GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGCTACTTAT ACCACCAAAA	CTGGCGCTGT CGTGAGAGCT AAAGCATGG AACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCA CACATGCTCA ATGAGGTCAC AGCTATATA	AGGACTAGAA GGTGGTTGGC AACTGATCCG GACTCAGACA ATGAAGCAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT TGGAGGAGA TTGAAGTCCG	120 180 240 300 360 420 480 540
	GTTCGGCGCC CGAAAGGAGT AAGGCCGCGG CGAGCTGCAT AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT GGAGTGGTTT TGAAGGTTTT	11 AAAGCGCGGA GAGGGCCGA GAGTGGAAG GGCGGCCCG GAGATGAAAG GGAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAG	21 GCGGAGGCCG GAGCCAGAT CGTCCGCCAT CATACCAAC CATACCAAC CATACCATCA TGCCAAATGC AAGATCTCT AGGATATGAA	AGGCAGAGG ACCATTTTGG GTTCTGCGAA GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGCTACTTAT ACCACCAAAA TGATGATGGC	CTGGCGCTGT CGTGAGAGCT AAAGCCATGG AACGAGGATG TCTGATGTA CTTCGGATCA CACATGGCTG ATGAGGTCAC AGCCTATATCA	AGGACTAGAA GGTGGTTGGC AACTGATCCG GACTCAGACA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT TGGAAGGAGA TTGAAGTCCG	120 180 240 300 360 420 480 540 600 660
60	GTTCGGCGCC CGAAAGGAGT AAGGCCGCGG CGAGCTGCAT AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAAATAT TGAAGGTTTC GGAGTGTTTTGAAGGTTTTCGAGGTTTTCGAGGTTTTCGAGGTTTTCGTGTATAT	11	21 GEGGAGGCCG GAGCCCAGAT CGTCCGCCAT AAGGCCAACT CTTTGTATGA CATACCTGTA TGCCAAATGC AAAGATCTCT AGGATATGAA AATTTGAACT ATTGAACTAGA AATTTGAACT CTCCATGGAA	AGGCAGAGG ACCATTTTGG GTTCTGCGAA GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGCTACTTAT ACCACCAAAA TGATGAGGAG ATTGAGGAGA	CTGGCGCTGT CGTGAGAGCT AAAGCCATGG AACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCA CACATGGCTC ATGAGGTCAC AGCCTATATA AGCCTATATA	AGGACTAGAA GGTGGTTGGC AACTGATCCG GACTCAGACA ATCAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT TTGGAGGAGA TTGAAGTCCG TATTAAAAAA	120 180 240 300 360 420 480 540 600 660 720
60	GTTCGCCGCC CGAAAGGAGT AAGGCCGCGG CGAGCTGCAT AGTTCTCGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT TGAAGGTTTT TGAAGGTTTT GTGTCTAAAA AAATAGCCAG GGACCAATC	11 	21 GCGGAGGCCG GAGCCCAGAT CGTCCGCCAT AAGGCCAACT CTTTGTATCAA CCATACCATA	AGGCGAGAGC ACCATTTTGG GTTCTGCGAA GCCTGCTTC ACAAAACCAG TATCAAAATT TGACCGCTTG ATTACGATTT TGCTACTTAT ACCACCAAAA TGATGATGGG ATGTTGAGCAG GGCACTTCCA	CTGGGGCTGT CGTGAGAGCT AAAGCCATGG AACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCA ATGAGGTCA AGCCTATATA ACTTCAGTC CTGATCAGTC CTGATCAGTC	AGGACTAGAA GGTGGTTGGC AACTGATCCG GACTCAGACA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGA TTGAAGTCCG TATTAAAAAA AAGGAGTCCT	120 180 240 300 360 420 480 540 600 660 720 780
60	GTTCGGCGCC CGAAAGGAGT AAGGCTGCAA AAGTCTGGAG GTCAGGTGGA AAATCGAAGG ATGGGAATAT GGAGTGGTT TGAAGGTTT TGAAGGTTAAA AAATAGCCAG GGAGCACATC	11 	21 GCGGAGGCCG GAGCCCAGAT CGTCCGCCAT AAGGCCAACT CTTTGTATCA TGATACCAAC CATACCTGTA TGCCAAATGC AAGATCTCT AAGATCTCT AAGATCTCT CTCGATGGAA CATGCGCCGA CCACCACTCC	AGGCAAGAGC ACCATTTGG ATTCTGCGAA GCTTCTGCGAA ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT ACCACCAAAA TGATGATGAGCAG ATGTGAGCAG CTTCACTCCC CTTCACTCCC ACCTCCAC CTTCACCTCC	CTGGGGCTGT CGTGAGAGCT AAAGCATGG AACGAGGATG CGACACTGT CTTCGGATCA ATGAGTCA AGCCTATATA ACTTCAGTCC CTGATCAGGC CTGATCAGGC CTGATCAGT CTCTTTGATT	AGGACTAGAA GGTGGTTGGC AACTGATCOG GACTCAGACA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG GAGCACTCAG TTGAAGTCCG TTTTAAAAAA AAGGAGTCCT AACTCATGGA TTAGAAGCCTA	120 180 240 300 360 420 480 540 600 660 720 780
60	GAGCACATTG	11	21 GCGGAGGCCG GAGCCCAGAT GGTCGCCAT AAGGCAACT CTTTGTATGA CATACCTGTA TGCCAAATGC AAAGATCTCT AGGATATGAA AATTTGAAGT CTCGATGGAA AATTTGAAGT CTCGATGGAA CATGCGCCCA CCACCACTCC TAAGAATACT TTGTACACTT	AGGCAAGAG ACCATTTTGG GTTCTGCGAA GCCTGCCTTC ACAAAACCAG ATTACAAATT TGGACCGCTTG ATTACAATT ACCACCAAAA TGATGATGAG ATTGAGGAG CGCACTTCCA CTTCACCTCC TGGCTAAGAA TTCTTCCTAC	CTGGGGCTGT CGTGAGAGCT AAAGCCATGG AACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCA AGCCTATATA ACTTCAGTCA CTGATCAGTC CTGATCAGTC CTGATCAGTC CTGATCAGTC CTGTTGATT CTATATTTTTG	AGGACTAGAA GGTGGTTGGC AACTGATCCG GACTCAGACA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT TTGGAGTCCG TATTAAAAAA AAGGAGTCCT AACTCATGGA TTGAAGTCT AACTCATGGA TTAGAAGCTA TTAGAAGCTA TTAGAAGCTA TTAGAAGCTA TTAGAAGCTA TTAGAAGCTA	120 180 240 300 420 480 540 600 660 720 780 840 900
60	GTTCGGCGCC CGAAAGGAGT AAGGCCGCG GAGCTGGAT AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT GGAGTGGTTT TGAAGGTTTT GAAGGTTAAA AAATAGCCAG GGAGCACATC CTCCTCTGTA AGGACTTTGT AGGACTTTCT AGGACTTTCT AGGACTTTCT AGGACTTTCT AGGACTTTCT AGGACTTTCT	11	21 GGGAGGCCG GAGCCCAGAT CGTCCGCAT AAGGCCACT TGTTATGA TGATACCAAA TGCCAAATGC AAAGATCTCT AGGATATGAA AATTTGAAGT CTCGATGGAA CATCCCCTAAGAATACT TAAGATACT TTGTACACTT TTGTACACTT TTGTACACTT TTGTACACTT TTGTACACTT TTGTACACTT	AGGCAAGAGC ACCATTTGG ATTCTGGAA GCTTGCTGCTTC ACAAAACCAG TATCAAATTT TGACGCTTAT ACCACCAAAA TGATGATGAGCAG ATGTGAGCAG ATGTGAGCAG TTACACTCC TGGCTAAGAA TTCTTCCTAC CAAGCTGGTC	CTGGGGCTGT CGTGAGAGCT AAAGCATGG AACGAGGATG CGACACTGTT CTTCGGATCAC ATGAGTCAC ATGAGTCAC ATGAGTCAC ATGAGTCAC ATGAGTCAC ATGATCAGTC CTGATCAGTC CTGATCAGTC CTCTTTTTTTCC TCTATATTTT	AGGACTAGAA GGTGGTTGGC AACTGATCOG GACTCAGACAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT TGGAGGAGAA TTGAAGTCCG TATTAAAAAA AAGGAGTCCT AACTCATGGA TTAGAGTCCT CACCACTCAGACTATTA CTAACTATTA	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
60	GTCGGCGCC CGAAAGGAGT AAGGCCGCGG CGAGCTGCAT AGTTCTGGAG GTCAGGTCGAA AAATCGACGC ATGGGAATAT TGAAGGTTTT TGAAGGTTTT TGAAGGTTTT TGAAGGTTTC GTGTCTAAAA AAATAGCCAG GGAGCACATC CTCCTCTGTA TAGACATTGT AGGACTTTCT GTTTTTTAGA	11	21 GGGGAGGCGG GAGCCAGAT CGTCCGCCAT AAGGCAACT CTTGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC TCCGATGGA AATTTGAACT CTCGATGGA CATGCCCCC TTAGGATACT TTGTACACT TTGTACACT CTATGTTGCC CTATGTTGCACT CTATGTTGCC CTATGTTGCC CTATGTGCAC CTATGTTGCC CTATGTTGCC CTATGTTGCC CTATGTTGCC CTATGTGCAC CTATGTTGCC CTATGTTCC CTATGTTGCC CTATGTTGCC CTATGTTGCC CTATGTTCC CTATGTTGCC CTATGTTCC CTATGTTC CTATGTTCC CTATGTTC CT	AGGCAGAGG ACCATTTGG ACCATTTGG GTTCTGCGAA GCCTGCCTTC ACCAAAACCAG TATCAAATTT TGCTACTTAT ACCACCAAAA TGATGATGGGA GGCACTTCCA CTCTACCTCC TGGCTAAGAA TTCTTCCTAC CAGGCTGGTA	CTGGCGCTGT CGTGAGAGCT AAAGCCATGG AACGAGGATG CGACACTGTT CTTCGGATCA ATGAGGCAC ATGAGGCAC ATGAGTCA AGCCTATATT ACTTCAGAC CTGATCAGAC GGCTTCACTC CTCTTTGATT CTTTTTTTC CTTTTTTTTC CTCAAACTCCT CGGTGAGCCG	AGGACTAGAA GGTGGTTGGC AACTGATCCG GACTCAGACA CTCTGTTAAG GAGCACTCAG CTGAAGAAA TTGGAGGAGA TTGAAGTCCC TATTAAAAA AACGAGTCCT AACTCATGGA TTIAGAAGTCT CTAACTCATGGA TTTAGAAGTCT CTAACTCATGGA CTTATGAAGTCA CTTACTAGAGCTA CTTACAAGCTA CTTACAAGCTA CTTACAAGCTA CTTACAAGCTA CTTACAAGCTA CTTACAAGC CTCCACCCGG	120 180 240 300 360 420 480 540 600 720 780 840 900 960 1020 1080
60	GTTCGGCGCC CGAAAGGAGT AAGGCCGCGG CGAGCTGCAT AGTTCTGGAG GTCAGGTCGAA AAATCGACGC ATGGGAAATAT TGAAGGTTTT TGAAGGTTTT GGAGTGAA AAATAGCCAG GGAGCACATC CTCCTCTGTA TAGACATTGC GTTTTTGTAGA AGTCCTCCCACTAGAA AGTCCTCCACACC CCCTCTACACA	11	21 GGGAGGCCG GAGCCCAGAT GGTCGCCAT AAGGCAACT CTTTGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC AAGGATCTCT AGGATATGAA AATTTGAAGT CTCGATGGAC CACCACTCC TAAGAATACT TTGTACACT CTATGTTGCC TCAAAGGTTT CTATGTTGCC TCAAAGGTTT	AGGCAGAGG AGCATTTTGG ATTCTGCGAA GCCTGCTTC ACAAAACCAG TATCAAATT TGACCGCTTG ATTACGATTT ACCACCAAAA TGATGATGATGATGATGATGATGATGATGATGATGATGAT	CTGGGGCTGT CGTGAGAGCT AAAGCATGG AACGAGGATG CGACACTGTT CTCGGATCA AGCCTATATA ACTTCAGGCC CTGATCAGAC GGCTTCACTC CTCTTGATT CTTCAGTCC TCTTTGATT CTTTAATTT CTTTTTTTC CCAAACTCCT CGGTGAGCCC GGCTTACCTA	AGGACTAGAA GGTGGTTGGC AACTGATCCG GACTCAGACAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT TTGGAGGAGA TTGAAGTCCG TATTAAAAGTCCG TATTAAAAGTCCG TATTAAAAGTCCT AACTCATGA TTAGAAGTCT TTTTGGTTTT GGCCTCAAGC AGTTGTTACA	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1080
60 65 70	GTTCGGCGCC CGAAAGGAGT AAGGCCGCAG AAGGCCGCAA AGTCTCGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT GGAGTGGTTT TGAAGGTTTT TGAAGGTTTAAA AAATAGCCAG GGAGCACATC CTCCTCTGTA TAGACATTGT AGGACTTTCT GTTTTGTAGA AGTCCCCA CCCCTACTCC	11	21 GGGAGGCCG GAGCCCAGAT CGTCCGCAT AGGGCAACT CTTTGTATGA TGATACCAAA TGCCAAATGC AAAGATCTCT AGGATATGAA AATTTGAAGT CTCGATGGAA CCACCACTCC TAAGAATACT TTGTACACTTA CTAAGATACT TAAGATACT TAAGATACT AAAGTTTAACTTAAC	AGGCAAGAGC ACCATTTGG ATTCGGAA GCTGCCTTC ACAAAACCAG TATCAAATTT TGACGCTTAT ACCACCAAAA TGATGATGAG ATGTGAGCAG ATGTGAGCAG TTTCTCCTAC TGGCTAAGAA TTCTTCCTAC CAAGCTGGTC GAGATCACAG	CTGGGGCTGT CGTGAGAGCT AAAGCATGG AACGAGGATG CGACACTGT CTCGGATCAC ATGAGTCAC ATGAGTCAC ATGAGTCAC ATGAGTCAC ATGAGTCAC ATGAGTCAC ATGATCAGAC CTCATTAGATC CTCTTTTGATT CTTTTTTTCC CTCAAACTCCT GCGTGACCC GCATTCCTAAAT CTCTTTAAAT	AGGACTAGAA GGTGGTTGGC AACTGATCOG GACTCAGACAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT TGGAGGAGAA TTGAAGTCCG TATTAAAAAA AAGCAGTCCT AACTCATGGA TTAGAGTCCT CTAACTATTA CTAACTATTA GGCCTCAAGC CTGACCCGG CTGCACCCGG AGTGGTTACA AAGCAGTCAC	120 180 240 300 360 420 600 660 720 780 840 900 1020 1080 1140 1200
60	GTTCGGCGCC CGAAAGGAGT AAGGCCGCGG CGAGCTGCAT AGTTCTGGAG GTCAGGTAGAA AAATCGACGTTT TGAAGGTTTT TGAAGGTTTT TGAAGGTTTT TGAAGCATTC CTCCTCTGTA TAGACATTCT AGGACTTTCT GTTTTTGTAGA AGTTCTCCCA GTTTTCTAGA AGTCCTCCCA CCCCTACTCC CTCGTGTTTTTTTTTGAGAAGTTTCT CCCTACTACA CCCCTACTCC CTGTGTTTTTTTTTT	11	21 GGGAGGCCG GAGCCCAGAT GGTCCGCCAT AAGGCCAACT CTTTGTATGA CATACCTGTA TGCCAAATGC AAGATATTGAACT AGGATATGAA AATTTGAACT CTCGGATGGAA CATGCCCCC TTGGACACTCC TAGGAATACT TTGTACACTA CTATGTTGCC TAAGAATACT TAAACATGGT TAAACATGGT TAAGATCTGT TAAACATGGT TAGATCCTGT TAGATCCTGT TAGATCCTGT TAGATCCTGT TAGATCCTGT TAGATCCTGT TAGATCCTGT TAGATCCTGT	AGGCAAGAG AGCATTTGG AGCATTTGG GTTCTGCGAA GCCTGCCTTC ACAAAACCAG TATCAAATT TGCTACTTAT ACCACCAAAA TGATGATGGAG GGCACTTCCA TTCTACTCC CTCACTCC CAAGCAGGGC GAGATCACAG TGTTAAGAA TCTTCTAC CAAGCTGGTC CAAGCTGGTC TAAGAA TACATTGAA TACATTTGAA TACATTTGAA TACATTTGAA TACATTTGAA TACATTTGAA CATTTCAATCCCA TACATTTCAACTCC CATTTCAATCCCA TACATTTCAACTCC CATTTCAATCCCA TACATTTCAACTCC CATTTCAACTCC CATTTCAACTCC CATTTCAACTCC CATTTCAACTCC CATTTCAACTCC CATTTCAACTCC CATTTCAACTCC CATTTCCAACTCC CACTCC CACTC CACTCC CACTC CACTCC CACTC CACTCC CACTCC CACTCC CACTCC CACTCC CACTCC CACTCC CACTCC CACTC CACTCC CACTC CAC	CTGGGGCTGT CGTGAGAGCT AAAGCATGG AACGAGGATG CGACACTGTT CTTCGGATCC CACATGGCTA AGGCTATATA ACTTCAGTCC CTGATCAGAC CTGTTCAGAC CTCTTTGATT CTTTTTTTC CTAAACTCCT CGGTGAGCC GCATCCTAACT CTCTTAATT TCTTTTTTC CGGTGAGCC CGCTTCCTAACT TCCTTAAAT TCTCTTAAAT TCTCTTAAAT TCTCTTAAAT TCTCTTAAAT TCTCTTAAAT TCTCTTAAAT TCTCTTAAAT TCTCTTAAAT TCACATGCAA	AGGACTAGAA GGTGGTTGGC AACTGATCCG GACTCAGACA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAA TTGGAGTCCG TATTAAAAA AAGGAGTCCT AACTCATGA TTAGAAGCTA TTTTGGTTTT CGACCTCAAGC AGTGTTACA AGGAGTCAC CTGCACCCGG AGTTGTACA AGCAGTCAC GTGTATTGTA	120 180 240 300 360 420 540 660 720 780 960 1020 1140 1260 1320
60 65 70	GTTCGGCGCC CGAAAGGAGT AAGGCCGCAG AAGGCCGCAA AATCCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT GGAGTGGTT TGAAGGTTT TGAAGGTTT AAATTCTAAA AAATAGCCAG GGAGCACATC CTCCTCTGTA TAGACATTGT AGGACTTTCT GTTTTGTAGA AGTCCCCA CCCCTACTCC CTCGTTATTTTAGCCAC CCCTATACTCC TTTGGCTGGAC CAAGCTTAGAG CAAGCTTAGAG CAAGCTTAGAG CAAGCTTAGAG TGGTCTGTATA	11	21 GGGAGGCCG GGGCCCAGAT CGTCCGCCAT AGGGCAACT CTTTGTATGA TGATACCACA CATACCTGTA AGGATATCAA AAGATCTCT AGGATATGAA CATGCACCACTCC TAAGAATACT TTGTACACTTA CCACCACTCC TAAGAATACT TTGTACACTTA AGCTGTAA CATGCTGTAACACTA TAAACATGCT TAAAAATAAAAAAAAAA	AGGCAAGAGC ACCATTTGG CTTCTGCGAA GCCTGCCTTC ACAAAACCAG TATCACATTT TGCTACTTAT ACCACCAAAA TGATGATGCAC ATGTGAGCAG CTTCACCTCC TGGCTAAGAA TTCTTCCTAC CAAGCTGGTC GAGATCACAG TACATTTGAACACA TACATTTGAACACA TACATTTGAA GTGTAATCACA TCTTTCATAC TACATTTGAA GTGTTATTCATAC CATTTTCATAC CATTTTCATTTCATAC CATTTTCATAC CATTTCATAC CATTTTCATAC CATTTCATAC CATTTTCATAC CATTTCATAC CATTTTCATAC CA	CTGGGGCTGT CGTGAGAGCT AAAGCATGG AACGAGGATG CGACACTGTI CTTCGGATCAC ATGAGTCAC ATGAGTCAC ATGAGTCAC ATGAGTCAC ATGATCAGGCC CTGATCAGAC CTCTTTTTTTCC CTCAAACTCCT GGGTGAGCCC GCATTCCTAC TCTCTTAAAT TTCTGGTCAT TCACAGCAGCAT CACACAGCAAT	AGGACTAGAA GGTGGTTGGC AACTGATCOG GACTCAGACA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG TTGAAGTACA TTGAAGTACA AAGGAGTCCT AACTCATGGA TTTAGAGTCCT ACTCATGGA TTTAGATTCC CCTGCACCGG AGTTGTTACA AAGCAGTCAT AGCACCGG AGTTGTTACA AAGCAGTCAC GTGTATTGGA	120 180 240 300 360 420 480 540 660 720 780 840 900 900 1020 1140 1200 1260 1320
60 65 70	GTTCGGCGCC CGAAAGGAGT AAGGCCGCGG GAGCTGCAT AGTTCTGGAG GTCAGGTCGAA AAATCGACGC ATGGGAATAT TGAAGGTTGT TGAAGGTTGT TGAAGGTTGT AAAATAGCCAG GGAGCAATC CTCCTCTGTT AGGACTTCT AGGACTTCT AGGACTTCT GTTTTTTTAGA AGTCCTCCCA CCCTACTCC GTGTGTTTT TTGGCGGAC CAAGCTAGAG TGGTCTGTAG	11	21 GGGGAGGCGG GAGCCCAGAT CGTCCGCCAT AAGGGCAACT CTTGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC CATACGTGA AAGATCTCT AGGATATGAA CATGCCCACTCC CTAGGAATACT TTGTACAACT TTGTACACTA CTATGTGGC CCACCACTCC CTAAGGATATC TAGACCTGTAC TAGACCTGT TAGACCTGT TAGACCTGT CTGAGATACA TAGATTATATATATATATATATATATATATATATATAT	AGGCAGAGG AGCATTTGG ATTCTGCGAA GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACAATTT TGCTACTTAT ACCACCAAAA TGATGATGGCA ATGTAGGCA ATGTAGCAG ATGTACACCC TGGCTAAGAA TTCTCCTAC CAAGCTGGTC ACAACTACAA TCATTCAAA AGGTCTTCT CAATTTCAAA AGGTCTTGTC CATTTTAATGAC TTTAATGAC TTGACATTTC	CTGGGGCTGT CGTGAGAGCT AAAGCATGG AACGAGATGT CTCGGATCAC ATGGGTCA ATGGGTCA ATGGTCAC ATGGTTACATC CTCTTTGATT CTTTTTTTTC CTTTTTTTTC CTGATCACC GGATTACATC CTCTTTACT CTCTTTTTTTC CTTTTTTTC CTTTTTTTC CGATCACC CGATTCCTAC TCTCTTAAAT TCTTTTATC TCTTTTATC TCTTTTATC TCTCTTAAAT TCTGTCAT TCACATGCAT ATACTACTT TCACATGCAT ATACTACTT TCACATGCAT ATACTACTT TCACATGCAT ATACTACTT TCACATGCAT ATACTACTT TCACATGCAT ATACTACTTT ACCATGCAT CACCATGCAT CACCATCAT CACCATGCAT C	AGGACTAGAA GGTGGTTGGC AACTGATCCG GACTCAGACA ATCAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAGAGAA TTGGAGAGAA TTGGAGGAGA TTAAAAAA AACGAGTCCT AACTCATGGA TTTAGAGTCCT CTAACTCATGGA CTAACTATTAA TTTTGGTTTT GGCCTCAAGC CTGCACCCGG AGTTGTACA AAGCAGTCAC GTGTATTGTA GTGAAGATCA GTGAAGATCA GTGAAGATCA GTGAAGATCA	120 180 240 300 360 420 480 540 660 720 780 900 900 900 1080 1140 1200 1320 1380
60 65 70 75	GTTCGGCGCC CGAAAGGAGT AAGGCCGCGA AAGGCCGCAT AGTTCTGGAG GTCAGGTGGA AAATCGACGG ATGGGAATAT GGAGTGGTT TGAACGTTTT GGAGCTTCTAAAA AAATAGCCAG GGAGCACATC CTCCTCTGTA TAGACATTCT GTTTTGTAGA AGTCCTCCC CCCTACTCC GGTGTGTTTT TTGGCTGAC CAAGCTAGAG TAGTTTGGGAA TATTTGGGAA TATTTGGGAT TATTTGGAT TATTGGAT TATTTGGAT TATTTGGAT TATTGGAT TATTTGGAT TATTTGGAT TATTTGGAT TATTGGAT TATTTGGAT TATTTGGAT TATTTGGAT TATTGGAT TATTGGAT TATTTGGAT TATTGGAT TATTGGAT TATTGGAT TATTTGGAT TATTTGGAT TATTGGAT TATTGGAT TATTTGGAT TATTTGGAT TATTTGGAT TATTTGG	11	21 GGGAGGCCG GAGCCCAGAT GGTCGGCAT AAGGCAACT CTTTGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC AAGGATATGAA AATTTGAACT CTCGAGTAC CACCACTCC TAAGAATACT TTGTACACT CTATACTGCC TAAGAATACT TAAACATGGT TAAACATGGT TAGACTAC TAGAGTACC TAGAGTACC TAGAGTACC TAGAGTACC TAGAGTATC TAGACTACT TAGACT TAGACTACT TAGACTACT TAGACT TA	AGGCAGAGG AGCATTTGG AGCATTTGG GTTCTGCGAA GCCTGCTTG ACAAAACCAG ATTACAATT TGCTACTTGT ACCACCAAAA TGATGATGGGG GGCACTTCCA TTCTACTCCT CTCACTCC CTCACTCC CAAGCTGGTC GAGATCACAG TGTTAATGAA GTTTAATGAG TGCACATTTCAA	CTGGCGCTGT CGTGAGAGCT AAAGCCATGG AACGAGGATG CGACACTGTT CTTCGGATCC CACATGGCTA ATGAGGTCA AGCCTATATA ACTTCAGTCC CTGATCAGAC GGCTTCAGTC GTGATCAGAC GGCTTCAGT TCTTTTTTC TCAAACTCCT GGGTGAGCCG GCATTCCTAAAT TTCTGGTCAT TCACATGGTA ATACTAATTT CACCATGGTA ATACTAATTT CACCATGGTA AGGGGACAGT	AGGACTAGAA GGTGGTTGGC AACTGATCCG GACTCAGACAA CTCTGTTAAG GAGCACTCAG CTGAAGAAA TTGGAGGAGA TTGAAGTCCT AACTCATGA TTTTAAAAAA TTTTTAAAAAA TTTTTGGTTTT GGCCTCAAGC AGTTGTACA AGCAGTCAC GTGTATTGAAGTCAC GTGTATTGAAGTCAC GTGTATTGAAGTCAC GTGTATTGAAGTCAC GGTGTATTGAAGAGTCAC GGTGTATTGTACAC GGTGTATTGTA	120 180 240 300 360 420 480 540 660 720 840 900 1020 1140 1200 1140 1320 1380 1440 1500
60 65 70	GTCGGCGC CGAAAGGAGT AAGGCCGCG GAGCTGCAT AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT GGAGTGGTTT TGAAGGTTGT GTGTCTAAAA AAATAGCCAG GGAGCACATC CTCCTCTGTGT AGGACTTCT GTTTTTTAGA AGTCCTCCCA CCCTACTCC GTGTGTTTT TTGGCTGTAC CAAGCTAGAG TGTCTGGAA CATGTGGGAA CATGTGGCTA	11	21 GGGGAGGCGG GAGCCAGAT CGTCGGCAT AAGGGCAACT CTTGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC AAGGATATGAA AATTTGAACT CTGGATAGAA CCACCACTCC TTGTACACT TTGTACAATT TTGTACAATT TTGTACACT TTGTACACT TTGTACACT TAGAATACT TAGATCTT TAGATCTT CCGATATT TAGATCAT ACATGGATT ACTTTCCTT CGTATTCTT CGTATCT CGTATCT CGTATCT CGTATCT CGTATCT CGTATCT CGTACCC CGTATCT CGTA	AGGCAGAGGC AGCATTTGG ATTCTGCGAA GCCTCCTTC TGACCGCTTG TATCAAATTT TGACCCTTG ATTACAATTT TGCTACTTAT ACCACCAAAA TGATGATGGCA ATGTCAGCTGCAC TGGCTAAGAA TTCTTCCTAC TCCCTCCC TGGCTAAGAA TTCTTCCTAC TACATTTCAA TGACTGGTC TGAATCACA TGTAATCACA TTCTTCTTAATGAC TTCACTTTCCAC TGCAATTTCAAA TTCTTTCAAA TTCTTTCAAA TTCTTTCAAA TTCTTTCAAA TTCTTTCAAA TTTTTCAAA TTTTCAAA TTTTTCAAA TTTTTCAAA TTTTTCAAA TTTTTCAAA TTTTTCAAA TTTTTCAAA TTCTTTCAAA TTCTTTTCAAA TTCTTTCAAA TTCTTTCAAA TTCTTTCAAA TTCTTTCAAA TTCTTTCAAA TTCTTTCAAA TTCTTTCAAA TTCTTTTCAAA TTCTTTCAAA TTCTTTCAAA TTCTTTTCAAA TTCTTTTTCAAA TTCTTTTTTTT	CTGGGGCTGT CGTGAGAGCT AAAGCCATGG AACGAGGATG CGACACTGTT CTTCGGATCAC AGCCTATATA ACTTCAGATCAC CTGATCAGAC GGCTTCACTC CTGTTTGATT CTTTTTTTCC TCTATAACTCCT CGATCAGAC GCATTCCTAC CGCTTAACTCC CGATCAGAC CCCTTTAAT TCTGATCAC CCCTTTAAT TCTGTCAT TCACATGCAC ATACTACTT CACCATGCAC ATACTACTT CACCATGCAC AGGGGACAGT TTGACCTGAAT AGGGGACAGT TTGACCTGAAT AGGGGACAGT TTGACCTGAAT AGGGGACAGT TTGACCTGAAT AGGGGACAGT TTGACCTGAAT AGATGCAT AGGGGACAGT TTGACCTGAAT AGATGCAT AGGGGACAGT TTGACCTGAAT AGATGCAT	AGGACTAGAA GGTGGTTGGC AACTGATCCG GACTCAGACA ATCAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAGAGAA TTGAAGTCCC TATTAAAAA AACGAGTCCT AACTCATGGA TTTAGAAGTCT CTAACTCATGGA CTAACTATTAA TTTTGGTTTT GGCCTCAAGC CTGCACCCGG AGTTGTACA AACGAGTCAC GTGTATTGTA GTCAAGTCAC GTGTATTGTA GTCAAGTCAC GTGTATTGTA GTCAAGTCAC GTGTATTGTA GTCAAGTCAC TTTCATGAGATCAC TTTCATGAGATCAC TTTCATGAGATCAC TTTCATGAGATCAC TTTCATGAGATGAA TTTCATGAGATGAA TTTCATGAGATGAA TTTCATGAGATGAA TTTCATGAGATGAA TTTCATGAGATGAA TTTTCATGAGAGATGAA TTTTCATGAGAGATGAA TTTTCATGAGAGATGAA TTTTCATGAGAAGATGAA TTTTCATGAGAAGATGAA TTTTCATGAGAAGATGAA TTTCATGAGAAGATGAA TTTTCATGAGAAGATGAA TTTTCATGAGAAGATGAA TTTTCATGAGAAGAATGAA TTTTCATGAGAAGAATGAA TTTTCATGAGAAGAATGAA TTTTCATGAGAAGAATGAA TTTTCATGAGAAGAATGAA TTTTCATGAGAAGATGAA TTTTCATGAGAAAA	120 180 240 300 360 420 480 540 660 720 780 900 900 1020 1140 1260 1320 1380 1440 1500 1500
60 65 70 75	GTTCGGCGCC CGAAAGGAGT AAGGCCGCGG CGAGCTGCAT AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAAATAT GGAGTGGTT TGAAGGTTTT TGAAGGTTTT TGAAGGTTTT TGACACATC CTCCTCTGTA TAGACATTGT GTTTTGTAGA AGTCCTCCC CCCTACTC CGTGTGTTTT TTGGCTGAC CAAGCTAGAG TATTTGGGAA CTTGTGGTA CTTGTGGAA CTTGTGGAA CTTGTGGAA CTTGTGGAA AGTCTTAGA	11	21 GGGAGGCCG GAGCCCAGAT GGTCGCGCAT AAGGCAACT CTTTGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC AAGGATATGAA AATTTGAACT TCTGATGAA AATTTGAACT CTGGAGAA CATGCCCCC TAAGAATACT TAGACACT CTAAAGTGTT TAAACATGGT TAAACATGGT TAGACTAC TATATATAAT ACATGGATTCCCC GGTATCCCC GGTATCCCC GGTATCCCCC GTAGCCCC TCTACACCC TCTACACCC TCTACACC TCTA	AGGCAAGAGC AGGCAGAGC AGGCATTTGG AGCATTTGG GTTCTGCGAA GCCTGCTTTC ACAAAACCAG TATCAAATT TGCTACTTAT ACCACCAAAA TGATGATGGG GGCACTTCCA TTCTACTCC CTCTACCTCC CAGGCAGGC GGAATACACAG TGTAATCACA TACATTGAA GTTTAATGAC GTTAATCACA TTCATTTCAA GTTTAATGAC TGCACATTTC CAATTTCAA GTTTAATGAC TGCACATTTC CCACTTTGGA AAACACCTGA AAACACCTGA AAACACCTGA AAACACCTGA AAACACCTGA TGGGTTTGGG AAACACTTGA AAACACCTGA TGGGTGTTGGT	CTGGGGCTGT CGTGAGAGCT AAAGCCATGG AACGAGGATG CGACACTGTT CTTCGGATCC CACATGGCTA ACGCCTATATA ACTTCAGTCC CTGATCAGAC CGCTATATA CTTCAGTCC CTGATCAGAC CCTGATCAGAC CCCTTTGATT TCTTTTTTC CGCTGAGCCA GCCATCCTAAAT TCCTGATCATA TCCTTAAAT TCCTTAAAT TCCTCTAAAT TCACATGCAA ATACAAGTCAT CACATGGTA ATACTAATTT CACCATGGTA TCACATGCAA ATACTAATTT CACCATGGTA TCACATGCAA ATACTAATTTAAAT ACGGGACAGT TTGACTGAAA CATTTTAAAAT ATCGAGGAAA CATTTTTAAAT ATCGAGGAAA ATCGAGGAAA ATCGAGGAAA ATCGAGGAAA CATTTTTAAAT ATCGAGGAAA ATCGAGAAA ATCGAGGAAA ATCGAGAAA ATCGAGAAAA ATCGAGAAAAAA ATCGAGAAAAAA ATCGAGAAAAAAAAAA	AGGACTAGAA GGTGGTTGGC AACTGATCCG GACTCAGACA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAA TTGGAGTCCG TATTAAAAAA AAGGAGTCCT AACTCATGA TTTAGAAGCTA TTTTGGTTTT GGCCTCAAGC CTGCACCCGG AGTTGTACA AGCAGTCAC GTGTATTGTA GTGAAGTCAC GGTGTATTGTA GTGAAGTCAC GGTGTATTGTA GTGAAGTCAC GGTGTATTGTA GTGAAGATGA ATCATCTGGC GGTGTGTGG GGAATTGGGG AGTTCACTGGA TTTGATGAAA TTTTGATGAAA	120 180 240 300 360 420 480 540 660 720 840 900 1020 1140 1220 1380 1440 1560 1560 1560
60 65 70 75	GTTCGGCGC CGAAAGGAGT AAGGCCGCG GAAAGGAGT AAGTCTGAG GTCAGGTGA AAATCGACGG GTAGGTGTT TGAAGGTTT TGAAGGTTT TGAAGGTTT TGACATTGT AGACATGT TAGACATTGT TAGACATTGT TTTTGTAGA AGTCTCCCA CCCTACTCC GTGTGTTTTTAGA CAGCTTAGAG TGTCTCGAC CAGCTTAGAG TGTTTTGGCTA TATTTGGCAA CTAGAGAAGG AGAGTTGAT CTAGAGAAGG AGAGTTGAT TCCAGTTTAT	11	21 GGGAGGCCG GGGCCCAGAT GGTCCGCCAT AGGGCAACT CTTTGTATGA TGATACCACA AGATACTGTA AGATATGAA AATTTGAATT TTGAATGA CCACACTCC TAAGAATACT TAAGAATACT TAAGATACT TAAGATATT ACAGGATACT ACAGTATCC GGTTATGTTT TTTTTTCCTTTT TTTTTTTTTT	AGGGGAGGGGAGGGGAGGGGAGGGGAGTGCAGAGGGGAGTGCAGGGGAGGGGGAGGGGGAGGGGAGGGGGGAGGGGGGAGGGG	CTGGGGCTGT CGTGAGAGCT AAAGCATGG AACGAGGATG CGACACTGTI CTTCGGATCAC ATGGCTC ATGAGTCAC AGCCTATATA ACTTCAGTCC CTGATCAGAC GGCTTACATG GTATAATTTC TCTATATTTCTGGTCAT TCACATGCAC AGCCTACATA TTCTGGTCAT ATCTCAAACTCCT AGGGGACAGT TCACATGCAA ATACTAAATT CACATGCAA ATACTAAATT CACATGCAA AGGGGACAGT AGGGGACAGT TTGACTGAAA CATTTTAAAT ATCCGAGAAA ATCCGAGAAA ATCCGAGAAA CATTTTAAAT TTGTATAATT TTGTATAATT TTGATCGAAA ATCCGAGAAA ATCCGAGAAA TTGTATAATT TGTATATAATT TGTTATAATT TGTTATAATT	AGGACTAGAA GGTGGTTGGC AACTGATCOG GACTCAGACA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG TTGAAGTACT TAGAGTCCT AACTCATGAG TTAGAGTCCT AACTCATGAT CTCAAGCAAA CTAACTATTA TTTTGGTTTT CGCCTCAAGC AGTTGTTACA GTGAAGATCA CTGAAGATCAC GTGAAGATCAC GTGTATTGTAC ATCATCTGGC GAAATTCGGC GAAATTCGGC AGTTCACTGAC TTTATGATGAAA TTTTTTCACCA TTTATGATTAC	120 180 240 300 360 480 540 660 720 780 840 900 1020 1140 1200 1260 1320 1440 1500 1620 1620
60 65 70 75 80	GTTCGGCGCC CGAAAGGAGT AAGGCTGCAA AGTCTCGAT AGTTCTGAT AGTTCTGAT GTCAGGTGGA AAATCGAAGC ATGGGAAATAT GGAGTGGTT TGAAGGTTGT TGAAGGTTGT CTCTCTTGT AGGACATTGT AGGACATTGT AGGACATTGT AGGACTTTGGAA AGTCCTCCCA CCCTACTCC GTGTTTTTTAGA CTCTCTGTAGA CTCTCTGAGAC CCCTACTCC CTGTGTTTTT TGGCTGGAC CAAGCTAGAC CTAGAGAAGG AGAGTTGAT CCTAGAGAAGG AGAGTTGATT TCCCAGTTTAT TCCCAGTTTAT TCCCAGTTTAT TCCCAGTTTAT TCCCAGTTTAT TCCCAAGTTTAT TCCAAGTTTAT TCCAAGTTAT TCCAAT TCCAAT TCCAAT TCCAAT TCCAAT TCCAAT TCCAAT TCCAAT TC	11	21 GGGGAGGCCG GAGCCCAGAT GGTCGCCCT AAGGGCAACT CTTTGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC CATACCTGTA TGCCAAATGC CCACCCC CTCGATGGAA CATGCCCGA CCACCCC CTAGGAATACT TTGTACACTA TTGTACACTA TTGTACACTA TAGATCTTCC TCAAGTGTT AAGCTGTATC TAGATCCTGT TAGATCCTGT TAGATCTTTCCC CTGAGATACA TATATTATA ACATGGATTT ACCAGTATCA AGTTTTCCCT TTCTTTTTTTTTT	AGGCAGAGGC ACCATTTGG GTTCTGCGAA GCCTGCCTTC ACCAAAACCAG TATCAAATTT TGACGCTTG ATTACAATTT TGCTACTTAT ACCACCAAAA TGATGAGGC ATGTCAGCTCCA CTTCACTCCA CCAAGCTGGTC GAGATCACAG TATATAATCAC TACATTTAAA ACTACTTGTAC TCACATTTCAAA TGTTTAATCAC TCACATTTCAAA TGTTTAATCAC TCACATTTCAAA TGTTTAATCAC TCACATTTCAAA TGTTTTAATCAC TCACATTTCAAA TGTTTTAATCAC TCACATTTCAAA TGTTTAATCAC TCACATTTCAAA TCTCACACC TCACATTTCAAA TCTCACACC TCACATTTCCAC TCACTTTCCACAC TCACATTTCCAC TCACATTTCCAC TCACATTTCCAC TCACATTTCCAC TCACATTCCAC TCACATTCCA	CTGGGGCTGT CGTGAGAGCT AAAGCATGG AACGAGATGT CTCGGATCAG ATGGGTCA ATGGGTCA ATGGGTCA ATGGTCAC ATGGTTAATTT CTTTTTTTGT CTCTTTTTTTGT CTTTTTTTTG CTCTATTTTTTT CTTTTTTTTT CTTTTTTTTT CTTTTTTTT	AGGACTAGAA GGTGGTTGGC AACTGATCOG GACTCAGACA ATCAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAGAGAA TTGAAGTCCT AACTCATGGA TTAGAAGTCCT AACTCATGGA CTAACACATGA CTAACACATGA CTAACACATGA CTAACACATGA CTAACACTATA TTTTGGTTTT GGCCTCAAGC CTGCACCCGG AGTGTTACCA GTGAAGATGA ATCATCTGG GCTGGTGTGG GCTGGTGTGG AGTCACATGA TTTTGTGTTTT TTTTTTTTTT	120 180 240 300 360 420 480 540 660 720 780 900 900 1020 1140 1260 1320 1380 1440 1560 1560 1620 1680 1740
60 65 70 75	GTTCGGCGC CGAAAGGAGT AAGGCCGCG GAAAGGAGT AAGTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT GAGTTTT TGAAGGTTT TGAAGGTTTA TAGACATTG CTCCTCTGTA TAGACATGC TTTTTTTTG TTTTTTTTG TTTTTTTTTT	11	21 GGGAGGCCG GAGCCCAGAT GGTCCGCCAT AAGGCCAACT CTTTGTATCAC CATACCTGTA TGCCAAATGC AAGATATCTA AGGATATGAA AATTTGAACT TCCGATGGAA CCACCACTCC TAAGAATACT TAGTCACT TAGACATGC CTAAGATACT TAGACATGC TAGACATGC TAGACATGC TAGACATGC TAGACATCC TAGACATCC TAGACATCC TAGACATCC TAGACATCC TAGACATCC TAGACATCC TAGACATCC TAGACTTT TAGATCCT TTTTTTTTTT	AGGCAGAGG AGGCAGAGGC AGGCATTTGG GTTCTGCGAA GCCTGCTTTC ACAAAACCAG TATCAAATT TGCTACTTAT ACCACCAAAA TGATGATGGGG GGCACTTCCA CTCTACTCCC CTCTACTCCC CAAGATACACAG TGTAATCACA TGTAATCACA TGTAATCACA TGTAATCACA TGTAATCACA GTTTAATCACA TGTAATCACA TCCACTTTGCA GTTAATCACA TCCACTTTGCA GTTAATCACA TTCACTTTGCA TCCACTTTGCA CTCTAGAAGA TCCTTTTGCA CTCTAGAAG CTTTTGTTTTT TGGGTTTTGC CTTCTAGAAG CTTTTTGTTTT TGGGTTTTGC CTTCTAGAAG CTTTTTTTTTT	CTGGCGCTGT CGTGAGAGCT AAAGCCATGG AACGAGGATG CGACACTGTT CTTCGGATCA AGCCTATATA ACTTCAGTCC CTGATCAGAC GGCTTCAGTC CTGATCAGAC GGCTTCAGTC CTCTTTGATT CTTTTTTTGC TCAAACTCCT CGCTGAGCCA GCATTCTAAT TCTGGTCAT TCACATGCAA ATACTACTT CACATGCAA ATACTATTT CACATGCAA ATACTATTT CACATGCAA ATACTATTT CACATGCAA ATACTATTT CACATGCAA ATACTATTT CACATGCAA ATACTATTTAAAT CACATGGAA CACTGGAA CACGGGAACAGGAA CTGATTTAAAT CTTTTTTCG GCAGGGAAG TGTTATAAT CGCAGGGAAG CGCAGTGGCG CGCAGTGGCCG CGCAGTGGCCA CGCAGGGAAG CGCAGTGCAA CGCAGGGAAG CGCAGTGGCCG CGCAGTGCCA CGCAGGGAAG CGCAGTGCGCG CGCAGTGCCG CGCAGTGCCG CGCAGTGCGCG CGCAGTGCGCG CGCAGTGGCGCG CGCAGTGCGCGCG CGCAGTGCGCGCG CGCAGTGCGCGCG CGCAGTGCGCGCG CGCAGTGCGCGCGCG CGCAGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC	AGGACTAGAA GGTGGTTGGC AACTGATCCG GACTCAGACA ATCAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGACA TTGGAGTCCG TATTAAAAA AAGGAGTCCT AACTCATGGA TTAGAAGTCCT AACTCATGGA TTAGAAGTCT CTAACTATTA TTTTGGTTTT GGCCTCAAGC CTGCACCCGG AGTTGTTACA AGGAGTCAC GTGTATTGTA GTCATGGG TTATTGTTTTCGTTTTT GGCCTCAAGC TTGCTGTGTGG AGTTGTTACA ATCATCTGGC GGTGTGTGGG GAAATTGGGG AGTCACATGA TTTGATGAAA TTTTTCCCA TTTAAGCTTTA TTGATGAAA TTTTTCCCA TTTAAGCTTTA	120 180 240 300 360 420 480 540 660 720 840 900 900 1020 1140 1200 1320 1380 1440 1500 1560 1680 1740 1860
60 65 70 75 80	GTTCGGCGCC CGAAAGGAGT AAGGCCGCAG AAGGCCGCAA AAGTCCAGG GTCAGGTGGA AAATCCACGC ATGGGAATAT GGAGTGGTT TGAAGGTTTT TGAAGGTTT CTACTCCAC CCCTACTCC GTGTGTTTTTTGAGA TGTTTGGAG TGTCTCCAA CCAGTTGAG TGTTTGTAGA AGTCCTCCA CCCTACTCC GTGTTTTTTTGGCTGAC CAGCTTAGAG TGGTCTTCTACA CTAGAGAAGG AGAGTTGAT CTAGAGAAGG AGAGTTGAT TCCAAGTTAT TCCCAAGTTTAT TCCCAAGAT TTTTTTTTTT	11	21 GGGAGGCCG GAGCCCAGAT GGTCGCCCT AAGGGCAACT CTTTGTATGA TGATACCAGA AGATCTCT AGGATACGA AAAGATCTCT AGGATACGAC CCACCACTCC TAAGAATACT TTGAAGTAT CCACACTCC TAAGAATACT TAAGATACT TAAACATGT TAAACATGT TAAACATGT TAAACATGT TAGATTCC TAAGATATA ACTGTTTCCCT TTGTTCCCT TTTTTTTTTT	AGGCAGGGC ACCATTTGG ACCAACTTTGG GTTCTGCGAA GCCTGCCTTC ACCAACACACACACACACACACACACACACACAC	CTGGGGCTGT CGTGAGAGCT AAAGCATGG AACGAGGATG CGACACTGT CTCGGATCAC ATGGCTC ATGAGTCAC AGCCTATATA ACTTCAGTCC CTGATCAGAC GGCTTAAATTC CTTAAATTC CTCATCAGAC GCATTCCTAC GCATCCTAC AGCCTACAGC AGCCTACAGC AGCCTACAGC AGCCTACAGC AGCCTACAGC AGCGGACAGC TCAAACTCCT AGCGGACAGCAG ATCCTACAATCCAA ATCCTAAATTC CACCATGCAA CATTTAAAT ATCTGATCAAT ATCCGGGAAAT CACTGGAA CATTTAAAT TTGTATAATT GTTTTTCGG GCAGTGGCG GCAGTGCGCG CATTTTAAAT TTGTATAATT TTTTTTCGG CAGTGGCG CAGTGCGCG CAGTGCCG CAGTGCCG CAGTGCCG CAGTGCCG CAGTGCCG CAGTGCCG CAGTGCCG CTCTCACAC CAGCAGCAGC CAGTGCCG CTCTCACAC	AGGACTAGAA GGTGGTTGGC AACTGATCOG GACTCAGACA ATCAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAGAGAA TTGAAGTCCT AACTCATGGA TTAGAAGTCCT AACTCATGGA CTAACACATGA CTAACACATGA CTAACACATGA CTAACACATGA CTAACACTATA TTTTGGTTTT GGCCTCAAGC CTGCACCCGG AGTGTTACCA GTGAAGATGA ATCATCTGG GCTGGTGTGG GCTGGTGTGG AGTCACATGA TTTTGTGTTTT TTTTTTTTTT	120 180 240 300 360 480 540 660 720 780 840 900 1020 1180 11200 1260 1380 1440 1560 1620 1680 1740 1860 1860 1860

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10	CA CARCALO CACO	CVALLACTAC	TENGATTE	TTTGGCTATG	TTAAGTCCTT	TGCTTTTGAT	2580
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15	COCACCOCAC	ATCACACCAC	TGTACTCCAG	CCTGGGTGAC	AAAGTGAGAC	TCTATCTCAA	2880
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45	ACTTCTCGAG	CACATCAAAG	CTTTGTATGA	ACAAAACCAG	TCTGATGTGA	ATGAAGCAAA	300
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          TIKPRHOSLL RNRRCTVAYL YDRLLRIRAL RWEYGSVLPN ALRFHMAAEE MEWFNNYKRS
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          TITCTAATAA TICTTGAAAC AGATAGTATT AATGTGTCAT ATTITTGCTG TIGTTTGTAT
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          ANANCTOCOT CTCTACANAN ANTAGANAN ATTAGCCAGG TGTGGTGGTG CATGCCTGTA
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          AAAAAGAAAT TAGGATCAAT TTGTCAATTT CTACAACAAC AACAACAAAA ACCCCTGTTG
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Seq ID NO: 162 Protein sequence: Protein Accession #: AAA68877.1

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	as ammoon mo	CACACCACCA	ል ልርሮል ልርሮ <b>ል</b> ቸ	GAATTTTTGA	CAGATGGCTA	TCAAGACTIG	1260
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	TTTGCTACAC	CTGTTTTATC	AATTGATGAA	CCATTAAATA	CACTAATAAA	TAAGCTTATA	4140
	01 MM C 0 C 1 MC	A A A CHEMINA A C	CTCCACCAAA	A CITE CITY TO THE	CTCCTAAGGT	ATTIGCIGGI	4200
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65	CCCCATCTTC	CCATTACAGC	TGTTTCTCCC	CACAGAGATG	GITCIGIAAC	CICAACAAAG	4320
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	<b>ምጥ እ ሮጥርርርርጥር</b>	CTCCTCAACA	TGGTGACACT	GATGATGATG	GTGATGATGA	TGATGATGAC	4440
	ACACCTACTC	ስጥርርርርምምልጥር	<b>САТТСАТАА</b> Б	TGTATGTCAT	GCTCATCCTA	TAGAGAATCA	4500
	CACCAAAACC	TAATGAATGA	TTCAGACACC	CACGAAAACA	GTCTTATGGA	TCAGAATAAT	4560
70	<b>ማርስ አጥርጥር ልጥ</b>	ACTCACTATC	TOAGAATTCT	GAAGAAGATA	ATAGAGTCAC	AAGTGTATCC	4640
, 0	TONGROUP CACTO	AAACTCCTAT	GCACAGAAGT	CCTGGTAAAT	CACCATCAGC	AAATGGGCTA	4680
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	GGATTCCCAC	AGTICCCCAAC	ATCATCTGTT	ACTAGCGAGA	WCICHOWNG!	GTTCCACGTT	5040
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	CAGAGCTGTA	CTGTTGACTT	' AGGTATTACA	GCAGACAGCT	CCAACCACCC	AGACAACAAG	5400
	CACAACAATC	CATACATAAA	TATYCTTCC	* ተልጥሮልጥሮ <b>ል</b> ፕል	GCAGGGTTAA	GCTAGCACAG	5460
85	CALCALCO DO	ACCATICATA	ACTENCTION	ን የልተልተር ል እንር	CCAATTATGT	TGATGGCTAC	5520
	AACAGACCAA	AAGCTTATAT	TO THE PARTY OF TH	. GGCCCACTGA	AATCCACAGC	TGAAGATTIC	2260
	יייייייייייייייייייייייייייייייייייייי	TATCCCARCE	TAATETYSEA	GTTATTGTCA	TGATAACAAA	CCTCGTGGAG	5640
	TOURDANTON						

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85
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Seq ID NO: 181 DNA sequence Nucleic Acid Accession #: Eos sequence

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	ACACAAAAAG	Vale Automotive to W	GACTTCTCAG	ACTGTGACTG	AACTGCCACC	TCACACTGTG	1740
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TCTAGAAGGC TGTCTAACAT ACCACATGAT TACATGAACT GTATGGTATC CATCTATCTC
                                                                                                         2280
                                                                                                         2340
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CATGTCTGTA TTTCAGGAGC AAACTCTTCA GGCTCCTTTT TATAAACTG GTGATTTTTC
                                                                                                         2460
                                                                                                         2520
65
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                                                                                                         2700
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70
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                                                                                                         3120
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                                                                                                         3180
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                                                                                                         3360
                                                                                                         3420
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                                                                                                         3480
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                                                                                                         3540
                                                                                                         3600
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85
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                                                                                                         3840
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5			ACACACATCA				4200
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20	CTTTCCAGGC	TGAGGGAAAT	TTTCTGAGAT	ICCMMAGIAN	CATTTAAAA	AAACTACTCT	5160
			TTTNTTTTAG				5220
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			TCCTGTGGCC				5460
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• •	CCTCCTTCTC	CTCCACAGTC	ACAAGTAACC	AAGGAACCTG	AAAGTGGATG	TGTAGCTATT	5640
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			CTCCCAAGTG				6180
			CCATCTATCC				6240
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10			CGTCCTGCCT				6360
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			CACCATGTTG				6660
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			ATCCCTTGGT				6780 6840
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50			GTAAGGCAAA				6960
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			AAACATCCAT				7140
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			TCAGAAGTAT				7320
			TTOGTAATCC				7380
<b>C</b> 0			GTCTTTGCCT				7440
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			TGCAATATAA GGGGGTGGGG				7620 7680
			CTTGTTTGGG				7740
65			GATTTAAATG				7800
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			TGTTAATTTA				7980
			ATGGCATGCC				8040
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			AGAAAATGTT				8280
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			TATTGGCCAT				8760
			CAGTAGGTAG				8820
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			GTGATTCAAA				9060
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         Seq ID NO: 214 Protein sequence:
Protein Accession #: NP_000546
10
                       11
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15
                                                                                                    120
         LVTIIRSGVK PRKAVRVLLN KKTAHSFEQV LTDITEAIKL ETGVVKKLYT LDGKQVTCLH
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MRRSKSFADS ANGTSSSQLS TPKSKQSPIS TPTSPGSLRK HKDLYLPLSL DDSDSLGDSM
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         Coding sequence: 312..644
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         Protein Accession #: NP_569734
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Coding sequence: 82..435
55
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                                                                                                      60
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                                                                                                    120
                                                                                                    180
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85
                                                                                                    300
         GCTTTTACCG GCACAGAGAA AGGGACCGCT GTTTGCCCTG CAATTGTAAC TCCAAAGGTT
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		/086443					
	CTCTTAGTGC	TCGATGTGAC	AACTCTGGAC	GGTGCAGCTG	TAAACCAGGT	GTGACAGGAG	420
	CONCATOCON	COGATGTCTG	CCAGGCTTCC	ACATGCTCAC	GGATGCGGG	TGCACCCAAG	480
	ACCAGAGACT	CCTAGACTCC	AAGTGTGACT	GTGACCCAGC	TGGCATCGCA	GGGCCCTGTG	540
	MACAGAGAGA	CHESTERCHEC	PACICACICAL	TTACTGGAGA	ACCCTGTGAT	AGGTGTCGAT	600
5	CACCEPIACE	TARRESTEAT	GGGGGGAACC	CTGAGGGCTG	TACCCAGTGT	TTCTGCTATG	660
-	CCCN TTCNCC	CACCTCCCCC	ACCOMPACAG	AATACAGTGT	CCATAAGATC	ACCTCTACCT	720
	TTCATCAAGA	TOTTGATGGC	TGGAAGGCTG	TCCAACGAAA	TGGGTCTCCT	GCAAAGCTCC	780
	ANTICCTCACA	CCCCCATCAA	CATCTCTTTA	GCTCAGCCCA	ACGACTAGAC	CCTGTCTATT	840
	THE PROPERTY OF THE PROPERTY O	ጥርርር እል ልጥተተ	CTTGGGAATC	AACAGGTGAG	CTATGGGCAA	AGCCTGTCCT	900
10	THE ROTTO COC	TOTOGACAGA	CCACCCAGAC	ACCCATCTGC	CCATGATGTG	ATTCTGGAAG	960
10	CALCACCACA	ACCCATCACA	GCTCCCTTGA	TGCCACTTGG	CAAGACACTG	CCTTGTGGGC	1020
	TORCOR ACRO	THERMONER	PTAAATTO	AGCATCCAAG	CAATAATTGG	AGCCCCCCAGC	1080
	THE RESERVE OF THE PROPERTY OF	TONGTATOTA	ACCUPATED CITCO	GGAATCTCAC	AGCCCTCCGC	ATCCGAGCTA	1140
	CT TT T	ATACACTACT	CCCTACATTG	ACAATGTGAC	CCTGATTTCA	GCCCGCCCTG	1200
15		COCACCA CCC	TOCOTTODAC	AGTGTATATG	TCCTGTTGGG	TACAAGGGGC	1260
13	**********	CCATTCTCCT	TOTACA	AGAGAGATTC	AGCGAGACTG	GGGCCTTTTG	1320
	CCA CONTOURA TO	TOTTOTALO	TETCARGGGG	GAGGGGCCTG	TGATCCAGAC	ACAGGAGATT	1380
	CORRES OF THE CALCE	CCATCACAAT	CCTGACATTG	AGTGTGCTGA	CTGCCCAATT	GGTTTCTACA	1440
	A COLATOCOCO	CONCOUNT	ACCTGCAAGC	CATGTCCCTG	TCATAACGGG	TTCAGCTGCT	1500
20	CACTCATCCC	CCACACCCAC	CACCITICATION	GCAATAACTG	CCCTCCCGGG	GTCACCGGTG	1560
20	W. Charles and the second	CONCRETE	CATGGCTACT	TTGGGGACCC	CTTTGGTGAA	CATGGCCCAG	1620
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0.5	Protein Ac	cession #:N	P_005553				
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Coding sequence: 126-752

PCT/US02/12476

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15	THE CACCATICAL	CALCALVALCALC	CCCTCAGAAT	GAGAGAGTCA	AGCTGGGCAG	AATCTCTCGC	780
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	WITH CITY CITY	CCACATTTTC	CATTGCATAC	TGGAAAAGAA	GCCAATCTTC	TIGCIAGIAA	960
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	TYTE CTATTA	<b>プ</b> ザプアムなですで	AGGAAAAACA	AGAAATTAAC	CCAGAGAGAG	TCTGGGTTTT	1200
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	MKDIDIGKEY	İIPSPGYRSV	RERTSTSGTH	RDREDSKFRR	TRPLECQDAL	ETAARAEGLS	60
	LDASMHSQLR	ILDEEHPKGK EDVWSLSKHE	YHHGLSALKP	PLWOEELNEV	ODNAGLESCM GPDAASLERV	TFSWLSSDAR VWIFCRTRLI	120 180
		LAGFSGPNFQ		KUNQLILLI	<b>C. D. D. C.</b>		
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		233 DNA sed id Accession		ster			
	_			21	41	51	•
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           Protein Accession #: Eos sequence
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	GAGCAACCTC CGACCCAGAG GCGGGGCCCA ACCTGCCACC GCTGTTGGGC	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG	ATCCAGACTC GGCGGCGCAG GGAGTCCGGG CGCGGGCGCC CCTTCCTGGG	CAGCGCCGCC CGAGCAGGC TTGCCCACCT CGAGCGAGTC	CCGGGCGCGG TCCCCGCCTT GCAAACTCTC ATGGCCAACG GCCATCGTCA	ACCCCAACCC AACTTCCTCC CGCCTTCTGC CGGGGCTGCA GCACTGCCCT	120 180
	GAGCAACCTC CGACCCAGAG GCGGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCAGTGG CGAGGGGCTG	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG TTCATTCTCG AGGATTTACT TGGATGTCCT	ATCAGACTC GGCGCGCAG GGAGTCCGGG CGCGGGCGCC CCTTCCTGGG CCTATGCCGG GCGTGTCGCA	CAGCGCCGCC CGAGCAGGGC TTGCCCACCT CGAGCGAGTC ATGGATCGGC CGACAACATC GAGCACCGGG	CCGGGCGCGG TCCCCGCCTT GCAAACTCTC ATGGCCAACG GCCATCGTCA GTGACCGCCC CAGATCCAGT	ACCCCAACCC AACTTCCTCC CGCCTTCTGC CGGGGTGCA GCACTGCCCT AGGCCATGTA GCAAAGTCTT	120 180 240 300 360 420
50	GAGCAACCTC CGACCCAGAG GCGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCAGTGG CGAGGGGCTT TGACTCCTTG CATCCTCTTG	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG TTCATTCTCG AGGATTTACT TCGATGTCCT CGGATGTATAG GGAGTGATTAG	ATCCAGACTC GGCGGCGCAG GGAGTCCGGG CGCGGGGCC CCTTCCTGGG CCTATGCGG GCAGTATCGCA GCAGCACATT CAATCTTTGT	CAGGGCGCC CGAGCAGGG TTGCCCACT CGAGGAGTC ATGGATCGGC CGACAACATC GACACCGGG GCAAGCAACC GGCACCGTT	CCGGGGGGGGGGGTCCCCGCCTTGCAAACTCTCATGGCCAACGGCCCCCAGATCCAGTCAGT	ACCCCAACCC AACTTCTCC CGCCTTCTGC CGGGGCTGCA GCACTGCCT AGGCCATGTA GCAAAGTCTT TGGTGGTTGG GTATGAACTG	120 180 240 300 360
	GAGCAACCTC CGACCCAGAG GCGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCAGTGG CGAGGGGCTG TGACTCCTTG CATCCTCCTG CTTGGAAGAC	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG TTCATTCTCG AGGATTTACT TGGATGTCCT CTGAATCTGA GGAGTGATAG GATGATAG	ATCCAGACTC GGCGGCGCCAG GGAGTCCGGG CCCTTCCTGGG CCTATGCCGG GCAGCACATT CAATCTTTGT AGAAGATGAG	CAGGGCCGCC CGAGCAGGGC TTGCCCACCT CGAGGGAGTC ATGGATCGGC CGACAACATC GAGCACCGGG GCAAGCAACC GGCCACCGTT GATGGCTGTC	CCGGGCGCGG TCCCCGCCTT GCAAACTCTC ATGGCCAACG GCCATCGTCA GTGACCGCCC CAGATCCAGT CGTGCCTTGA GGCATGAAGT ATTGGGGGTG	ACCCCAACCC AACTTCCTCC CGCCTTCTGC CGGGGCTGCA AGCCATGCCCT AGGCCATGTA GCAAAGTCTT TGGTGGTTGG GTATGAAGTG CGATATTTCT	120 180 240 300 360 420 480 540 600
50	GAGCAACCTC CGACCCAGAG GCGGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCAGTGG CGAGGGGTTG TGACTCCTTG CATCCTCTTG CTTTGCAGGT TTTTTCAGGT ATTCTATGAC	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG TTCATTCTCG AGGATTTACT TGGATGTCCT TGGATGTCAT GGATGATAGG GATGAGGTGC CTGGCTATTT CCTATGACCC	ATCCAGACTC GGCGGCSCAG GGAGTCCGGG CCCTTCCTGGG CCTATGCCGG GCGTGTCGCA GCAGCACATT CAATCTTTGT AGAAGATGAG TAGTTGCCAC CAGTCAATGC	CAGCGCCGCC CGAGCAGGGC TTGCCCACCT CGAGCGAGTC CGACAACATC GGACAACATC GACAACATC GGCACCGGT GATGGCTGT GATGGTAT CAGTACGAA	CCGGGCGGG TCCCCGCTT TCCCCGCCTT GCAAACTCTC ATGGCCAACG GCCATCGTCA GTGACCGCCC CAGATCCAGT CGTGCCTTGA GCCATGAAGT ATTGGGGTG GCCATAGAA TTTGGTCAGG	ACCCCAACCC AACTTCCTCC CGCCTTCTCC CGCGTTCTCC CGCGCTCCA CGCATGTA CCAAAGTCTT TCGTTCGTTCGTTCGTTCGTTCGTTCGTTCTTCCC CGTTCAACGA CTCTCTTCAC	120 180 240 300 360 420 480 540 600 660 720
50 55	GAGGAACCTC GAGCGAGGGCCCA ACCTGCCACC GCTGTGCACC GCCCCAGTGG CCACCTCCTGCACC CATCCTCCTC CTTGGAACAC TCTTGCAGGT ATTCTATGAC	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG GCTAGCCAG TTCATTCTCG AGGATTTACT TGGATGTCCT CTGAATCTCA GAGTGTAG GATGAGGTGC CTGGCTATTT CTGGTTTCTCG CTGGCTATTT CTGGTTCTC	ATCCAGACTC GCGCGCCAG GGAGTCCGGG GCAGTCCTGGG CCTTATGCCGG CCTATGCCGG CCTATGCCGG CCAGTCCAG CAATCTTTGT AGAAGATGAG TAGTTGCCAC CAGTCAATGC TCTGCCTTCT	CAGGGCCGCC CGAGGAGGGC TTGCCCACCT CGAGGAGTC CGAGGAGTC ATGGATCGGC GCAACATCT GAGCACCGGC GCAAGCAACCT GATGGCTGTC AGCATGGTAT AGCATGGTAT CAGGTACCGAG GGGAGGTGCC	CCGGGCCGGG TCCCGCCTT GCAACTCTC ATGCCAACG GCCATCGTCA GTGACCGCC CAGATCCAGT GGCATGAAGT ATTGGGGTA ATTGGGGTG GGCATGAAGT ATTGGGGTCAGG CTACTTTGCT CTACTTTGCT	ACCCCAACCC AACTTCCTCC GGCTTCTGC GGGGCTGCA GGACTGCCCT AGGCCATGTA GCAAAGTCTT TGGTGGTTGG GTATGAAGTG CGATATTTCT TCGTTCAAGA CTCTCTTCACA GTTCCTGTCCA	120 180 240 300 360 420 480 540 600 720 780
50	GAGCAACCTC GACCCAGAG GCGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCAGTGG GCCCAGTGG GATCCCTG CATCCTCCTG CTTGGAAGAC TCTTCCAGGT TCTTCCAGGT TCTTCAGGT TCTTGCAGGAT TCTTATGAC TGGCTGGGCT CCGAAAAACA TAACAACTAC	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG TTCATTCTCG AGGATTACT TGGATGTCCT CTGAATCTGA GATGAGTGC CTGCATATTT CCTATGACCC GCTGCTTTCC GCTGCTTTACC GTGTGACACA	ATCCAGACTC GGCGGCCCG GGAGTCCGGG CCTATGCCGG CCTATGCCGG CCTATGCCGC GCAGCACATT CAATCTTGT AGAAGATGAG TAGTTGCCAC CAGTCAATGC TCTGCCTTCT CAACAACAAG GAGGCAAAAG	CAGGGCCGCC CGAGGAGGGC TTGCCACT CGAGGAGTC CGAGGAGTC CGACACCGC GGACACACC GGCACCGT GATGGATAC AGGTGTAT CAGGTACCAG GGAGGTTCC GCCTATCCA GGAGAAATCA GGAGAAATCA	CCGGGCGGG TCCCGGCTT TCCCGGCTT GCAACTCTC ATGGCCAACG GCCATCGTCA GTGACCGCC CAGATCCAGT ATTGGGGGTG GGCATGAAGT ATTGGTCAGG CTACTTTGGT AAACCTGCAC TGTTGAAACA	ACCCCAACCC AACTTCCTCC CGCCTTCTCC CGCGTTCTCC CGCGCTCCC AGCCATGTA GCAAAGTCTT TGGTGGTTGG GTATGAAGT CGATATTTCT TCGTTCAAGA CTCTCTTCAC GTTCCTGTCC CTTCCAGCG AACCGAAAT	120 180 240 300 360 420 480 540 600 720 780 840 900
50 55	GAGCAACCTC GAGCGACCCA GCTGCCACC GCTGTCACC GCTGTTGGGC GCCCCAGTGG CATCCTTC CATCCTCCTG CATCGTCACAC TCTTGCAGGA ATTCTATGAC TGGCTGGGCT CCGAAAAACA GAAAGACTAC GGACATTGAGGATTGAGGACTT	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG GCCACCTTCG CCTGAGCCAG TTCATTCTCG AGGATTTACT TGGATGTCCT CTGAATCTGA GATGAGTATAG GATGAGTATT CCTATGACCC GCTGCTTCTC ACCTCTTACC GTGTGACACA ATACTATCATA	ATCCAGACTC GGCGGCCAG GGAGTCCGGG GGAGTCCCGGG CCTATGCCGG CCTATGCCGG CCGTGTCCCA GCAGCACATT AGAAGATGAG TAGTTGCCAG CAGTCAATGC TCTGCCTTCT CAACACAAG GAGCAAAAT TAGAGACAAG TAGTTAGAAG TAGATTAGAAG TAGAACAAAG TAGAACAAAG TAGAACAAAG TAGAAACAAAG TAGAAACAAAG TAGAAACAAAG TAGAAAACAAAG TAGAAAACAAAG TAGAAATTAAG	CAGGGCCGCC CGAGGAGGGC TTGCCCACCT CGAGGAGTC CGAGGACTC CGAGCAACATC CAGCACCGC CCAAGCAACCT GATGCTACT CAGCACCGTT CATGCTACT CAGCACCGTT CAGCATCGTC CAGCACCGTT CAGCATCGTAC CAGCTACCAA CGGAGGTGCC CCCTATCCA ACCTTAGAAT	CCGGGCGGG TGCCGGCTT TGCCGACTT GCAACTCTC ATGGCAACG GCCATCGTCA GTGACCGCC CAGATCCAGT GGCATGAAGT ATTGGGGTG GGCATGAAGT ATTTGGTCAGG CTACTTTGCT AAACCTGCAC TGTTGAAACA TTTTGGGTATT	ACCCCAACCC AACTTCTCC CGCCTTCTCC CGCGTTCTCC CGCGTTCTCC CGCATGTCCT AGGCCATGTA GCAAAGTCTT TCGTGGTTCG GTATGAAGT CTGTTCAAGA CTCTCTTCAC CTTCCTCAC GTTCCAGCGG AACCGAAAAT GTAATCTGAA	120 180 240 300 360 420 480 540 600 720 780 840 900
50 55 60	GAGCAACCTC GACCCAGAG GCGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCCAGTGG GCATCCCTG CATCCTTC CTTGGAAGAC TCTTGCAGGT ATTCTATGAC TGGCTGGGCT CCGAAAAACA GAAAGACTAC GGACATTGAG GTATGGTATT ABACATGGCT	AGCTTCTAGT AGCTTCTAGCAG GCCACCTTCG CCTGAGCAG TTCATTCTCG AGGATTACT TGGATGTCCT CTGAATCTGA GATGAGTGC CTGGCTATTT CCTATGACCC GCTGCTATTC ACCTCTTACC GTGTGACACA ATACTATCAT ACAAAACAAA	ATCCAGACTC GGCGGCGCG GGAGTCCGGG GCCTCCTGGG CCTATGCCGG GCAGTCCGCA GCAGCACATT CAATCTTTGT AGAAGATGAG TAGTTGCCAC TCTGCCTTCT CAACACAACA	CAGGGCCGCC CGAGGAGGGC TTGCCCACCT CGAGGAGTC CGAGGAGTC GGCACACCT GAGGACACC GGCACCGT GATGGCATGC AGCATGGTAT CAGGTACGA GGGAGGTGCC GCCCTATCCA AGCATGTAT ACCTTAGAAT AAAAACCCAT	CCGGGCGGG TCCCGGCTT TCCCGGCTT GCAACTCTC ATGGCCAAG GCCATCGTCA GTGACCGCC CAGATCCAGT GGCATGAAGT ATTGGGGTG GGCATATAGAA TTTGGTCAGG CTACTTTGGT AAACCTGCAC TGTTGAAACA TTTGGTAAT TTTGGTATT AGGAGGAAG	ACCCCAACCC AACTTCTCC CGCGTTCTGC CGCGTTCTGC CGGGGCTGCA GCACTGCCT AGGCCATGTA GCAAAGTCTT TCGTTGGTTGG CGTATGAAGTG CTGTTCAACGA CTCTCTTCAC GTTCCTGCC CTTCCAGCGC AACCGAAAAT GTAATCTGAA ACTCAGTGCT ATTTTACCAT	120 180 240 300 360 480 540 600 720 780 840 900 960 1020 1080
50 55	GAGCAACCTC GGAGCACAGA GCGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCAGTGG GCAGGGCTC TGACTCCTCG CTTGCAGCA TCTTCCAGGT ATTCTATCAC TGGCTGGCT CCGAAAAACA GAAGACTAC GGACATTCAG GGACATTCAG GTATGTGATT AAACATGGCT	AGCTTCTAGT CTTCTCCAGC GCACCTTCG CCTGAGCCAG TTCATTCTCG AGGATTACT TGGATGTCCT TGGATGTCTC TGGATGATAG GATGAGTGC CTGGCTATT CCTATGACCC GCTGCTTACC GCTGCTTACC ACCTCTTACC ATACTACACA ATACTATACAT ACAAAACAAA TAATCTATT	ATCCAGACTC GGCGGCGCG GGAGTCCGGG GGAGTCCGGG CCTTATGCOGG CCTATGCOGG CCTATGCOGG CCAGTCCAG CAGCACATT AGAAGATGAG TAGTTGCAC CAGTCAATGC TCTGCCTTCT CAACACAAG GAGCAAAAG TAGTTATAGG CAAACAACA TAACATTAGG CAAACAACA TAACATTAGC CAACAACAAC TAACATTATGC CAACAACAAC TAACATTATGTTCTT TAGTTATCTT	CAGGGCCGCC CGAGGAGGGC TTGCCCACCT CGAGGAGTGGC ATGGATCGGC GCAACATC GAGCACGG GCAACGTT GATGGCTGT AGCATGGTAT AGCATGGTAT AGCATGGTAT AGCATACGAA GGGAGGTGCC GCCTATCCA AGCATACTACAA AAAACCCAT TCCTCAATAT	CCGGGCGGG TCCCGCCTT TCCCGCCTT TCCAACTCTCA ATGGCAACG GCCATCGTCA GTGACCCCC AGATCCAGT GTGACTCAGT ATTGGGGTG GCAATAGAA ATTGGTCAGG CTACTTTGCT AAACTGCAC TGTTGAAACA AGGGGTAT GGGAAGGGAT GGGAAGGGAA	ACCCCAACCC AACTTCTCC CGCCTTCTCC CGCGTTCTCC CGCGTGCCCT AGGCCATGTA CCAAAGTCTT TGGTGGTTCG GTATGAAGT CTGTTCAAGA CTTCCTTCAC CTTCCAGCG AACCGAAAAT GTAATCTGA ACTCAGTGCT ATTTACCAACA ACTCAGTGCT ATTTTACCAACA ACTCAGTGCT ATTTTACCAACA ACTCAGTGCT ATTTTACCAACA ACTCAGTGCT ATTTTACCAACA ACTCAGTGCT ATTTTACCAAAA	120 180 240 300 360 420 480 540 600 660 720 960 1020 1080 1140
50 55 60	GAGCAACCTC GACCCAGAG GCGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCAGTGG GCCCAGTGG GATCCTCG CATCCTCCTG CATCCTCCTG CATCTCCAGG ATTCTATGAG TATTCTATGAG GAAAACAC GGAAAACAC GAAAGACTAC GGACATTGGA GTATGGTATT AAACATGGCT TTGTATTACT TATATATACT TATATATAGAG CTCATTATGAT	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG TTCATTCTCG AGGATTACT TGGATGTCTA GGATGATAG GATGAGTGC CTGGATCTATT CCTATGACCC GCTGCTCTTACC GTTGTACACC GTTGTACACA ATACTATCAT ACAAAACAAA	ATCCAGACTC GGCGGCCCG GGAGTCCGGG GCCCTCTCTGGG CCTATGCCGG CCTATGCCGC GCAGCACATT AGAAGATGAG TAGTTGCAC CAGTCAATGC CAACAACAA TAACATACG CAACAACAACAA TAACTTCTT GAGTAATCAT TACATTCTTT GAGTAATCAT TACATTCTTT TACATTATAA	CAGGGCCGCC CGAGGAGGGC TTGCCCACCT CGAGGAGTC CGAGGAGTC CGACACCGC CGACACCTC GACACCGC GCACACCGT GATGGTAT CAGGTACCAC GGCACCGTT CAGGTATC CAGCTACCAA CCTTACCAA ACCTTAGAAT AAAAACCCAT TCCTCAAATAG CTCAAATAG TCTATAAAAT ATATCTCTAAA	CCGGGCGGG CCAAACTCTC ATGGCAAAG GCCATCGTCA GTGACCGCCC CAGATCCAGT GTGACCGCCC CAGATCCAGT ATTGGGGGTG GCCAATAGAA TTTGGTCAGG CTACTTTGCT AAACCTGCAC TGTTGAAACA TTTGGGTATT GTGTTAAAAT ATGGGGAAG GGGAAGGGAAG	ACCCCAACCC AACTTCCTCC CGCCTTCTCC CGCCTTCTCC CGCGCTCCC AGCCATGTA GCAAAGTCTT TCGTTCGTTCGTCCAACG CTTCCTCCACC CTTCCACCC CTTCCACCC CTTCCACCC ACCCAAAAT GTAATCTGAA ACTCAGTGCT ATTTTACCAT GCTCCTTAAA AAAATACTATT GTATTTAATT GTATTTAATT	120 180 240 360 420 480 540 660 720 780 840 960 1020 1080 1140 1200 1260
50 55 60	GAGCAACCTC GACCCAGAG GCGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCCAGTGG GATCCCTTG CATCCTTCCTG CATCGTCCTG CATCGTCCTG CATCGTCCTG CATCGTCCTG CATCATAGAC TGGCTGGCT CGAAAAACA GAAAGACTAC GGACATTGAG TATGTATT TATATATACA TTGTATTATAC TATATATACA CCCATATTGTA	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG TTCATTCTCG AGGATTACT TGGATGTCCT CTGAATCTGA GAGTGTATT GCATGTATACT GCTGCATTTCTC GCTGTATACT GCTGCTATTT ACCTATTCTC ACCTCTTACC GCTGCTACACA ATACTATCAT ACAAACAAA TAATCTATT TATGATATA TGATATATA TGATATATA TGATATATA TGAACTAGT GAAGAGTTT	ATCCAGACTC GGCGGCGCG GGAGTCCGGG GCAGTCCTGGG CCTATGCCGG GCAGCACTT CAATCTTTGT AGAAGATGAG TAGTTGCCAC CAGTCAATCC TCTGCCTTCT CAACACAATG TAACATACAG TAACATACAG TAACATACAG TAACATACAA ATTGCTTTAAAAAATTGCTATTAAAAAAAAAA	CAGGGCCGCC CGAGGAGGGC TTGCCCACCT CGAGGAGTCGC CGAGCAACATC GAGCACGGC GCACACCGT GATGGCACGGC GCACGGTACGCA GGGCACCGTT GATGGCTGTC GATGGTATCACA GGGAGAAATC GAGGAAATCA ACCTTAGAAT AAAAACCCAT TCCTCAATAT ACTCAAATAG TCTATTAAAA TATCTCTAAAA TATCTCTAAAA	CCGGGCGGG TCCCGGCTT TCCCGCCTT GCAACTCTC ATGGCCAAG GCCATCGTCA GTGACCGCC CAGATCCAGT CGTGCCTTGA ATTGGGGTG GGCATGAAGT ATTGGTCAGG CTACTTTGCT AAACCTGCAC TGTTGAACA TTTGGGTATT GTGTTAAAAT ATGGGGAAG GGGAGGGGAG GGGAGGGGAG ATAGACAGTA ATAGGTAAAT GTGCTTAATAT	ACCCCAACCC AACTTCTCC CGCGTTCTCC CGCGTTCTCC CGCGTGCATGTA GCAAAGTCTT TCGTGGTTCGG GTATGAAGTG CGATATTTCT TCGTTCAAC GTTCCTTCAC GTTCCTTCAC GTTCCTGCC CTTCCAGCGG AACCGAAAAT GTAATCGAA ACTCAGTGCT GCTCCTTAAA AAATACTATT GTATTTAACTATT ACATATGTAA	120 180 240 300 360 420 480 540 600 720 840 900 900 1080 1140 1200 1260 1320
50 55 60	GAGCAACCTC CGACCCAGAG GCGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCAGTGG GCCCAGTGG GCCCAGTGG GCCCAGTGG GCCCCAGTGG CATCCTCCTG CATCCTCCTG CATCCTCTG CATCCTCTG ATCTTCAGG ATTCTATGAC GAAAAACA GAAAAACTAC GGACATTGG GTATGGTATTACT TATATATAGA TATATATAGA CTCATTATGT CCATATTGT CCATATTGGT CATTATTATG CATCAATTAGAT CAGTCAATTA	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG TTCATTCTCG AGGATTACT TGGATGTCGT CTGAATCTGA GGAGTGATAG GGAGTGATAT CCTAGAGCAGT CTGGATTATCT CCTATGACCC GCTGCTTCTC ACCTCTTACC GCTGTGACACA ATACTATCAT ACAAAACAAA	ATCCAGACTC GGCGGCGCG GGAGTCCGGG GCAGTCCGGG CCTATGCCGG CCTATGCCGG CCTATGCCGG CCAATCTTGT AGAAGATGAG TAGTTCCCAC CAGTCAATGC TCACCACAG GAGCAAAAG TAACATTAC CAACAACAA TAACATTACG TACATACTTTT TACATGTTTT TACATGTTTT TTCTTTCATTA	CAGGGCCCCC CGAGGAGGCC TTGCCCACCT CGAGGAGGTC CGAGGAGTC CGACACCGC CGACACCTC CAGCACCGGC CGACACCTC CAGCACCGGC CGACACCTC CAGCACCGTC CAGCACCGTC CAGCACCGTC CAGCACCGTC CAGCACCGTACCA CACCTTACCAA CCTTTCAATAT ACTCAATAT ACTCAATATAAAA TTTCTTTTCC CTTCATGCTT CCTTCATCCTAACCCTTTCCCTACCCTTCCCTACCCTCCT	CCGGGCGGGGGGGGGAAACTCTC GCAAACTCTC GCAAACTCTC GCAAACTCTC GTGACCGCCC CAGATCCAGT GTGACCGCCC CAGATCCAGT ATTGGGGGTG GGCAATAGAA TTTGGTCAGG CTACTTTGGT TTGGTAAAC TTTGGGTATT AGGAGGGAAG GGGAAGGGGT ATAGGAAGGA	ACCCCAACCC AACTTCCTCC CGCCTTCTCC CGCCTTCTCC CGCCTTCTCC CGCCATGTA GCAAAGTCTT TGGTGGTTGG GTATGAAGT CGATATTTCT TCGTTCAACA CTCTCTTCAC CTTCCTGCCC AACCGAAAAT GTAATCTGAA ACTCAGTGCT ATTTTACCAT GCTCCTTAAA AAAATACTAAT ACATATGTAA AAGACCTAGC TATACTTATT	120 180 240 300 360 420 480 600 600 780 840 900 1020 1080 11200 1260 1320 1320 1340
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	GAGCAACCTC GACCCAGAG GCGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCCAGTG GAAGGGCTG TGACTCCTTG CTTGGAAGAC TCTTGCAGGT ATTCTATGAC TGGCTGGCT CGAAAAACA TGAATGACTA TATATATAGA CTCATTATAT CAGTTATATC CAGTTATATAT CAGTCAATA CTAATTTTTA	AGCTTCTAGT AGCTTCTAGCAG GCCACCTTCG CCTGAGCAG GTCATCTCG AGGATTACT GGATGTCCT CTGAATCTGA GAGATGTATA GATGAGCAG GCACTATTT CCTATGACCC GCTGCTATTC GCTGCTATTC ACCTCTTACC GTGTGACACA ATACTATCAT ACAAAACAAA	ATCCAGACTC GGCGGCGCG GGAGTCCGGG GCAGTCCTGGG CCTATGCCGG GCAGTCCCGC GCAGTCCCGCAATCCTTTGT AGAAGATGAG TAGTTGCCAC TCTGCCTTCT CAACACATGT TAACACAAGA TAACATACG CAAACAAACA ATTACTTCTT AGAGTATCATTTT AGAACAAACA ATTACTTCTT TACATGTTTT ATACTTAAAA ATTGGTATTT ATACTTCATT TCTTCATTA TCTTTCATTT TCTTTCATTT TTCTTCATTT TATAGCACTTG	CAGGGCCGCC CGAGGAGGGC TTGCCCACCT CGAGGAGTCGC CGAGGAGTCGC CGACAACATC GAGCACGGC GCACACGTT GATGGCTGTC GATGGCTGTC GATGGCTGTC GATGGCTGTC GATGGTATC GAGTACCA GGGAGAAATC ACCTTAGAAT AAAAAACCCAT ACTCAAATAT ACTCAAATAT ACTCAATAT ACTCAATAT ACTCAATAT ACTCAATAT ACTCAATAT ACTCAATAT CCTTATGAT TTTCTTTTTC GCTTTGGGTG CTTCATGGTT	CCGGGCGGG CCAAACTCTC GCAAACTCTC GCAAACTCTC GCGAACTCTCG GCGATGTCAGG GCGATGAGT ATTGGGGTG GGCATGAAGT ATTGGGGTG GGCATGAAGT ATTGGGGTG GGCATGAAGT ATTGGGGTTAGAGC TTTGGTCAGG CTACTTTGCT AAACCTGCAC TTTGGGAACA TTTGGGTATT GTGTTAAAACA TTTGGGTATT GTGTTAAAACA TTTGGGTATT GTGTAAACA GGGAAGGGGT ATAGACAGTA ATAGGTAAACT GCCTTTTCAAAC CCCCTTTTCCAC GCCCTTTTCCAC GCCCTTTTCAAAC CCCCTTTTCCAC	ACCCCAACCC AACTTCTCC CGCGTTCTCC CGCGTTCTCC CGCGTGCAC CGCGTGCAC CGCAAGTCTA GCAAAGTCTT TCGTGGTTCGAC GTATGAACTG CCATTCTAC GTTCCTGTCAC GTTCCTGCC CTTCCAGCGC AACCGAAAAT GTAATCTGAA ACTCAGTGCT GCTCCTTCAAC GTTCCTGAA AAATACTTAT GTATTTAACTAT GTATTTAATT ACATATGTAA AAGACCTAGC TATGTTAAT TTGTTTTTTTTTT	120 180 240 360 420 540 600 720 780 840 900 960 1020 1140 1260 1320 1380 1440 1500
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	GAGCAACCTC CGACCCAGAG GCGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCAGTGG GCCCAGTGG GCCCAGTGG GCCCAGTGG GCCCAGTGG CTGATCCCTC CTTGGAACAC TCTTGCAGGT ATTCTATGAC GAACATTCAG GAACATTCAG GAACATTCAG GTATGTATTACT TTGTATTACT TATATATAGA CTCATTATTGT CCATATTTATT CAGTCAAATA CTAATTTTTTCA	AGCTTCTAGT CTTCTCCAGC CCTGAGCCAG CCTGAGCCAG TCATTCTCG AGGATTACT TGGATGTCCT TGGATGTCT CCTGATCTGA GAGTGACT CCTGATCTGA GATGAGTGC CTGGCTATT CCTATGACCC GCTGCTTCTC GTGTGACACA ATACTATCAT TACTATATT CCTTCCCATT TATGTATATAT TGATTACTC AGGATGAT CCATAATCTT CATTACTC AGGATGAT CCATAATCTT CTCTATTCTCC	ATCCAGACTC GGCGGCGCG GGAGTCCGG GGAGTCCGG GCAGCACC CCTTCCTGGG CCTATGCCGG CCTATGCCGG CCTATGCCGG CCTATGCCGG CCTATGCCGG CCTATGCCGC CAGCCACT TAGTCACC CAGCCACAT CAACACCAAG GAGCAAAACA TTACCTCAT TACATGCTATT ATACTTAAAA ATTGGTATAT TCTTCATTA TCTTTCATTA TCTTTCATTA TCTTTCATTA TCTTTCATTA TCTTTCATTA TCTATCATTA TCTATCATCATCATCATCATCATCATCATCATCATCATCA	CAGGGCCCCC CGAGCAGGGC TTGCCCACCT CGAGCAGGGC TTGCCCACCT CGAGCAGGCC CGACCACCT CAGCACCGC CGACACACT CAGCACCGGC CGACCACCGT CATGCATCCA GGCACCGT CATGCATACCA CGCTATCCA CAGCATACCA CACCTACCA CACCTACCA CACCTACCA CACCTACCA CACCTACAATC TCCTCAATAT TACTCAAATC CCTTTAGAT TTTCTTTTTC CCTTTTGGTG CTTCATGCT CACCTTAT CACCTTCAT CACCTTAT CACCTTAT CCTCATCTTAT CCTTTTGGTG CTTCATCCTTAT CACCTTCAT CACCTT	CCGGGCGGGGGGGGGGAGGGGAGGGGAGGGGAGGGGGAGGGGGG	ACCCCAACCC AACTTCCTCC CGCCTTCTCC CGCCTTCTCC CGCCTTCTCC CGCCTTCTCC CGCCATGTA GCAAAGTCTT TGGTGGTTGG GTATGAAGTG CTATCAACA CTCTCTTCA CTTCCTTCAC GTTCCAGCGG AACCGAAAAT GTAATCTGA ACTCAGTGCT ATTTTACCAT GCTCCTTAAA AAATACTATT GTATTTAATT ACATATGTAA AAGACCTAGC TATGTTTTTT TTGTTTTTGTG TAGTTTTTTATT TTGTTTTTGTG TAGTTTCTAA	120 180 240 360 420 540 660 720 780 840 960 1020 1080 1140 1260 1380 1440 1560
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	GAGCAACTC GAGCCAGAG GCGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCAGTGG GCGCCAGTGG GCAGGGGCTC TGACTCCTCG CTTGCAGC TTGTCAGCT TTGTATAGA GAAGACTAC GGAAGACTAC GGACATTAGG GTATGGTATT TAAATATAGA TCAATTAGT CCATATTGT CCATATTGT CCATATTGT TCATTTTTT TTTTTTTTA TTTCATTGC TTGTTTTTTTTTT	AGCTTCTAGT CTTCTCCAGC GCACCTTCG CCTGAGCCAG CTGATCTCTC AGGATTACT TGGATGTCCT TGGATGTCCT CTGATCTGA GATGAGTGC CTGGCTATT CCTATGACCC GCTGCTTACC ACCTCTTACC ATCTTACC ATCTTACT ACAAACAA	ATCCAGACTC GGCGGCGCG GGAGTCCGGG GCAGCCAG CCTATGCCGG CCTATGCCGG CCTATGCCGC GCAGCACATT AGAGACATGA TAGTTGCAC TCTGCCTTCT CAACACAAG TAACATTACG CAAACAAACA TAACATATCT TACATGTTT TAACTATATT TTCTTCATT TTCTTCATT TTCTTCATT TATACGCCTTC TGAGCACTT TATACGCACACAAAA ATTGCTATTA	CAGGGCCGCC CGAGGAGGGC TTGCCACT CGAGGAGTC CGAGGAGTC CGAGCACACT CAGGCACCGT CAGCACACGC CGACAACAC CGCACCGTT CATGGCTGTC CAGGTACCAC CGCCTATCCA CAGGTACCA CATGTACATAT CATCATATAAA CATTTCATA CATCATCATA CATCATCATCA CATCATCATCATA CATCATCATCATCA CATCATCATCA CATCATCATCATCA CATCATCATCATCATCATCATCATCATCATCATCATCATC	CCGGGCGGG CCAAACTCTC GCAAACTCTC GCAAACTCTC GCAACGCACGG GCCATCGTCA GTGACCGCCC CAGATCCAGT GGGCATGAAGT ATTGGGGGTG GGCATGAAGT ATTGGGATCAGG CTACTTTGCT AAACCTGCAC TTTGGAAACA TTTGGGTATT GTGTTAAAACA TTTGGGAAGGGAA	ACCCCAACCC AACTTCTCC CGCGTTCTCC CGCGTTCTCC CGCGTTCTCC CGCGTGCATGTA GCAAAGTCTT TCGTCGTTCAC GTATGAACTG CGATATTTCT TCGTTCAAC GTTCCTTCAC GTTCCTGCC CTTCCAGCGC AACCGAAAAT GTAATCTGAA ACTCAGTGCT GCTCTTAAA AAAATACTATT GTATTTAATT GTATTTAATT ACATATCTTAT TTGTTTTTTTTT TTGTTTTTTTTTT	120 180 300 360 480 540 660 720 840 900 900 1020 1140 1200 1320 1380 1440 1560 1560 1680
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	GAGCAACTTC GAGCCAGAG GCGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCAGTGG GCCCAGTGG GCCCCAGTGG GCCCCAGTGG GCCCCAGTGG GCCCCAGTGG CATCCTCCTC CTTGGAACAC TCTTCCAGGT ATTCTATAGAC GAAAACTAC GAAAACTAC GAAATTCAT TATATATAGA TATATATAGA CTCATTATATC CCATATTCAT CCATATTCAT TATATATA	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG TTCATTCTCG AGGATTACT TGGATGTCGT CTGAATCTCA GGAGTGATAG GGAGTGATAG CTATGACTCG CTGGCTATT CCTATGACCC GCTGCTTCTC GCTGTTACC GCTGTTACC GCTGTTACC GCTGTACACA ATACTATCAT TACATATCAT TACATATATAT	ATCCAGACTC GGCGGCGCG GGAGTCCGGG GGAGTCCGGG GCAGTCCGGG CCTATGCGG CCTATGCGG CCTATGCGG CCTATGCGG CCTATGCGG CAATCTTTGT AGAAGATGAG GAGCAAATG CTACCACAG GAGCAAAAG TAACATTACG CAACACAACA	CAGGGCCCCC CGAGGAGGCC TTGCCCACCT CGAGGAGTC CGAGGAGTC CGAGCACGGC CGACACACTC CAGCACCGGC CGACACACTC CAGCACCGGC CGACACCGT CAGCACCGGC CGCACACTT CAGGTACCAA CGCACCGT CACCTTACAA CTCCAATAT ACTCAATAT ACTCAATAT ACTCTATTACAA CTTCATTCA	CCGGGCGGGGGGGGGAAACTCTC GCAAACTCTC GCAAACTCTC GCAAACTCTC GTGACCGCCC CGGATCGACG GGCATCGTCA GGCATGAAGT ATTGGGGGTG GGCATTGAACT TTTGGTCAGG CTACTTTGCT TGTTGAAACA ATGGGGATG ATGGGATAGAA ATGGGATAGAA ATGGGGATGAACA TTTGGTAAACA TTTGGTAAACA TTTGGTAAACA TTTGGTAAACA TTTGGTAAACA TTTGGTAACATTT ATGCTACATTT CCTTACACTTA AGCCCTTAT GCCTACATTTT CATTCCCCCA GTTTTTATATC CCGGCCTTTTCCACCCCA TTTTTCCCCCCA GTTTTTATATATC	ACCCCAACCC AACTTCCTCC CGCCTTCTCC CGCCTTCTCC CGCCTTCTCC CGCCTTCTCC CGCCATGTA GCAAAGTCTT TGGTGGTTGG GTATGAAGT CGATATTTCT TCGTTCAACA CTCTCTTCAC CTTCCTGCCC AACCGAAAAT GTAATCTGAA ACTCAGTGCT ATTTTACCAT GCTCCTTAAA AAGACCTAACT GTATTTAATT ACATATGTAA AAGACCTAGC TATACTTATT TTGTTTTGTC TAGTTTCTAA CATGACCAAA AGCACTCTTC GGTGTTCTAAA ACCCACAAA ACCCACAAA ACCCACAAA ACCCACTCTC GGTGTTGTAA CCCCTAAACT	120 180 300 360 480 540 660 720 780 900 906 1140 1260 1320 1380 1440 1500 1500 1620 1620 1640 1740
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	GAGCAACTC GAGCCAGAG GCGGGCCCA ACTGCCACC GCTGTTGGGC GCCCAGTGG GCGCCAGTGG GCGCCCAGTGG CCAGGGCTC TGACTCCTC CTTGCAGC TTGTCACC CTTGCAGC TTCTTCAGC TGGCTGGCT TGGCTGGCT TGGCTGGCT TGGCTGGC	AGCTTCTAGT CTTCTCCAGC GCACCTTCG CCTGAGCCAG CTGATCTCTC AGGATTACT TGGATGTCCT TGGATGTCCT TGGATGTAGT GATGAGTGC CTGGATATA CATAGACCC GCTGCTTACC ACCTCTTACC ACCTCTTACC ATATACAT AAAAACAAA TAATCTTATT TGATTACAT TCATTACTC AAGGTGAC AAGATGTT CCTAATCAT TCATTACTC AAGGTGAT TCATTACTC AAGAGTGAT TCATTATTCT CCTAATCTC TCATTATTTATTAC CATAATCTT TCATTATTATTAC CATAATCT TCATTATTTAT	ATCCAGACTC GGCGGCGCG GGAGTCCGGG GCGCGGCGCC CCTTCCTGGG CCTATGCGG GCAGCACATT AGAAGATGAG TAGTTGCAC TAGTTGCAC TAGTTGCAC TAGTTGCAC TAGTTAGT TAGAACAACAA TAACAACAAG ATACTTATT TACATTATT TCTTCATTA TATTAAATT ATACCACAC TAACACAAG TAACATATAC CAATTTAAACT TAAATTAAACT TTAAAGTT TTTAAAGTT TTTAAAGTT TTTAAAGTT TTTAAAGTT TTTAAAGTT TTTAAAGTT TTTAAAGTT TAAATTGTAT	CAGGGCCGCC CGAGGAGGGC TTGCCCACT CGAGGAGGGC TTGCCCACCT CGAGGAGGCACGG CGACAACATC GAGCACGGG GCACCGTT GATGGCTGTC AGGATGGTAT CAGGTACGA GGAGAAACC GCCCTATCCA ACCTTAGAAT ACCATATAAAA TATCTCTAAATT ACTAAATGG CTTCAGGTG CTTCAGGT CTTCAGGT CTTCAGGT CTTCAGGT ACATTTCATA TTTGGAGCA ATCCTGTAC AGCTGCATGC AGCTGCATGC CTTATTCATA TTTGGAGCA TTTGGAGCA AGCTGCATGC AGCTGCATGC CTTATTCATA ATCCTGTAC AGCTGCATGC CTTATTCATA TTTGGAGCCA AGCTGCATGC CTTATTCATA AGCTGCATGC CTTATTCATA AGCTTGCATGC AGCTGCATGC CTTATTCATA AGCTTGCATGC AGCTGCATGC CTTATTCATA AGTTTCCCA AGCTGCATGC	CCGGGCGGG CCAAACTCTC GCAAACTCTC GCAAACTCTC GCAACCGCCC GGATCCAGT GTGACCGCCC CAGATCCAGT GGGCATGAAGT ATTGGGGGTG GGCATGAAGT ATTGGGGTTG AACCTGCAC TGTTGAAACA TTTGGTAATT AGGAGGGAA ATAGGAAGT ATAGGAGGAAT AGGACGGAA GCGAAGGAGT ATAGACAGTA ATAGGTAAACA GCCTTTTAAAT GCCTTTTAAAT GCCTTTTGCAC GCCCTTTTCA AACCCTTAT TGTTGACCAT TGTTGCCCCA GTTTTAAATT TTTGTTAAAT TTTTGTT TTTTTGCCCCA GCCTTTTTCAATT TTTTGCCCCA GTTTTAATT TTTTGCCCCA GTTTTATATT TTTTGCCCCA GTTTTATATT TTTTCCCCCA GTTTTATATT TTTTCCCCCA GTTTTATATT TTTTCCCCCA GTTTTATATT TTTTCCCCCA TTTTTATATC TTTTTTTT	ACCCCAACCC ACTTCTCC CGCGTTCTCC CGCGTTCTCC CGCGTTCTCC CGCGTTCTCC CGCGTGCTCA CGCAAGTCTT CGTGGTTCG CGAAGTCTT TCGTTGAACTG CGTTCACC CTTCCACCG CTTCCACCG AACCGAAAAT GTAATCTGAA ACTCCTTCAC GTCCTTCAC CTTCCAGCCC TATATCTTAA TATATCAAT CGTCCTTAAA AAATACTATT CGTATTTAATT ACATATGTAA AAGACTACC TATATCTTATT TTGTTTTTTTT TTGTTTTTATT TAGTTTTTTTT	120 180 360 460 480 540 600 600 600 1020 1080 1140 1260 1380 1440 1560 1620 1680 1740 1860
50 55 60 65 70 75	GAGCAACTIC GAGCCAGAG GCGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCAGTGG GCCCAGTGG GCCCCAGTGG GCCCCAGTGG GCCCCAGTGG GCCCCAGTGG GCCCCAGTGG GCCCCAGTGG CATCCTCCTG CTGGAAGAC TCTTGCAGGT ATTCTATGAC GAAAATCAG GAAAATCAT AACATTGGTATT AAACATGGCT TTGTATTACT TATATATAGA CTCAATTAGAT CCATATTGAT CCATATTTAT TTTATTATAC TTATATTACAT TTATATTACT TTATATTACT ACCTATTTTAT ACCTTTTTTAT ACCTTTTTTAT ACCTTTTTTATACTTTTATACTTTTCT TATATACTTTCC GATAATCTTGC GATAATCTTGC GATAATCTTGC GATAATCTTGC GATAATCTTGC GATAATCTTGC GATAATCTGC GATAATCT	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG GCACCTTCG CCTGAGCCAG TCCATTCTCG AGGATTACT TGGATGTCGT CTGAATCTGA GGAGTGATT CCTATGACCC GCTGCTATT CCTATGACCC GCTGCTTCTC ACCTCTTACC GTTGACACA ATACTATCAT TACATATCAT TACATATATAT TATGATATTAT TCATTTACTC CTCATTACTC CTCATTTACTC CTCATATCTC CTCATATCTC CTCATATCTC CATTATTACT CCTCTACC CATTATTACT CCTCTTACC CATTATTACT CCTCTTACC CATTATTACT CCTCTTACC CATTATTACT CCTCTTACC CTCTTTACT CCTCTTTCC TATTATTAC CCTCTTTCC TATTATTC CTCTTTCATT CCTCTTTCATT CCTCTTTCATT CCTCTTTCATT CCTCTTTCATT CCTTTTCATT CCTCTTTCATT CTCTTTCATT CTCTTTTCATT CCTCTTTCATT CTCTTTTCATT CTCTTTTCATT CTCTTTTCATT CTCTTTTCATT CCTCTTTCATT CTCTTTTCATT CCTCTTTCATT CTCTTTTCATT CCTCTTTCATT CTCTTTTCATT CTCTTTTT CTCTTTTT CTCTTTT CTCTTTT CTCTTTT CTCTTTT CTCTTT CTCTTT CTCTTT CTCTTT CTCTTT CTCTTT CTCTTT CTCTTT CTCTTT CTCTT CTT CTCTT CTCT CT	ATCCAGACTC GGCGGCGCG GGAGTCCGGG GGAGTCCGGG GCAGTCCGGG CCTATGCGG CCTATGCGG CCTATGCGG CCTATGCGG CCTATGCGG CCTATGCGG CCAGCACAT CAATCTTTGT AGAAGATGAG GAGCAAAAG CAACCAAG CAACCATGC CAACCACACA CAATCATTCTT ATACTTAAAA ATTGGTATAT TCTTCATTA ATAGCACTTG TTTAAAGGACTGA CCAACTGAGAC CCAATTGAGT TTTTAAGGTATTATT TTTTCATTA TAATTGTAT TTTTTATTATTATTATTATTATTATTATTATTATTA	CAGGGCCCCC CGAGGAGGCC TTGCCCACCT CGAGGAGGTC TGCCCACCT CGAGGAGTC CGAGCACGGC CGACACACTC CAGCACCGGC CGACACACTC CAGCACCGGC CGACACACTC CAGCACGGTC CAGCACGGTC CAGCACCGTT CAGGTACCAA CCTTAGAATT ACACATATAAAA TATCCTTATAA TATCTTTTCC CACTTAGATT TCTTTTCGGTGC CATCGTACT TTTGGAGGA ATCCTGAATT TCTTAGTTT TTTGGAGGCA ATCCTGATT TTTTGGAGGCA TCCTTATTCATA TTTTTCATTTCCT CTTTTTCCTTTCCT CATCTTATT TCTTTTCCT CATCTTATT TCTTTTCCT CTTTTTCCT CTTTTTCCT CTTTTTCCT CTTTTTCCT CTTTTTCCCA CTTTTTCCCA CTTTTTCCCA CTTTTTCCCA CTTTTATCATA CTTTTTCCCA CTTTATCATA CTTTTTCCCA CTCTGAACAA	CCGGGCGGGGGGGGGAAACTCTC GCAAACTCTC GCAAACTCTC GCAAACTCTC GCGAACTCTC GTGACCGCC CAGATCCAGT GTGACCGCC CAGATCAGT GGCATGAAGT ATTGGGGTGG GGCAATAGAA TTTGGTCAGG CTACTTTGCT TGTTAAAAT AGGACGGAAG GGGAAGGGGT ATAGGAAGT ATAGGAAGTA ATAGGACGTAA TTGGTAAAT CCTTTGCTCC CAGCCCTTTTCC TCTGACCCAT TTTGCTCCCCA GTTTTTATAT CCTTACCCCT TTTTTCTCCCCA GTTTTTTTTCTC CTGACCCAT TTGTAATAT AGTGTAATTA	ACCCCAACCC AACTTCCTCC CGCCTTCTCC CGCCTTCTCC CGCGCTCCCT AGCCATGTA GCAAAGTCTT TGGTGGTTGG GTATGAAGT CGATATTTCT TCGTTCAACA CTCTCTTCAC CTTCCTGCCC AACCGAAAAT GTAATCTGAA ACTCAGTGC AACCGAAAAT GTAATCTGAA ACTCAGTGCT ATTTTACCAT GCTCCTTAAA AAGACCTAACT TTATTTAGTT TAGTTTTATT TTGTTTTGTT	120 180 300 360 480 540 660 720 780 900 900 1260 1260 1320 1440 1500 1620 1680 1620 1680 1860 1920 1980
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	GAGCAACCTC GACCCAGAG GCGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCAGTGG GCCCAGTGG GCCCAGTGG GCCCAGTGG GATCCTCG CTGGAAGAC TCTTCCAGGT ATTCTATGAC GAAAACATA GAAAGACTAC GGAAATACA TAATATAGAC TTGTATTACT TATATATAGAC TAATATATAGAC TAATATATAGAC TAATATATAGAC TAATATATAGAC TAATATATAGAC TAATATATAGAC TAATATATAGAC TAATATATACT TAATATATAGAC TAATATATACT TAATATATAGAC TAATATATACT TAATATATAGAC ACAACATTA ACCTTTTGT TAACCTTTGA ACCTTTTGT TAATCTTCC GATAATCTCC GATAATCTCC GATAATCTCC	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG GCACCTTCG CCTGAGCCAG AGGATTTACT GGAGTGTCT TGGATGTCGT CTGAATCTGA GGAGTGATAG GTTGACTCA GGAGTGATAG CTGGCTATTC CCTATGACCC GTGTGACACA ATACTATCAT ACAAAACAAA	ATCCAGACTC GGCGGCGCG GGAGTCCGGG GGAGTCCGGG GCGCGCGCC CCTTCCTGGG CCTATGCCGG CCTATGCCGC GCGTTCGCA CAATCTTGT AGAAGATGAG TAGTTGCAC CAACAATCA TACTTCT GAGACAATT TCTTCATTA ATAGCACTAG TATCTTCATTA ATAGCACTAG TATCTTCATTA ATAGCACTAG TATCTTCATTA ATAGCACTAG TATACTAAAA ATTGGTATAT TCTTCATTA ATAGCACTAG TAACACAAGAC TTCCACACA CCAATTGAGT TTTTAAGCTA TTTTAAGCTA TTTTAAGCTT TTTTAAGCTT TTTTAAGCTT TTTTAAGTT TTTTCTCTTTA TTGCCTCTTT TTTTACGTTT TTTTCCTTTT TTTTCCTTTT TTTTCCTTTT TTTTCACTTT TTTTCACTTT TTTTCCTTTT	CAGGGCCGCC CGAGGAGGAGT CGAGGAGGAGT CGAGGAGAGC CGACACACT CAGGGACACGG CGACACACT CAGGCACCGG CGACACACT CAGGCACGGT ATGCATACGAC GGCACCGTT CAGGTAT CAGGTAT CAGGTACCA CGCCTATCCA ACCTTAGAAT AAAAACCCAT TCCTCAATAT ACTCAAATAG TTTCTTTTC CCTTTAGGTG CTTCATAGTA ACATTCATA ACATTCATA ACATTCATA ACATTCATA CTTCAGAGGCA ATCCTGACCA ACCTTACACA ACCTTACACA CCTTATTCATA CTTCATATTCATA CTTCATACCA CTTATTCATA CTTTCCCCA CTTATTCATA CCTTTACACA CCTTATTCATA CCTTTACACA CCTTATTCATA CCTTTACACA CCTTATTCCCA CTTATTCCCA CTTATACCA CATCTTAACCA CATCTTTAACCA CATCTTTACCA CATCTTTACCA CATCTTTACCA CATCTTTACCA CATCTTTACA CATCTTTACA CATCTTTACA CATCTTTACA CATCTTTACA CATCTTTACA CATCTTTACA CATCTTTAC CATCTTAC CATCTTTAC CATCTTTAC CATCTTTAC CATCTTTAC CATCTTTAC CATCTTTAC CATCTTTAC CATCTTTAC CATCTTTAC CATCTTAC CA	CCGGGCGGGGGGGGGGAAACTCTC GCAAACTCTC GCAAACTCTC GCAAACTCTC GCAAGGCAACG GCGATCGACG GGCATCGACG GGCATGAAGT ATTGGGGGTG GGCATGAAGT ATTGGGGATG GGCATGAACA TTTGGTCAGG CTACTTTGCT AAACTCTGCAC TGTTGAAACA TTTGGGTATT GTGTTAAAAT ATGGGTAAT GTCTTAAAT CCTTTGCAC AAGCCCTTAT GCCTACATTT TCTGACCCAT GTTTCCCCCA ATTTCCCCCA CTTTTTCCCCA CTTTTCCCCA CTTTTTCCCCA CTTTTTCCCCA CTTTTTCCCAC CTTTTTCCCACA CTTTTTCCTAAACA CTTTTAAATT AGTGTAATTA AGTGTAATTA AGTGTAATTA AGTGTAATTA AGTGTTAATA CAGTTAGAACA CAGTAGAACA CAGTTAGAACA CAGTAGAACA CAGTAGAA	ACCCCAACCC AACTTCTCC CGCCTTCTCC CGCCTTCTCC CGCGCTCCC CGCCCTTCTCC CGCCATGTA GCAAAGTCTT TCGTTCGTCGGTTCG CGATGTTCC CTTCCACCG CTTCCACCG CTTCCACCG ACCCAAAAT GTAATCTGA AACTCAGTGC ATTTTACCAT GCTCCTTAAA AAAATACTATT TGTTTTAAT TACATATGTAAA AAGACCTAGC TATATTTAAT TACTTTATT TTGTTTTCTG TAGTTTCTAA AGCACCAAA AGCACTCTTG GGTGTTGTAA CCCCTAAACT TCATGCGTTT TTCTTGGAGT TCTTTCTACC AGGTAGTGTG TCTTTCTACC AGGTAGTGTG TCTTCTACC AGGTAGTGTG TCTTCTACC AGGTAGTGTG	120 180 300 360 480 540 660 720 720 720 1080 1140 1200 1260 1380 1490 1560 1680 1740 1860 1920 1920 1920 1920 1920 1920 1920 192
50 55 60 65 70 75	GAGCAACCTC GACCCAGAG GCGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCACTGG GCCCCACTGG GCCCCACTGG GCCCCACTGG GCCCCACTGG GCCCCACTGG GCCCCACTGG GCCCCACTGG CATCCTCCTG CATCCTCCTG CATCCTCCTG CATCCTCAGG AATCTATGAC GAAAAACA GAAAAACA GAACATTAGG CTATTATTACT TATATATAGA CTCATTATTGT CCATAATTACT TATATTTTTAC TTATTTTTTA ACCTTTTTTAC CACAACTTTA ACCTTTTTTC TATATTTTTTTT	AGCTTCTAGT CTTCTCCAGC CCTAGCCAG GCACCTTCG CCTAGCCAG GCACCTTCG CCTAGCCAG GCACTTCG CCTGAGCCAG AGGATTACT TGGATGTCAT CCTATGACTGA GATGACTAC CTGGATATT CCTATGACCC GCTGCTTCTC CTGATATCT CCTATGACCA GTGTCACAC ATACTTACAC GTGTACACAA TAATCTTATT GCTTCCCATT TCATTTACTC AAGGATGATT TCATTTACTC AAGGATGATT TCTCTATTACTC AATTATTTAC CCTGTTGACC AATTATTTAC CCTGTTGACC AATTATTTAC TCTCTATTACTC AAGTTATTT TCTCTTTTACTC TCTATTACTC TTGATTGAT TCCCCATTCC TTGATTGAT TCCCATTCC TTATTAGAT TCCCATTCC TAATAGGTT TAATAGGTT TACTACAATAT ACTCCATACA ACTCTCATA	ATCCAGACTC GGCGGCGCG GGAGTCCGGG GGAGTCCGGG GCAGCGCGC CCTTCCTGGG CCTATGCCGG CCTATGCCGG CCTATGCCGG CCTATGCCGG CCTATGCCGG CCTATGCCGC CAGTCAATGC CAGTCAATGC CAGTCAATGC TAACCAAG GAGGCAAAAG TAACATACG CAAACAAACA TTACTTCTT ATAGTATTAT TCTTCAATT ATAGCACTTG TCAATTCATTT ATAGCACTTG TCAATTCATTT ATAGCACTTG TCAATTCAAT	CAGGGCCCCC CGAGCAGGGC TTGCCCACT CGAGCAGGGC TTGCCCACT CGAGCAGGGC TTGCCCACT CGAGCAGGCC CGACACACT CGACACCGGC CGACACACT CGACACCGGC GCACACCGT AGCATGGTAT CAGGTACGAA CGCTATCCA GAGAAAATCA ACCTTAGAAT TCCTCAATAT ACTCTAAATAT ACTCTATAAAA TTTCTTTTTC CACTTTAGGGC CATCGTTAGGGC CATCGTATCAT TTTGGAGGCA ATCCTGTATC TTTGGAGCA CCTTATCATA TTTTGCAGGC CTTATCATA TTTTGCAGGC CTTATCATA TTTTGCAGGC CTTATCATA TTTTGCAGGC CTTATCATA TGTTTTCCCA GCTGAACAA GCTGAACAA GCTGTAACAC GCTGTAACAA GCTGTAACAC	CCGGGCGGGGGGGGGATCCCCCAAACTCTCGCACATTGGCAAACTCTGGCATGGCATGGACACTTGGCAAGGCAACACTTGGTCAAGCGCACTTGAAACCACTGAAACCACTTCAAACCACTTCAAACCACTTAAAACTTCCCACACCCCTTTTAAAACAGCACACACTTTAAACCACTTACAACCCTTTCAAACCATTACAACCATTACAACCATTACAACCATTACAACCATTAAACTTTCCCACCA	ACCCCAACCC AACTTCCTCC CGCCTTCTCC CGCCTTCTCC CGCCTTCTCC CGCCTTCTCC CGCCATGTA GCAAAGTCTT TGGTGGTTGG GTATGAAGT CTATCTTCAC CTTCCTGTCC CTTCCAGCCG AACCGAAAAT GTAATCTCAA CTCCTTCAC CTTCCAGCCG AACCGAAAAT GTAATCTGAA ACTCAGTGCT ATTTTACCAT GCTCCTTAAA AACTACTATT TGATTTAATT ACATATCTAAT TAGTTTTTTTTTT	120 180 300 360 480 480 600 660 720 720 720 1080 1140 1260 1380 1440 1560 1680 1680 1740 1860 1860 1980 1980 1980 1980 1980 1980
50 55 60 65 70 75	GAGCAACCTC GACCCAGAG GCGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCAGTGG GCGCCAGTGG GCGCCAGTGG GCAGGGGCTC TGACTCCTCG CTTGCAGGC TTGTCAGAGAC TCGCAGAAAACA GAAGACTTAG GGACATTAGG GTATGTATTACT TTATATTAGA TAATTAGAC TCAATTAGAC TCAATTAGAC TCAATTAGAT TCAATTAGAT TCAATTAGAT TTTAATTAGAT TTTCATTGGT AGCCAACATTA TTTTCATTGGT TAATTTTTC TATATCTTC TATATCTTC TATATCTTC TATATCTTC TATATCTTC TATATCTTC TATATCTTC TATATCTC GATAAACTT TTTTTC TATATCTC AATATTAAT TTTTTTC TATATTTCC TTTCATTGGT AATATTAAT TTTTTTTC TATATTTCC TTTCATTGGT TATATTTTCC TTTCATTGGT TATATTTCC TTTCATTGGT TATATTTCC TTTCATTGGT TTTTTTTTC TTTTTTTCC TTTCATTGGT TTTTTTTTC TTTTTTTTCC TTTCATTGGT TTTTTTTTCC TTTCATTGGT TTTTTTTTCC TTTCATTGGT	AGCTTCTAGT CTTCTCCAGC GCACCTTCG CCTGAGCCAG GCACTTCG CCTGAGCCAG TTCATTCTCG AGGATTACT TGGATGTCCT TGGATGTCCT CTGAATTAG GATGAGTGC CTGCATATT CCTATGACCC GCTGCTTACC GCTCTTACC ATACTACA ATACTATATA TATTCTTATATA TGATACTAGA GAGAGTGAT TCATTACTC AAGATGAT TCATTATTAC CCTGTTGACC AATATTATTA CCATATTCAT TCATTATTATTAC CATATTCAT TTGATTGACC AATATTTTTTTTTC TTGATTGACC AATATTTTTTTTTT	ATCCAGACTC GGCGGCGCG GGAGTCCGGG GGAGTCCGGG GCGCGCGCC CCTTCCTGGG CCTATGCCGG CCTATGCCGC GCGTGTCGCA CAATCTTGT AGAAGATGAG TAGTTGCAA CAACAATCA TACTTCTT GAGAACAATCA TACTTCTT GAGAACAATCA TACTTCTT TACATCAATCA TACTTCTT TACATTAAAA ATTGGTATAT TCTTCATTA ATAGGACTTG TTAAACTAA TTCCACACA CCAATTGAGT TTTTAAGCTA TTTTAAGTTA TTGTCTCTTTA TTGAGATAAT ACTCTCATTC AGAACATGAAA ACTCTCAATC	CAGGGCCGCC CGAGGAGGACT CGAGGAGGACT CGAGGAGACCGC CGACACACT CAGGCACCGC CGACACACT CAGCACCGC CGACACACT CAGCACCGC CGACACACT CAGCACCGC CGCCACCGT CAGCACCGT CAGCACCGT CACCACC CCCCTATCCA ACCTTAGAAT AAAAACCCAT TACTCAAATAG TTCTTAATAT ACTATATATA ACTATTCATA TTTCTTTTC CCTTTAGGGC CTTATTCATA AGCTGCACC CTTATCCTA AGCTGCACC CTTATCCAA ACCTTAGACAC CTTATCACA CCTTATACAC CTTATCACAC CTTATCACAC CTTATCCCACC CTTATCCCAC CTTATCCCAC CTTATCCAC CTTATCCCAC CTTATCCAC CTTATCCCAC CTTATCCCAC CTTATCCCAC CTTATCCAC CTTATCCCAC CTTATCCAC CTTATCCAC CTTATCCCAC CTTATCCCAC CTTATCCAC CTTATCCAC CTTATCACAC CCACTCTAACCA CACCACTCTAACCA CACCACTCTAACCA CACCACTCTAA	CCGGGCGGGGGGGGGAAACTCTC GCAAACTCTC GCAAACTCTC GCAAACTCTC GCAACTCTC GCAACCGCCC CGGATCGACG GGCATCGACG GGCATGAAGT ATTGGGGGTG GGCATGAAGT ATTGGGGATG GTTGAACA TTTGGTAAACA TTTGGTAAACA TTTGGGAAGGAAGGGAAG	ACCCCAACCC AACTTCCTCC CGCCTTCTCC CGCGTTCTCC CGCGCTCCC AGCCATGTA GCAAAGTCTT TCGTTCGTCGGTTCG GTATGAAGTG CGATATTTCT TCGTTCACC GTTCCAGCG AACCGAAAAT GTAATCTGAA ACTCAGTGC ATTTACCAT GCTCCTTAAA AAAATACTATT TGTTTTAATT ACATATGTAA AAGACCTAC TATGTTCTAA AGGACCTACT TAGTTTCTAA AGGACCTACT TAGTTTCTAA AGGACCTACT TAGTTTCTAA AGGACCTACT CGTGTTTCTAA CATATGTTAT TTGTTTTGT TAGTTTCTAA AGGACCTAC CGTGTTGTAA TCATGCGTTT TTCTTGGAGT TCTTCACC AGGTAGTGTG ACACACGTAC CAAAACCTAC	120 180 300 360 480 540 660 720 720 720 1080 1080 1260 1260 1380 1440 1620 1680 1680 1740 1860 1920 1980 2160 2160 2160 2160
50 55 60 65 70 75	GAGCAACCTC GGACCAGAG GCGGGCCCA ACCTGCCACC GCTGTTGGGC GCACCAGTG GCACCAGTG GCACCAGTG GCACCAGTG CATCCTCCTC CTTGGAACAC TCTTCAGAGA ATTCTATGAC GGACATTCAG GAAGACTAC GGACATTCAG GTATGTATTACT TTATATATAGA CTCATTATATC TATATATATACA CTCATTATAC TTATATTTTT TTATATTTTT TTATTTTTT TTATATCT GATAAACT CCATTATTGT CCATTATTCT TTGTTTCAG ACCCAAGAG GTGATAAATT TTTATTTTTT TTATATCTTC GATAATCTG TCTTTTTTTT TTATATCTG TTATATCTG TTATATCTTTT TTATATCTG TTATATCTTTT TTATATCTG TTTATTTGCT TTTATTTGCT TTTATTTGCT TTTATTTGCT TTTATTTGCT TTTATTTGCT TTTATTTGCT TTTATTTGCT TCTATGTCAACTACATCAT	AGCTTCTAGT CTTCTCCAGC CCTGAGCCAG GCACCTTCG CCTGAGCCAG GCACCTTCG CCTGAGCCAG AGGATTACT TGGATGTCT CCTGAATCTGA GATGAGTGCC CTGGCTATT CCTATGACCC GCTGCTTCTC CCTGATTTACC GTTGACACA ATACTTACT GCTTCCCATT TCATTACTC AAGAGTGAC AGAGAGTGAT TCATTACTC AAGAGTGAC ATACTTAT TCATTACTC AAGATGATT TCATTACTC AATATCTT TCATTACTC AATATCTT TTCATTACTC AATATCTT TTCATTACTC AATATCTT TTCATTACTC TTCATTACTC TTCATTACT TTCATTACTC TTCATTACT TCCATTCC TTCATTACC TTCATTCC TTCATTACC TTCATTCC TTCATTC	ATCCAGACTC GGCGGCGCG GGAGTCCGGG GGAGTCCGGG GCAGTCCGGG CCTATGCCGG CCTATGCCGG CCTATGCCGG CCTATGCCGG CCTATGCCGG CCTATGCCGG CCTATGCCGC CAGTCAATGC CAGTCAATGC CAGTCAATGC CAACACAAG GAGGCAAAAG TAACATAGG CAAACAAACA TATCTTCTT ACATGTATTA TCTTCAATA TCTTCAATA TCTTCAATA TCTTCAATA TCTTCAATA TCATCAATGAT TTAAATGTAT TCTCCACACA AAATCAGAAC TCCACTCATC AGACACTGAA TCCTCCATCC AGACACTGAA TCCTCCATCC AGACACTGAA TCCTCCATCC AGACACTGAA TCCTCCCTCTC	CAGGGCCCCC CGAGCAGGGC TTGCCACT CGAGCAGGCC TTGCCACT CGAGCAGGCC CGAGCACT CGAGCACCC CGACCACT CAGCACCC CGACCACT CAGCACCC CGACACACT CACCACC CGACACCC CGACACCGT CACCACC CGCCACCGT CACCACC CACCACC CACCACC CACCACC CACCACC	CCGGGCGGGGGGGGGATCAGAGGGAACCAGTTTAAAACATTTGGCAACGGCCTTTAAACATTGGTAAAACATTTGGTAAAACATTTGGTAAAACATTTGGTAAAACAGTAAAAACCTTTAAACATTTGGACAAGAGGGAACGGTAACAAGAGAGGGAACGGTAACATTTGGACAAAACCTTTAAACTTTGCAACATTAAACATTAAACAGTAAAAACCTTTAAACAGTAAAAACCTTTAAACAGTAAAAAACCTTAAAAAAAA	ACCCCAACCC AACTTCCTCC CGCGTTCTCC CGCGTTCTCC CGCGTTCTCC CGCCATGTA GCAAAGTCTT TGGTGGTTGG GTATGAAGTG CTATCCATCC CTTCCAGCCG AACCGAAAAT GTAATCTGAA CTCCTTCAC ACTCCTTCAC ATTTACCAT GCTCCTTAAT GTATTAATT ACATATGTAT TTGTTTTTTT GTATTTATT TTGTTTTTTT TTGTTTTTTT TTGTTTTTTT TTGTTTTTT	120 180 300 360 480 540 660 720 720 720 1080 1020 1080 1140 1500 1500 1620 1620 1680 1740 1860 1980 1980 2040 2160 2220 2228
50 55 60 65 70 75	GAGCAACCTC GACCCAGAG GCGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCAGTGG GCGCCAGTGG GCGCGCCAGTGG GCGCGCCAGTGG CCAGAGGGCTG CTTGCAGCT CTTGCAGGT ATTCTATGAC GGAGGATTGG GGAGGATTGGG GTATGGTATT AAACATGGCT TTGTATTACT TTATATTACT TTATATTACT TTATATTACT TTTCATTGGT AGCCAACATTA ACCTTTTTTT TATATTCTT TATATTACT TTTCATTGGT AGCCAACATT TTTGTTTTTT TATATCTTC GATAACTTGCT TATATTACT TTTTTTTTTT	AGCTTCTAGT CTTCTCCAGC GCACCTTCG CCTGAGCCAG TCATTCTCCAGC GCACTTCG CTGAATTACT TGGATGTCCT TGGATGTAGT GATGAGTGC CTGCATTTG CCTGATTAGC GCTGCTATT CCTATGACCC GCTGCTTACC GCTGCTTACC ATACTACAC ATACTATATA TAATCTTATT TGATTCATATA TGATACTAGC AGAGATGATT TCATTTATTAC CCATTTATTAC CATTTATTATTAC CATTTATTATTAC TCATTTATTATTAC TCATTTATTATTAC TCATTTATTATTAC TCATTTATTATTAC TCATTTATTATTAC TCATTTATTATTAC TCATTTATTATTAC TCATTTATTATAC TCATTTATTATAC TCATTTATTATAC TCATTTATATAC TCATTTATTATAC TCATTTATATAC TCATTTATATAC TCATTTATATAC TCATTTATATAC TCATTTATATAC TCATTTATATAC TCATTCAT	ATCCAGACTC GGCGGCGCG GGAGTCCGGG GGAGTCCGGG GCAGTCCGGG CCTATGCGG CCTATGCGG CCTATGCGG CCTATGCGG CCATGCTGG CAATCTTGT AGAAGATGAG TAGTTGCAAC CAGTCAATGC CAACAACAA TAACTTGT TAGACAACAA ATTGCTATAT TATCTTCATT ATAGTATAT ATAGTATAT TCTTCAATT ATAGCACTGG CAAATCAGT TTTAAAA ATTGGTATAT TCTTCAATT ATAGTATAT TCTTCAATT ATAGCACTGG CCAATTGAGT TTTTAAAGTA TTCACACACA CCAATTGAGT TTTTAAGCTA TTGAGTATTTT TCTCTCTTA TTGAGTATTT TCTCTCTTA TTGAGTATAT TCTCTCTTCT CAGTGCCTTC CAGTCTTCTTGTC CAGTGCCTTC CAGTCTTTTTGCCTCA CATGTTTTTTGCCTCA CATGTTTTTTG	CAGGGCCGCC CGAGGAGGACT CGAGGAGGACT CGAGGAGACCGC CGACACACT CGAGGACT CGAGCACCGC CGACACACT CAGCACCGC CGACACACT CAGCACCGCC CGACACACT CAGCACCGCC CGACACACT CAGCACCGT CAGCACCGT CAGCACCGT CAGCACCGT CAGCACCGT CACCTACCA ACCTTAGAAT ACTCAAATAG TTCTTAGAT ACATTCATA ACTCTAAAT TTCTTTTTC CCTTTAGGTG CTTCATCCT ACATTTCATA TTTGGTGACAT TTTGGAGGC ATCCTGAACA TTTGAACAC CTTATACAC CCTTATCCC CTTCTCTCAC CGTCCTCCT CCTCTTCTCAC CTTCTCTCAC CTTCTCTCAC CTTCTCTCAC CTTCTCTCAC CTTCTCTCAC CTTCTCTCAC CTTCTCTCAC CTTCTCTCC CTTCTTCTCC CTCTCTTCC CTCTCTTCC CTCTCTTCC CCACCC CTCTCTTCC CCTCTTCTC CACCCC CTCTCTTCC CCACCC CCACCC CCACCC CCACCC CCACCC CCACC CCACCC CCACC CCACC CCACCC CCACC	CCGGGCGGGGGGGGGAAACTCTC GCAAACTCTC GCAAACTCTC GCAAACTCTC GCAAACTCTC GTGACCGCCC CGGATCGAGG GGCATCGAGG GGCATGAAGT ATTIGGGGGTG GGCATGAACT TTTGGTCAGG GTGACTTGAACA TTTGGTTAAAAT GTGTTAAAAT ATGGTAAAACT ATAGGGGAAGGGAA	ACCCCAACCC AACTTCCTCC CGCCTTCTCC CGCCTTCTCC CGCCTTCTCC CGCCTTCTCC CGCCTTCTCC CGCCATGTA GCAAAGTCTT TGGTGGTTGG GTATGAAGT CGATATTTCT TCGTTCACC CTTCCACGCG AACCGAAAAT GTAATCTGAA ACTCAGTGCT ATTTTACCAT GCTCCTTAAA AACTCAGTGT TATTTAATT ACATATGTAA AAGACCTATT TTGTTTTGTG TAGTTTCTAA CATGACCAAA AGCACTCTTC CGTGCTCTAAA ACCCACTAAACT TCATGCGTT TTTCTGGGGT TTTCTGGAGT TTTCTGGAGT TCTTCTGAC AGGTAGTGTC ACACACGTAC CAAAACCTAC CAAAACCTAC CAACTGAACA GCTCTATTCC	120 180 300 360 480 540 660 720 720 720 1080 1080 1020 1260 1260 1260 1260 1260 1260 126

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                                                                                               2700
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30
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                                                                                                180
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        THICTICCT GAGATITAGI TICTICATO INCLUSION CONTROL CAGGAGGATACT CAGGAGGCTA AGGTGGGGAG GTCCCTCAAG CCCACGAATT CAAAGCTGCA ATGCATTATC ATTACAGCTG
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                                                                                               1200
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Seq ID NO: 248 DNA sequence
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		CARACTER CC	A JAN TAINED WALK	CCACCTCCAT	TTCCCAGCAG	GGCMCICIC	120
10		~~~~~~~~~	COCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCO	CCCTGCCCT	TUTTUUC	GILLIGUEL	180
		~~~~~~~~	CCCCACCCCCC	CALCALATER SEC.	AGCCTCTGGC		240 300
		MANAGE CTC		TCCAATTAAT	TUTGGGTGGA	CIIGIICE	360
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15							480
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		~~~~~~~~~~	CCCANCRCC	VCCV LALLIANT		MONUNCIOIO	960 1020
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25		COCARCACA	TACCCACCC	CGAGACGGCC	TTCACATACG	CCGIGAGCAC	1140
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20	CGACAACATC	GACTATGGCT	ACCGCTTTGC	CAAGGAGITC	GTGGACGCCC	TCCACAACAA	1380
30		000100100C	CCTACGAGAG TGTACAACCT	CCCALCYLATA	GCCTGCAAGT	CCCATCCCT	1440
		more a country	ひとりひてはつはった	GCTGCAGCTG	GCAGACTICU	GCAMGIGG	1500
		8 8 CC 8 C 8 8 CT	N CONTRACTOR	CCCCCCCATG	CGGCTCAACA	GCCGGGGGG	1560
		OMORROS COO		CCCCACCACA	CAAGACCIGG	TCIACAICUA	1620 1680
35		~~~~~~~~~~	TGCGCAATGA AGGGCATGGA	CACCACCIAN	The Literature	COCHOOCCO	1740
		WINDS AND COL	TOTAGACIGA	GCGCTGCCAC	TGCAAGTTCC	ACTOGIGETO	1800
		TOCALOADET	CCACGGAGAT	CCTTGGACCAG	TITIGITGICA	MOTMOTOGGT	1860
		3 CMC3 CCCCC	へんせんしんじょうになる	CCCCCTTATT	TATAGAAAGT	ACAGIGATIC	1920
40		CONTROL OF A A A A	L V andredschutz V de	TTTTCCCCAA	GAATTGCAAC	COGAACCALL	1980 2040
	TITTITCCTG	TTACCATCTA	AGAACTCTGT CCACGAAAAA	GGTTTATTAT	GTGGATCTTT	GAAAAGGTAA	2100
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		A COURT A PARTY OF	*************************************	CACAAGAATG	TCATATTUTU	AAGGAAAAA	2460
		*************************************	TAAAATT	ATTCCATTIG	CAGACAGACC	GICATATICI	2520
50	3 3 M 3 C CTC 3 T	CARATTICCC	CAGCAGGGAG	GAAAGTCCCC	AGAAATTAAA	AMMILIAMA	2580
	COMPANIES INCOME	**************************************	ن لمان و لان الملت	TTATAAGAAT	TUGGATTUC	GATTIGIANA	2640 2700
	AAGACCCCCA	ATGATTCTGG	ACACTAGATT	TTTTGTTTGG	AATTATAATA	TTGAACATAA GTAGAAATAA	2760
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55	CCACTCCACC	ACACCAGACA	<b>ACCTATTGA</b>	GGAAAAACAG	TGAAATCCAC	CITCUTCITC	2880
	3 C3 CTC3 CCC	י רייורייוריירירינא חית	· ^~T^CCTCTT	GTGATGTGAT	GCTGGCCAC	TTTCCAAACG	2940 3000
	GCAGCTCCAC	TGGGTCCCCT	TTGGTTGTAG	GACAGGAAAT	GAAACATTAG	GAGCTCTGCT	3060
	TGGAAAACAG	TTCACTACT1	AGGGATTTT	COTANTGGAN	TTCACAGAGO	TGAGGAGCAG TGTTGCAGCG	3120
60	TO THE STREET	• ለጥርልጥርርፕሮፕ	· СТТТАСАТТА	TCCACTCATG	CTTCTCCTA	TGTACTGCAG	3180
•	CTCT A CCTT A	. ልልልጦሚሚሚሮር	CAGTGTACTT	GAACAGITGO	ATTTATAAGG	, CCCCAMMIGI	3240
	COMMENT NAMED	· ምርርርርርር እጥአባ	י רייראאאמדריי	TACATA	ACATATATA	ATATATACAT	3300 3360
	ATATATAAAT	ATAAATATAA	ATATATCTCA	TTGCAGCCAG	TGATTTAGAT	TTACAGCTTA	3420
65	Ammoon 1 2 2 2	Land A chitalographics .	י רייירים מכוריירים	CCCTGTGGCC	· CCGCTGTGA:	CATACCCIGA	3480
05	CCACCACCA	CCAACCTCCT	TTCTGAGGA	GAAGCTTGAG	TTCTGACTC/	CIGARATGEG	3540
	mammaccamac	• አአርአጥለጥርጥ	لململمك الماملسات	CTGCCTCACC	CCTTTGTCTC	CANCELCENI	3600
	TTCTGTTCAC	TITGTGGAGA	GGGCATTACT	TGTTCGTTAT	AGACATGGAG	GTTAAGAGAT	3660 3720
70	ATTCAAAACI	CAGAAGCATC	CACACTACT	CICTITICI	TCCCTAAGG	GCAGAATGGA ATATTCAGCC	3780
70	CACTACATAC	* ATACCUTTUT	և <u>Վուլովովոկսկուն և</u>	TATETTETT 1	TAAGGACAC	TCTTTCCAAA	3840
	CAGGCCATCA	AATATGTTCT	TATCTCAGAG	TTACGTTGTT	TTAAAAGTT	r GGAAAGATAC	3900
	ACATCOPTOTY	* ATACCCCCC	TTAGGAGGTT	GGGCTTTCAT	' ATCACCTCA	CCAACIGIGG	3960
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75	ATAATGATAT	TCACATCCCC	ATGTCACTT	TTTCCTTTT	ATTATACAA	AACCATGAAG	4140
	At W Contralistantial Laboratory	AATTICTAA!	TCAGATTGT7	r ccitittagi	GACTCATGT	TATGAAGAGA	4200
	CONTRACTOR CONTRACTOR	ACABTCCTAC	CATATANA C	: AAACTATTI	ATGTAAAAT	A TICTACATGE	4260
00	CATTCAGATA	TTATGTATAT	CTTCTAGCC	TTATTCTGT/	CTTTTAATG	COTTATTCCA	4320 4380
80	GTCTTGCGTC	ATTTGTATA	TTCACTGGT	r TAAAAAAACAA	ACAICGAAA	GCTTATTCCA	4,500
	AATGGAAGAT	AGAATATAA	ATAAAACGT	. ACITOINAD			
	Sea ID NO	: 249 Prote:	in sequence	:			
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MAGSAMSSKP FLVALAIFFS FAQVVIEANS WWSLGMINPV QMSEVYIIGA QPLCSQLAGL
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KLWSVHGQKR LQEFLADMGL PLKQVKQRFQ AMDISLKERU REMIEESANK FGKEDNRVQT
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                                                                                                                        1200
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                                                                                                                          720
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		COMPROMOS C	COTOTOTO	AACAAGCTGC	AGGITTUTGUU	CARCOCCIC	360
15			WALL S CHANGE AND A CHANGE OF THE PARTY OF T	CALL LALL LALL	GTAALCAGCT	GIIGCAGAIC	420
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	001 0001 001	TO COMPANY OF THE PARTY OF THE	CONCONTRACT	CTCAACCGIC	TTACTCICI	IGGGWATTCC	840
	OPPOSITOR OF THE PROPERTY OF T	THE PROPERTY OF THE PROPERTY O	CATCTTCCC	CCCATGCCCA	ACCIGCGGGA	GCTTTGGCTC	900
	MARCACA ACC	<b>み こりかしててててて</b>	TCTACCCGAC	AATGTCTTCA	GCAACCTCCG	CCAGTIGCAG	960
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50	*********	CCTTACCCAC	CCACACTGTA	CCTGTGTGTT	TCAGCCCAGC	CAATGTCCGA	1380
	***********	መር አጥተ አጥር አጥ	<u> </u>	GTTGCTGTTC	CAAGCGTCCA	TGTCCCTGAG	1440
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47	A GOOD CONTO	TOTATA	ጥር እ አርርጥጥር ጥ	CCCCTTGATT	TTCTGCTCCT	GAAGGCAGGG	2280
	THE RESERVE OF THE PROPERTY OF	CCTCAAAGAA	CACTTCAAAC	CATTTAACTG	GTTTCTTAAG	AGCCGTCAAT	2340
	OR COOKSONIE	THE COLOR PICE	DADAAANAT	AGAAGGAAAA	TCATGCCGCT	CAGTTCCTGG	2400
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	CANTOTAGTO	TAAT	GTGGTAAAAT	TCTCCATCAA	CATCACAGTC	AGCTGGCAGC	3300
	THE REPORT OF THE PARTY OF THE	יייים איייים איייים איייים איייים	LCACCAGGCG	ACACGGGGGT	ACACCGATGG	GICACACIGG	3360
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	CCTATTCCT	CCACTACCC	TGACATTGG	GCACCTTCC	CTCCAGCCAC	AGGCTGACCI	4380
	CACCCCCACT	የ ርምሮርምር አር ልባ	CACACCACC	· AGGAGCACCO	TAGGTGAGGC	GIGAGGGCCC	4440
	COMM N MCMC	* * **********************************	· distributed and a party of the party of th	• ተናናናር ልጥር ልር ፤	A GTGGTTGGAT	GGAGCCATIG	4500 4560
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WO 02/086443
Seq ID NO: 295 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-816

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Protein Accession #: Eos sequence

PCT/US02/12476 WO 02/086443

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                                                                                     1620
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85
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.0		CCCCC CACAC	ACACCCCAT.	GGCCACCTCC	ATGGGCCTGC	TOUTGUIGUI	180
.0		CHARLE COCK CC	CONTRACTOR OF THE PARTY OF THE	GACGGGAGCT	GACACGGAGG	CGGTGGTCTG	240
		GGGGGGGT 1 C1	CALL CANADA	CCCCAAGCTG	AGUSCIGUE	AGGCCCAGAA	300 360
		CAGAAOGGGG GTACTGGCCC	* COMPANY TO THE	CCCTAGGGGA	GLLLTGALLG	CEMOGNIGNO	420
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		TOGTGCATCT AACOGCCTGC					660
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		COCON COLD COL	المراو وبالشابية	CALITATION	TICULIUU	Widciaga	1260
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	TGAGGAGGGC	TACGTCCTGG GGGGGCCCCC	CCGGGGAGGA	CGGGACTCAG	AACACACAAG	GGTCCTTCCA	1500
	amama a arrea	COCCOCCCC	CCCRCCRCCC	CCCAAATGGG	GTCTCTTGCA	CCATGGGGCC	1560
		CONTRACTOR OF THE	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	CCATGAGGAG	GACAAAGGAG	DUMMUMMUM	1620
35			CAACAGCCAG	TYTYCZĄCAAGG	GGCCCCGAGG	GCACCCCAA	1680 1740
		ACCACAAGTA	CALCICITY OF THE	ACCCCTCTCG	ACCUALCULA	GCAICCAICA	1800
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	CONCORCA A A C	THE REPORT OF THE PROPERTY OF	CTACAGACAC	TAGAGTCACC	AGCCACCATC	CICAGAGCII	2160
4.5	TGAACTCCCC	ATTCCAAAGG	GGCACCCACA	TTTTTTTGAA	AGACTGGACT	GGAATCTTAG	2220 2280
45		**************************************	СА АССТОТОТ	GTTGGCGTGC	CACGGTGGGG	TTTCTACGGG ATTTCGTGAC	2340
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	accompance & Co	* ACCCTCGGGG	TARGGGGGCTC	CCCTGAATAT	CTTCTCTGCI	CACFICCACC	2460 2520
50	ATCTAAGAGG	AAAAGGTGAG	TTGCTCATGC	TGATTAGGAT	AAGAAGATCI	TGTTTCTCTT	2580
30	mon naccon a	(こと)からかからない。	CTCCAAACAT	TTCTTTACAI	TIGCATICCE	CCATTTOGCC	2640
	A COLD ON A CTO	**************************************	マにひせる ひてにすて	GACATCCTCC	AGAATGGCCA	GAAGIGCAAI	2700
	TAACCTCTTA	GGTGGCAAGG	AGGCAGGAAG	TGCCTCTTTA	ANCTICAT	TTCTAATAGC AAGTGCATTA	2760 2820
55	CA COMOTOTO	• ጥሮክ ስርጥሮ ስ ሮሽ	TAATCTACC	CCCTAGGGCG	AGAGAGGCCA	GGGATTTGTT	2880
33	as as as as as a	**************************************	CATCCAAATC	TACTGAGGTT	ACCACACAC	TGACTACGGA	2940
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60	TO A A CYCCOM	2 ATCATCCACT	· GTGTTTGA	AGTTGTCATI	TTAAAGCATI	TIAGCACAGI	3180
•	man ma amaca	Charterate	· ልርርርልጥርርር	GATTTTAAAI	CCTGAAGTG	GGGTGGGGGA	3240 3300
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	mmmmm x C 3 C C	* ************************************	• ሮልአልርርርልሞባ	TABATTATAI	CCTCATTITI	AAAGTTACAT	3420
65		**************************************	• ሮ አሞልልፕሮሮልር	TOTATACTG1	GCACTCTTT	TCTCTCTCTC	3480
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	CACTTAAAT	YEAAADDYAA A	CAACATTTC	CCCTCTGGG	CTIGAAAAI	CCAACATCAG CTTGCCCTTA	4200
	THE REPORT OF THE PARTY OF THE	C TCARCCACAC	• ልተተጥርጥርጥር ነ	TTGGCTTCCC	: ACAGCCCCA	A CGCAGTCIGI	4260
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05	**********	C CTC333C3C	· Artelated Table	י איריריטיזייטידייטיי	r TTTTGCTGT	T ACTITGAAGC	4620
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         WINSPOIVEL YNRLLORCEL NRHTTEAAAG ALQNITAGDR RWAGVLSRLA LEQERILNPL
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         NPHDIVIFHE LKQPRAPDAC ELSVQPNGGC EYLCLPAPQI SSHSPKYTCA CPDTMWLGPD
MKRCYRDANE DSKMGSTVTA AVIGIIVPIV VIALLCMSGY LIWRNWKRKN TKSMNFDNPV
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WO 02/086443 Seg ID NO: 414 DNA sequence Nucleic Acid Accession #: XM_084007 Coding sequence: 138..2405

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			AAATAATATT				
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	Sea ID NO.	417 Protein	semence				
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	MDICE A VINCAY	COURT TYPE	DD173.7	ON CAMPOCETURE	CEPPOT REUN	ACTAPUNICOT	60
85	MPKHAHWGAL	PAAPTTPMCH	PRVALACPHP	CACIARREAN	CILKOTHOAL	VOTATE ATTY	
0.)		0000000		TRATES OF T		CANTEL DALLANCE	120
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	NLGFNSIQAL QTLQGLSNLM	SETSFAGLTK RLHIDHNKIE	LELLMIHGNE PIHPQAFNGL SMLRNMPLLE	TSLRLLHLEG	NLLHQLHPST	FSTFTFLDYF	

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	GG1 000G1 CG1	CCCTCCATCA	ስጥተተርተር <u>ና</u> ልር	TGGAGGAAGA	TGAAGCTTCT	ACCTUGCAAA	1200
	TOTO TO TO A CA	ከጥር <b>ሶር</b> ሶ ቤርርጥ	TGTCAGTGGG	GTTTATTTCC	AAGGGACCAC	CATCGGCATG	1260
45	COCCCS STATES	<b>ጥር እርር ር እጥርጥር</b>	CACGGCAGAC	CAGTCTGGGG	GAATTGTCAT	GGACCATICA	1320
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	CCNACACCCT	CCACCCACTC	CAGCAACTCC	TGTGACCTCC	CAGAGTTCTG	CACAGGGGGC	1800
£ € .	AGCCCTCACT	GCCCAGCCAA	CGTGTACCTG	CACGATGGGC	ACTCATGTCA	GGATGTGGAC	1860 1920
55	GGCTACTGCT	ACAATGCCAT	CTGCCAGACT	CACGAGCAGC	TCA ATTCTCC	ACICIOGOA	1980
	CCAGGTGCTA	GTGGCAAAGT	CTCCAACACT	TOTTTGCCA	AATGCGAGAT	GAGAGATGCT	2040
	AAATOTOGAA	AAATCCACTG	TCAAGGAGGT	GCCAGCCGGC	CAGTCATTGG	TACCAATGCC	2100
	COMPACCATAC	***************	CCCCCTGCAG	CAAGGAGGCC	GGATTCTGTG	CCGGGGGACC	2160
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65	THE PROPERTY OF THE PARTY OF TH	CTGCCCGGATT	TGTGGTTTAT	CTCAAAAGGA	AGACCTTGAT	ACGACIGCIG	2520
05	<b>プライス へる みみずみ</b>	BCBBCACCAC	CATTGAAAAA	CTAAGGTGTG	TGCGCCCTTC	CCGGCCACCC	2580
	COTOCOTTO	* አአርርርርርርርርር	GGCTCACCTC	GGCCACCTTG	GAAAAGGCCI	GATGAGGAAG	2640
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50	CCAACTACC	COACCTGTGC	TTATGGTACC	AGATGCAGCT	CAAGAGATC	CAAGTAGAAT	3480
	CTCACTTGAT	PTASSITTATES	CCCCATCTC	GGCCAGAGCC	AAGGGGCIT	AGGTCCAGGC	3540
	ጥርጥርጥጥጥርር	TOTAL	CCCCTGTGCC	CCTTGACAAC	: TGGCAGGCAG	GCTCCCAGGG	3600
0.5	NON CONTROCCO	CARATCTCC	TTCTCCCCAC	CAAGCTTTGC	TGAGAACCT	GGTTGCAGAC	3660
85	<b>れたに入れてです</b>	100 ACCTCTACCC	· ACACCAGGAT	· AGAGACTGG	LACACTAGAC	AGCCAGAACI	3720 3780
	TCACCTCAC	TOTAL CONTRACTOR	CTGAGCATGT	TTGGAAGGG	TCTGTAGTG	CALTCAAGGC	3840
	GGTGCTTGA	r agaaatgcca	AGCACTTCT	Treruscit	, ICCITICIA	G AGCACTGCCA	

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10	Seq ID NO: Nucleic Ac:	458 DNA sec id Accession sence: 187	#: NM_001	999.2			
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	CONCORCO	V-A-CC-L-A-A-A-A-A-A-A-A-A-A-A-A-A-A-A-A-	TOTTGGGGTT	GGGGGAGCCG	GTGTGGGGGC	CGGGGGACAG	1440
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5		A COURS & CALCOL	ACMINICAL PROPERTY.	GTTGACAACC	GIGIGGGGA	CIGCIMCCIO	4740
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                                                                                         1500
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	W O 02/						
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C 0			TAATTTAATT				5280
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85	CITITOCCAA	COMMENTALIG	ACCTGTATAA	Paratoria ICI	GCACAGGACA	TACTGCATCT	6840
0.5	TTTTGCATTG	CCTACATGAC	MCCIGTATAA	TACABATTAC	TARCTTTCOT	ANTATATACT	6900
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WO 02/086443 PCT/US02/12476 LSMIVLLPRE IDGLQKLEEK LTAEKLMEWT SLQNMRETCV DLHLPRFKME ESYDLKDTLK 300

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5	Nucleic Ac:	466 DNA sec id Accession uence: 50	1 #: NM_001	1910.1			
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		INYLDMEYFG					120
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	* CCCX CDTEC	DATENIC DATELE	HARCOCTEVA	AAASAGVDDP	HOHGRGVALA	DFNRDGKVDI	300
	THE PROPERTY OF THE PARTY OF TH	LVIOVETHEK	MASSULUCION	FSMPSPVRTV	ITADFDNDOE	LEIPFNNLAY	360 420
5	A COLUMN CALL	VIRREHGDPL QGFNNNWLRV	UPPTREADA	RGAKVVLYTK	KSGAHLRIID	CGSGYLCEME	480
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PCT/US02/12476

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                   TATTILITED DESCRICOLS INVIDENCES VISTOFERLE VLAVFASTVL AQLGALFILE ESAERFLEOP EHTGRILUG TEVALCENLE TMLSIRNKOF AYVSEAASTS WLQEHVADLS RSLCGIFGL SSIFLPRMNP FVLIDLAGAF ALCITYMLIE INNYFAVDTA SALAIALMTF GTMYFMSVYS GKVLLQTTPP HVIGQLDKLI REVSTLDGVL EVRNEHFWIL GFGSLAGSVH VRIRRDANEQ MVLAHVTNRL YTLVSTLTVQ IFKDDWIRPA LLSGFVAANV LNFSDHHVIP MPLLKGTDDL BUCKTSTOLD FORTINGOUS TORMINGEL BELGATOGUE FORTINGOUS COMMUNICATION OF FILENDERS OF THE PROPERTY OF THE PRO
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                    SSMLNQGLGV PGIGATQGLR TGFTNIPSRY GTNNRIGQPR P
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                                                                                                       4380
          ATCAGTTTCT CTACAAAGTG ATCCTCAGCC TTGTGAGCAC AAGGCAGGAA GAGAATCCAT
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AGTCTTTAGT TTAACACAGA AAGGGGTGGG GGGACTCACA TCTGAGCATT GTTTTCCTCT
                                                                                                       4500
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          TCCTAAAATT AGGCAGGAAA ATCAGTCTAG TTCTGTTATC TGTTGATTTC CCATCACCTG
                                                                                                       4620
40
          ACAGTAACTT TCATGACATA GGATTCTGCC GCCAAATTTA TATCATTAAC AATGTGTGCC
TTTTTGCAAG ACTTGTAATT TACTTATTAT GTTTGAACTA AAATGATTGA ATTTTACAGT
                                                                                                       4680
          ATTICTAAGA ATGGAATTGT GGTATTTTT TCTGTATTGA TTTTAACAGA AAATTTCAAT
TTATAGAGGT TAGGAATTCC AAACTACAGA AAATGTTTGT TTTTAGTGTC AAATTTTTAG
                                                                                                       4800
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         CTGTATTGT AGCAATTATC AGGTTTGCTA GAAATATAAC TTTTAATACA GTAGCCTGTA
AATAAAACAC TCTTCCATAT GATATTCAAC ATTTTACAAC TGCAGTATTC ACCTAAAGTA
GAAATAATCT GTTACTTATT GTAAATACTG CCCTAGTGTC TCCATGGACC AAATTTATAT
                                                                                                       4920
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          TTATAATTGT AGATTTTTAT ATTTTACTAC TGAGTCAAGT TTTCTAGTTC TGTGTAATTG
                                                                                                      5100
          TITAGITTAA TGACGTAGIT CATTAGCIGG TCTTACICTA CCAGITITCI GACATIGIAT
                                                                                                      5160
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                                                                                                      5220
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ATGGTTTTTA TCCAAGGAAT TGCAAAAATA AATATAAATA TTGCCATTAA AAAAAAAAA
                                                                                                      5280
          AAA AAAAAAAA AAAAAAAAA
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55
         Protein Accession #: EOS sequence
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          MVPKASKITP HWGKCNMSSD GSEHSLEGQK PPLENQIYCF DADRFSSFEE AVKGKGKLRA
60
          LSILFEVGTE ENLOPKAIID GVESVSRFGK QAALDPPILL NLLPNSTDKY YIYNGSLTSP
                                                                                                       120
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                                                                                                        180
          SYTGKEEIHE AVCSSEPENV QADPENYTSL LVTWERPRVV YDTMIEKFAV LYQQLDGEDQ
         TRHEFLITDGY QDLGAILANL LPAMSYVLQI VAICINGLYG KYSDQLIVDM PTDNPELDLP
PELIGTEEII KEEEEGKDIE EGAIVNPGRD SATNQIRKKE PQISTTTHYN RIGTKYNEAK
                                                                                                        300
                                                                                                        360
65
          TNRSPTRGSE PSGKGDVPNT SLNSTSQPVT KLATEKDISL TSQTVTELPP HTVEGTSASL
                                                                                                        420
         NDGSKTVLRS PHMNLSGTAE SLNTVSITEY EEESLLTSPK LDTGAEDSSG SSPATSAIPF
                                                                                                        480
         ISENISOGYI FSSENPETIT YDVLIPESAR NASEDSTSSG SEESLKOPSM EGNVWFPSST
          DITAOPDVGS GRESFLOTNY TEIRVDESEK TTKSFSAGPV MSQGPSVTDL EMPHYSTFAY
                                                                                                        600
         PPTEVTPHAF TPSSRQQDLV STVNVVYSQT TQPVYNEASN SSHESRIGLA EGLESEKKAV IPLVIVSALT FICLVVLVGI LIYWRKCFQT AHFYLEDSTS PRVISTPPTP IFPISDDVGA
                                                                                                       660
70
         IPIKHPPKHV ADLHASSGFT EEPETLKEFY QEVQSCTVDL GITADSSNHP DNKHKNRYIN
IVAYDHSRVK LAQLAEKDGK LTDYINANYV DGYNRPKAYI AAQGPLKSTA EDFWRMIWEH
NVEVIVMITN LVEKGRRKCD QYWPADGSEE YGNFLVTQKS VQVLAYYTVR NFTLRNTKIK
                                                                                                       780
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         KGSQKGRPSG RVVTQYHYTQ WPDMGVPEYS LPVLTFVRKA AYAKRHAVGP VVVHCSAGVG
RTGTYIVLDS MLQQIQHEGT VNIFGFLKHI RSQRNYLVQT EEQYVFIHDT LVEAILSKET
                                                                                                       960
75
         EVLDSHIHAY VNALLIPGPA GKTKLEKOFO LLSOSNIQOS DYSAALKOON REKNRTSSII
PVERSRVGIS SLSGEGTDYI NASYIMGYYQ SNEFIITQHP LLHTIKDFWR MIWDHNAQLV
                                                                                                      1080
                                                                                                      1140
          VMIPDGQNMA EDEFVYWPNK DEPINCESFK VTLMAEEHKC LSNEEKLIIQ DFILEATQDD
                                                                                                      1200
         YVLEVRHFQC PKWPNPDSPI SKTPELISVI KEEAANRDGP MIVHDEHGGV TAGTFCALTT
LAHQLEKENS VDVYQVAKMI NLMRPGVFAD IEQYQFLYKV ILSLVSTRQE ENPSTSLDSN
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80
         GAALPDGNIA ESLESLV
         Sea ID NO: 580 DNA sequence
         Nucleic Acid Accession #: EOS sequence
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         Coding sequence: 148-4632
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	CACACATACG	CACGCACGAT	CTCACTTOGA CTCCCCCTCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCCGCA	120
	~~~~~~	COCCACA COC	TOTALANTA	AKTOOTAA	AACGTTTCCT	CGCTTGCATT	180
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	CHRONICA NO.	ACAPTCCCTC	CTCCTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300 360
		CC2 2 COMP 2 2	CCCAAAACAA GAAACTTAAA	THE PARTY OF THE PER	GGGATAAAAC	ATCATIGGAA	420
	***********	TOTAL BANKS	TOCCAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
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	AAATGCAATA	TGTCATCTGA	TGGATCAGAG TGATGCGGAC	CATAGTITAG	AAGGACAAAA	ACCACTCAAA	600 660
		20mm 20200	TT A TOTAL ATTEN	THEFT	TTUGGACAGA	AUAAAATIIG	720
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15			C V V CALLED AND	CCAAACTCAA	CIGACAAGIA	TIACATTIAC	840 900
			TCCCTGCACA CCAGTTGGCT				960
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	03 0mm003 m0	CACACCACCA	ስስርርስስርር <b>ስ</b> ቸ	GAATTTTTGA	CAGATGGCTA	TCAAGACTIG	1260
	COMMONSTANCE	TONBERROTT	CCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AUTAUCCATA	1320
	TO	COTTATATE	AAAATACAGC	GACCAACTGA	TTGTCGACAT	GCCTACTGAT	1380
25	AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAACTG	CTGGTAGAGA	CAAGGAGGAG CAGTGCTACA	1440 1500
	22002220002	CCANANACCA	<b>ACCCCAGATT</b>	TCTACCACAA	CACACTACAA	TOGCATAGGG	
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20	N N COCONC N TVC	TTCCCAATAC	<b>ተፈፈፈተተተ</b>	TCCACTTCCC	AACCAGTCAC	TAAATTAGCC	1680 1740
30	0 1 2 COM 1 COM	CAR CONTRACTOR OF THE PERSON O	AAATCATCCC	TCTAAAACTG	TTCTTAGATC	TCACACTGTG TCCACATATG	1800
	A A COMPOSITION OF CASE	CCACTCCAGA	ATCCTTAAAT	ACAGTTTCTA	TAACAGAATA	TGAGGAGGAG	1860
		CCS COMPTERS &	COTTEATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920 1980
35	GCAACTTCTG	CTATCCCATT	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTTCCTCC AAATGCTTCC	2040
33	01101000000000000000000000000000000000	COMPANIES OF THE SECOND	TOTORCARCAA	TCACTAAAGG	ATCCTTCTAT	GGAGGGAAA	2100
	ORGANICATOR C	CTACCTCTAC	ACACATAACA	GCACAGCCCG	ATGITGGATC	AGGCAGAGAG	2160
	* COMMECTIC	አር አርተስ አሞተል	CACTGAGATA	CGTGTTGATG	AATCTGAGAA	GACAACCAAG GGAAATGCCA	2220 2280
40	CIN THE S THE CHIES	COMPRECION	TOAACT	GAGGTAACAC	CTCATGCTTT	TACCCCCATCC	2340
70	TOCACACAAC	A CC A TITTCCT	CTCCACGGTC	AACGTGGTAT	ACTCGCAGAC	AACCCAACCG	2400
	CONTRACTOR	ACCCCACTAA	TACTACCCAT	GAGTCTCGTA	TTGGTCTAGC	TGAGGGGTTG	2460 2520
	GAATCCGAGA	AGAAGGCAGT	TATACCCCTT	TOGAGGAAAT	CAGCCCTGAC	TTTTATCTGT	2580
45	TACTTACACC	ስ/ ስ/ ተለር ተለር ስጥ (C	CCCTAGAGTT	ATATCCACAC	CTCCAACACC	TATCTTTCCA	2640
1.5	N TOTAL NAME OF THE PARTY OF TH	ATTECCACE	ATTCCAATA	AAGCACTTTC	CAAAGCATGT	TGCAGATTTA	2700
	CATGCAAGTA	GTGGGTTTAC	TGAAGAATTT	GAGACACTGA	AAGAGTTTTA	CCAGGAAGTG AGACAACAAG	2760 2820
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50	CALAIAS CALCE V V V	ACCATCCCAA	ACTGACTGAT	TATATCAATG	CCAATTATGT	TGATGGCTAC	2940
	AACACACCAA	AACCTTATAT	TGCTGCCCAA	GGCCCACTGA	AATCCACAGO	TGAAGATTTC	3000 3060
	TGGAGAATGA	TATGGGAACA	TAATGIGGAA	CCTGCCGATG	GGAGTGAGGA	CCTCGTGGAG GTACGGGAAC	3120
	THE THE CALL OF THE PARTY OF TH	CTCAGAAGAG	TGTGCAAGTG	CTTGCCTATT	ATACTGTGAG	GAATTTTACT	3180
55	CTARCAAACA	CAAAAATAAA	AAAGGGCTCC	CAGAAAGGAA	GACCCAGTGG	ACGTGTGGTC	3240
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	CACTCCACTC	CTCCAGTTGG	AAGAACAGGC	ACATATATTG	TGCTAGACAG	TATGTTGCAG	3420
	CACATTOAAC	ACCARCCARC	ተርተሮልልሮልሞል	TTTGGCTTCT	TAAAACACAT	CCGTTCACAA	3480
60	AGAAATTATT	TGGTACAAAC	TGAGGAGCAA	TATGTCTTCA	TTCATGATAC	ACTGGTTGAG TGTTAATGCA	3540 3600
		CHCC & CC & CC	**************************************	AAGCTAGAGA	AACAATTCCA	GGGTCTCACT	3660
		CCCCCCACTC	CAGAGGCACA	ATCTCGGCTC	ACTGCAACCT	TCCTCTCCCT	3720
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	CAACCCACACAC	ACTACATCA A	TGCCTCCTAT	ATCATGGGCT	ATTACCAGAG	CAATGAATTC	3900
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70	CATAATGCCC	AACTGGTGGT	TATGATTCCT	GATGGCCAAA	ACATGGCAGA	AGATGAATTT CACTCTTATG	4080 4140
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80	CTABBATTAC	GCAGGAAAAT	CAGTCTAGTT	CTGTTATCTC	TTGATTTCCC	ATCACCTGAC	4740
	<b>スペイススペデザイ</b>	* ATCACATAGO	ATTCTGCCGC	CAAATTTATA	TCATTAACA	TGTGTGCCTT	4800
	TOTALONAGAC	TTGTAATTT	CTTATTATG1	TTGAACTAAA	ATGATTGAAT	TTTACAGTAT	4850
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	TAAAACACTC	TTCCATATG	TATTCAACAT	TTTACAACTC	CAGTATTCAG	CTAAAGTAGA	2100
	AATAATCTG7	TACTTATTG	AAATACTGC	CIAGIGICIC	. CAIGGACCAI	ATTTATATTT	2200

	TAGTTTAATG	ACGTAGTTCA	TTTACTACTG TTAGCTGGTC TTGTTTCAGC	TTACTCTACC ATGTAATTTT	AGTTTTCTGA AACTTTTGTG	CATTGTATTG	5220 5280 5340 5400
5	GGTTTTTATC AAAAAAAAAA	CAAGGAATTG AAAAAAAAAAA	CAAAAATAAA A	TATAAATATT	GCCATTAAAA	AAAAAAAA	
10	Seq ID NO: Protein Acc	581 Protein ession #: E	n sequence: OS sequence	•			
10	1	11	21	31	41	51	
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	MRILKRFLAC	IQLLCVCRLD	WANGYYRQQR KFQGWDKTSL	KLVEEIGWSY	TGALNQKNWG	KKYPTCNSPK	60 120
15	DEVICETABRE	CKOMSSDGS	PHSI-EGOKEP	LEMOIYCFDA	DRFSSFEEAV	KGKGKLRALS	180
	TI.EWWITERN	LDEKATIDGV	ESVSRFGKOA	ALDPFILLNL	LPNSTDKYYI	YNGSLTSPPC	240
	TOTUDATURK	DTVSISESOL	AVFCEVLTMO	OSGYVMLMDY	LONNFREQQY	KPSRQVFSSY	300 360
	TGKEEIHEAV	CSSEPENVQA	DPENYTSLLV NMSYVLQIVA	ICTNGLYGKY	SDOLIVDMPT	DNPELDLPPE	420
20	T.TOPPETTER	FFFCKDIFFG	ATUNPERDSA	TNOIRKKEPO	ISTTTHYNRI	GTKYNEAKTN	480
	RSPTRGSEFS	GKGDVPNTSL	NSTSQPVTKL	ATEKDISLTS	QTVTELPPHT	VEGTSASLND	540 600
	GSKTVLRSPH	MNLSGTAESL	NTVSITEYEE VLIPESARNA	SEDSTSSGSE	PSLKDPSNEG	NVWFPSSTDI	660
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	LVIVSALTFI	CLVVLVGILI	YWRKCFQTAH FETLKEFYQE	FYLEDSTSPR	VISTPPTPIF	PISDDVGAIP	900
	A VIDUS DURTA	CLAPKTCKLT	DYINANYVDG	YNRPKAYIAA	OGPLKSTAED	FWRMIWEHNV	960
	ENTIMITED V	EKCESKCDOY	WPADGSEEYG	NFLVTOKSVO	VLAYYTVRNF	TLRNTKIKKG	1020
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	GTYIVLDSML	QQIQHEGTVN	IFGFLKHIRS TKLEKQFQGL	QRNYLVQTEE TLSPRLECEG	TISAHCNI.PL	PGLTDPPTSA	1140 1200
	SRVAGTILLS	OSNIOOSDYS	AALKQCNREK	NRTSSIIPVE	RSRVGISSLS	GEGTDYINAS	1260
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	PECUFACIEC	AANREGPMIV VOPLYKVILS	LVGTRQEENP	STSLDSNGAA	LPDGNIAESL	YQVARMINLM ESLV	1440
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	CACACATACG	CACGCACGAT	CTCACTTCGA	TCTATACACT	GGAGGATTAA	AACAAACAAA	60
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<i></i>	AGTTCAGAAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACCAGCCT	TCTTGTTACA	1140
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						ATTCTCTGGA	1620
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75	ACAGAAAAAG	ATATTTCCTT	GACTTCTCAG	ACTGTGACTG	AACTGCCACC	TCACACTGTG TCCACATATG	1740
15		CHUCCICITY	AAAIGAIGGC	ACAGTTTCTA	TAACAGAATA	TGAGGAGGAG	1860
	AACTTGTCGG	GGACTGCAGA	AICCITAAAT				
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	AACTTGTCGG AGTTTATTGA GCAACTTCTG	CCAGTTTCAA CTATCCCATT	GCTTGATACT CATCTCTGAG	GGAGCTGAAG AACATATCCC	AAGGGTATAT	ATTTTCCTCC	1980
80	AACTTGTCGG AGTTTATTGA GCAACTTCTG GAAAACCCAG	CCAGTTTCAA CTATCCCATT AGACAATAAC	GCTTGATACT CATCTCTGAG ATATGATGTC	GGAGCTGAAG AACATATCCC CTTATACCAG	AAGGGTATAT AATCTGCTAG	ATTTTCCTCC	1980 2040
80	AACTTGTCGG AGTTTATTGA GCAACTTCTG GAAAACCCAG GAAGATTCAA	CCAGTTTCAA CTATCCCATT AGACAATAAC CTTCATCAGG	GCTTGATACT CATCTCTGAG ATATGATGTC TTCAGAAGAA	GGAGCTGAAG AACATATCCC CTTATACCAG TCACTAAAGG	AAGGGTATAT AATCTGCTAG ATCCTTCTAT	ATTTTCCTCC AAATGCTTCC GGAGGGAAAT	1980
80	AACTTGTCGG AGTTTATTGA GCAACTTCTG GAAAACCCAG GAAGATTCAA GTGTGGTTTC AGCTTTCTCC	CCAGTTTCAA CTATCCCATT AGACAATAAC CTTCATCAGG CTAGCTCTAC AGACTAATTA	GCTTGATACT CATCTCTGAG ATATGATGTC TTCAGAAGAA AGACATAACA CACTGAGATA	GGAGCTGAAG AACATATCCC CTTATACCAG TCACTAAAGG GCACAGCCCG CGTGTTGATG	AAGGGTATAT AATCTGCTAG ATCCTTCTAT ATGTTGGATC AATCTGAGAA	ATTTTCCTCC AAATGCTTCC GGAGGGAAAT AGGCAGAGAG GACAACCAAG	1980 2040 2100 2160 2220
80	AACTTGTCGG AGTTTATTGA GCAACTTCTG GAAAACCCAG GAAGATTCAA GTGTGGTTTC AGCTTTCTCC TCCTTTTCTG	CCAGTTTCAA CTATCCCATT AGACAATAAC CTYCATCAGG CTAGCTCTAC AGACTAATTA CAGGCCCAGT	GCTTGATACT CATCTCTGAG ATATGATGTC TTCAGAAGAA AGACATAACA CACTGAGATA GATGTCACAG	GGAGCTGAAG AACATATCCC CTTATACCAG TCACTAAAGG GCACAGCCCG CGTGTTGATG GGTCCCTCAG	AAGGGTATAT AATCTGCTAG ATCCTTCTAT ATGTTGGATC AATCTGAGAA TTACAGATCT	ATTTTCTCC AAATGCTTCC GGAGGGAAAT AGGCAGAGAG GACAACCAAG GGAAATGCCA	1980 2040 2100 2160 2220 2280
	AACTTGTCGG AGTTTATTGA GCAACTTCTG GAAAACCCAG GAGGTTTCA GTGTGGTTTC AGCTTTCTCC TCCTTTTCTG CATTATTCTA	CCAGTTTCAA CTATCCCATT AGACAATAAC CTTCATCAGG CTAGCTCTAC AGACTAATTA CAGGCCCAGT CCTTTGCCTA	GCTTGATACT CATCTCTGAG ATATGATGTC TTCAGAAGAA AGACATAACA CACTGAGATA GATGTCACAG CTTCCCAACT	GGAGCTGAAG AACATATCCC CTTATACCAG TCACTAAAGG GCACAGCCCG CGTGTTGATG GGTCCCTCAG GAGGTAACAC	AAGGGTATAT AATCTGCTAG ATCCTTCTAT ATGTTGGATC AATCTGAGAA TTACAGATCT CTCATGCTTT	ATTTTCCTCC AAATGCTTCC GGAGGGAAAT AGGCAGAGAG GACAACCAAG GGAAATGCCA TACCCCATCC	1980 2040 2100 2160 2220 2280 2340
80 85	AACTTGTCGG AGTTTATTGA GCAACTTCTG GAAAACCCAG GAGGATTCAA GTGTGGTTTC AGCTTTCTCC TCCTTTTCTG CATTATTCTA TCCAGACAAC GTATACAAT	CCAGTTTCAA CTATCCCATT AGACAATAAC CTTCATCAGG CTAGCTCTAC AGACTAATTA CAGGCCCAGT CCTTTGCTA AGGATTTGGT GTGAGACACC	GCTTGATACT CATCTCTGAG ATATGATGTC TTCAGAAGAA AGACATAACA CACTGAGATA GATGTCACAG CTTCCCAACT TCTCCAACT TCTCCAACCT	GGAGCTGAAG AACATATCCC CTTATACCAG TCACTAAAGG GCACAGCCCG CGTGTTGATG GGTCCCTCAG GAGGTAACAC AACGTGGTAT TCCTACAGTA	AAGGGTATAT AATCTGCTAG ATCCTTCTAT ATGTTGGATC AATCTGAGATCT CTCAGGATCT ACTCGCAGAC GTGAAGTCTT	ATTTTCCTCC AAATGCTTCC GGAGGGAAAT AGGCAGAGG GACAACCAAG GGAAATGCCA TACCCCATCC AACCCAACCG TCCTCTAGTC	1980 2040 2100 2160 2220 2280 2340 2400 2460
	AACTTGTCGG AGTTTATTGA GCAACTTCTG GAAAACCCAG GAGGATTCAA GTGTGGTTTC AGCTTTCTCC TCCTTTTCTG CATTATTCTA TCCAGACAAC GTATACAAT	CCAGTTTCAA CTATCCCATT AGACAATAAC CTTCATCAGG CTAGCTCTAC AGACTAATTA CAGGCCCAGT CCTTTGCTA AGGATTTGGT GTGAGACACC	GCTTGATACT CATCTCTGAG ATATGATGTC TTCAGAAGAA AGACATAACA CACTGAGATA GATGTCACAG CTTCCCAACT TCTCCAACT TCTCCAACCT	GGAGCTGAAG AACATATCCC CTTATACCAG TCACTAAAGG GCACAGCCCG CGTGTTGATG GGTCCCTCAG GAGGTAACAC AACGTGGTAT TCCTACAGTA	AAGGGTATAT AATCTGCTAG ATCCTTCTAT ATGTTGGATC AATCTGAGATCT CTCAGGATCT ACTCGCAGAC GTGAAGTCTT	ATTTTCCTCC AAATGCTTCC GGAGGGAAAT AGGCAGAGAG GACAACCAAG GGAAATGCCA TACCCCATCC	1980 2040 2100 2160 2220 2280 2340 2400 2460

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WO 02/086443
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	GG1 GGG1 1 M1	TOTAL CONTRACTOR IN	CCTCAATGGC	CTCATGGCCA	TCCAGCTGCA	GAACAACCAG	1200 1260
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		N COCCE C & CCC	ስር አር ርር አጥር እር	ገንግግግ <b>ተ</b> ልጥልላል	CATCCTGGGC	TTTTCCCCAGA	2820
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PCT/US02/12476

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20		670 DNA se id Accession uence: 11	n. #: Eos se	edreuce			
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                                                                                           660
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                                                                                            900
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85
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Seq ID NO: 686 DNA sequence

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			TCCATCTATG			ATGTCAATAA	1080
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	FOUL ICTOORD	TIMITAIN	Ranakiak				
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	Seq ID NO: Nucleic Ac:	688 DNA se	equence	31	41	<b>51</b>	
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	Seq ID NO: Nucleic Act Coding sequents	688 DNA seid Accession Dence: 18	equence 1 #: NM_009 70 21	31   AGCATCOGAT	CCGGCGACTT	CCAAGCTCCG	60
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40 45	Seq ID NO: Nucleic Aci Coding sequ 1 ATGACAGGAG TTCAGACGT TCAGCTACCTGG AACGGCTCCG TACCACCAGT GAACTGACCG AGGACTATTT TACCTCGCCT	688 DNA sid Accession pence: 18°  11   TGTTTGACAG CCGCAGCTAT ATTCTATGG CCGGAGCTA ACGCCGCGAGCTA ACGCCGCGAGCTATTCCAGCTT TGCCGGAACG	equence a #: NM_005 70 21 AAGGGTCCCC GCACCATCCG CTACAGCCCT CCCAGCCAAA CTACAACCGC GAGAATGGTG TCAGCTGGCC CGCGAGCTGCC CGCGAGCTGCC	31   AGCATCCGAT TCTCAGGAAT ACGGGGGGAG AACCCCTACC GCTTATGCCG GCTCCAAGCG AATGCCAAAC GCATTACAGA GCATTACAGA GCCGCCTCGC	CCGGCGACTT CGCCAACTT CCCCGCACGG AGTATCAGTA ACTATAGCTA CCACCAACCA CAAAGAAAGT GAAGGTTTCA TGGGATTGAC	CCAAGCTCCG GCCCGAGTCT CTACTGCTCT TCACGGCTG GCTAGCTCC GCCAGAGAAA TCGTAAACCC GAAGACTCAG ACAAACACAG	120 180 240 300 360 420 480 540
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40 45 50	Seq ID NO: Nucleic Aci Coding sequ  1   ATGACAGGAG TTCAGACTACCG CTTACCTCGG AACGGCTCCG TACCACAGT TACCTCGCT GAAGTGACCG TTACCTCGCCT GTGAAAATCT ATGCCCCCG CCAGCGGTGT CCTCCGACCT ACAAGTGCAC CTGCCGCCTG	688 DNA seid Accession lence: 18°  11   TGTTTGACAG CCGCAGCTAT ATTCTGATAG ACCGCGGCGC AGCCGAGGT ATTCAGATATTCAGATAGCACATTCAGAAAGCAACACTCC CCAGCTCAATCCAGCT CCAGCTCAATCCCGGGACCCCAACCAGCCCAACCACCACCACCACCACCA	equence a #: NM_005 70 21   AAGGGTCCCC GCACCATCCG CTACAGCCCT CCCAGCCAAC CTACAACCGC GAGAATGTG CAAACGGC GAGAATGTG CAAAGATCC CACCTCCAGC CACCTCCAGC CCAGCGTCT CCCAGCGTCT CCCAGCGTCT CCAATTCCCAC ACTCTATTAG	31   AGCATCCGAT TCTCAGGAAT ACGGGGGGAG AACCCCTACC GCTCTATGCCG GCTCCCAAGCG AATGGCAAAC GCATTACAGA GCCCGCTCGC AAGATCAAGA GACCCAATGG GACCTACCTGG AGCTACCTGG	CCGGCGACTT CCCGCACGG AGTATCAGTA ACTATAGCTA ACTATAGCTA CCACCAACA CAAAGAAAGT GAAGGTTTCA AGATCATGAA CGTGTAACTC GCCACCACCC AGAACTCACCA	CCAAGCTCCG GCCGAGTCT CTACTGCTCT TCACGGCGTG GCCAGAGAAA TCGTAAACCC GAAGACTCAG AACAGCACAAA TCATACACAG AAACGGCGAG TCATGCCCAC ATCCTGGTAC	120 180 240 300 360 420 480 540 600 660 720 780
40 45 50 55	Seq ID NO: Nucleic Ac: Coding sequ  1   ATGACAGGAG TTCCAGACGT TCAGCTACCTCGG AACGGCTCCG TACCACCAGT TACCACCAGT TACCACCAGGT TACCACCAGGT TACCTCGCCT ATGCCCCCGG CCAGCGGTGT CCTCCGACCT ACAAGTCAG CTGGCGCTG Seq ID NO:	688 DNA 86 id Accession lence: 18'  11    TGTTTGACAG CCGCAGCTAT ATTCTGACTA ATTCTATGG CCGGAGGTA ACGCGGAGGTA ACGCGGAGGTA ACGCGAGGTA ACGCGAGGGGGGGGGG	equence a #: NM_005 70 21   AAGGGTCCCC GCACCATCCG CTACAGCCT CAAAGCTCTC CCCAGCCAA CTACAACGC TAGAACGTC TAGACTGGC GAGAATGTG TAGCTGGC CACCTCCAGC CAAAGATC CAAAGATC CAAACGTC CAAAGATC CAACTCCAGC GGGGTCCTCC CAATTCCCAC ACTCTATTAG	31   AGCATCCGAT TCTCAGGAAT ACGGGGGGAG AACCCCTACC GCTCTATGCCG GCTCCCAAGCG AATGGCAAAC GCATTACAGA GCCCGCTCGC AAGATCAAGA GACCCAATGG GACCTACCTGG AGCTACCTGG	CCGGCGACTT CCCGCACGG AGTATCAGTA ACTATAGCTA ACTATAGCTA CCACCAACA CAAAGAAAGT GAAGGTTTCA AGATCATGAA CGTGTAACTC GCCACCACCC AGAACTCACCA	CCAAGCTCCG GCCGAGTCT CTACTGCTCT TCACGGCGTG GCCAGAGAAA TCGTAAACCC GAAGACTCAG AACAGCACAAA TCATACACAG AAACGGCGAG TCATGCCCAC ATCCTGGTAC	120 180 240 300 360 420 480 540 600 660 720 780
40 45 50	Seq ID NO: Nucleic Ac: Coding sequ  1   ATGACAGGAG TTCCAGACGT TCAGCTACCTCGG AACGGCTCCG TACCACCAGT TACCACCAGT TACCACCAGGT TACCACCAGGT TACCTCGCCT ATGCCCCCGG CCAGCGGTGT CCTCCGACCT ACAAGTCAG CTGGCGCTG Seq ID NO:	688 DNA seid Accession lence: 18°  11   TGTTTGACAG CCGCAGCTAT ATTCTGATAG ACCGCGGCGC AGCCGAGGT ATTCAGATATTCAGATAGCACATTCAGAAAGCAACACTCC CCAGCTCAATCCAGCT CCAGCTCAATCCCGGGACCCCAACCAGCCCAACCACCACCACCACCACCA	equence a #: NM_005 70 21   AAGGGTCCCC GCACCATCCG CTACAGCCT CAAAGCTCTC CCCAGCCAA CTACAACGC TAGAACGTC TAGACTGGC GAGAATGTG TAGCTGGC CACCTCCAGC CAAAGATC CAAAGATC CAAACGTC CAAAGATC CAACTCCAGC GGGGTCCTCC CAATTCCCAC ACTCTATTAG	31   AGCATCCGAT TCTCAGGAAT ACGGGGGGAG AACCCCTACC GCTCTATGCCG GCTCCCAAGCG AATGGCAAAC GCATTACAGA GCCCGCTCGC AAGATCAAGA GACCCAATGG GACCTACCTGG AGCTACCTGG	CCGGCGACTT CCCGCACGG AGTATCAGTA ACTATAGCTA ACTATAGCTA CCACCAACA CAAAGAAAGT GAAGGTTTCA AGATCATGAA CGTGTAACTC GCCACCACCC AGAACTCACCA	CCAAGCTCCG GCCGAGTCT CTACTGCTCT TCACGGCGTG GCCAGAGAAA TCGTAAACCC GAAGACTCAG AACAGCACAAA TCATACACAG AAACGGCGAG TCATGCCCAC ATCCTGGTAC	120 180 240 300 360 420 480 540 600 660 720 780
40 45 50 55	Seq ID NO: Nucleic Ac: Coding sequ  1   ATGACAGGAG TTCAGACTACCG CCTACCTCGG AACAGCTCCG TACCACCAGT GAAGTGACCG AGGACTACTT ATGCCCCCGG CCAGCGGTGT CCTCCGACCT ACAAGTGACC ACAAGTGACC Seq ID NO: Protein Acc	688 DNA seid Accession sence: 18'  11   TGTTTGACAG CCGCAGCTAT ATTCTGACTA ATTCTATAGG AGCCGAGCTA ATTCAGACTA TTCCAGCTT TGCCGGAACG GGTTTCAGAA AGCACAGTC CCAGCTCAAT CCTCCGGGACCCAACCAGTC CCAGCTCAAT CCTCCGGGACG GG Proteiession #: N	equence  a #: NM_005  21    AAGGGTCCCC GCACCATCCG CTACAGCCTC CCCAGCCAA CTACAACCGC GAGAATGTG CAAAAGATCC CAGCGAGCTG CAAAAGATC CAACTCCAG CAGCTCAGC CAGCTCAGC CACTCAAG CTACTACTAC CACTCATCAG CACTCATTAG  IN po05212.1	31 AGCATCCGAT TCTCAGGAAT ACGGGGGGAG AACCCTIACC GCTTATGCCG GTCCCAAGCG AATGCAAAC GCCCCTTGC AAGATCAAGA GACCCAATGG GCCTCGCTCA AGCTACTGG CGCTCGCTCA AGCTACCTGG	CCGGCGACTT CCCCGCACGA GTATCAGTA ACTATAGCTA ACTATAGCTA CCACCAACCA CAAAGAAAGT GAAGGTTCA AGATCATGAA CGTGTAACTC GCCACCACCC AGAACTCTGC CGGGCTCCTT	CCAAGCTCCG GCCGAGTCT CTACTGCTCT TCACGGCGTG GCCAGAGAAA TCGTAAACCC GAAGACTCAG ACAACACAG AAACGGGGAG TCATGCCCAC ATCCTGGTAC ACAGCACCCAC ATCCTGGTAC ACAGCACCCG	120 180 240 300 360 420 480 540 600 660 720 780
40 45 50 55	Seq ID NO: Nucleic Ac: Coding sequ  1   ATGACAGGAG TTCCAGACGT TCAGCTACCTCGG AACGGCTCCG TACCACCAGT TACCACCAGT TACCACCAGGT TACCACCAGGT TACCTCGCCT ATGCCCCCGG CCAGCGGTGT CCTCCGACCT ACAAGTCAG CTGGCGCTG Seq ID NO:	688 DNA 86 id Accession lence: 18'  11    TGTTTGACAG CCGCAGCTAT ATTCTGACTA ATTCTATGG CCGGAGGTA ACGCGGAGGTA ACGCGGAGGTA ACGCGAGGTA ACGCGAGGGGGGGGGG	equence a #: NM_005 70 21   AAGGGTCCCC GCACCATCCG CTACAGCCT CAAAGCTCTC CCCAGCCAA CTACAACGC TAGAACGTC TAGACTGGC GAGAATGTG TAGCTGGC CACCTCCAGC CAAAGATC CAAAGATC CAAACGTC CAAAGATC CAACTCCAGC GGGGTCCTCC CAATTCCCAC ACTCTATTAG	31   AGCATCCGAT TCTCAGGAAT ACGGGGGGAG AACCCCTACC GCTCTATGCCG GCTCCCAAGCG AATGGCAAAC GCATTACAGA GCCCGCTCGC AAGATCAAGA GACCCAATGG GACCTACCTGG AGCTACCTGG	CCGGCGACTT CCCGCACGG AGTATCAGTA ACTATAGCTA ACTATAGCTA CCACCAACA CAAAGAAAGT GAAGGTTTCA AGATCATGAA CGTGTAACTC GCCACCACCC AGAACTCACCA	CCAAGCTCCG GCCGAGTCT CTACTGCTCT TCACGGCGTG GCCAGAGAAA TCGTAAACCC GAAGACTCAG AACAGCACAAA TCATACACAG AAACGGCGAG TCATGCCCAC ATCCTGGTAC	120 180 240 300 360 420 480 540 600 660 720 780
40 45 50 55	Seq ID NO: Nucleic Ac: Coding sequ  1   ATGACAGGAG TTCAGACGT TCAGCTACCCG CCTACCTCGG AACGGCTCCG TACCACCAGT GAAGTGACCG CGTAAAATCT TACCTCCGCCT GTGAAAATCT ATGCCCCCGG CCAGCGGTGT CCTCCGACCT ACAAGTGCAG Seq ID NO: Protein Acc	688 DNA seid Accession Lence: 18'  11   TGTTTGACAG CCGCAGCTAT ATTCTGACTA ATTCTATAGS CCGGAGCTAT ACGCCGAGGTT ACGCCGAGGTT ACGCCGAGGTT ACGCCGAGGTC ACGCCAGGTT CGCGGAACG GGTTTCAGAA ACGCACAGTC CCAGCTCAGT CCAGCTCAGT CCAGCTCAGT CCAGCTCAGT CCAGCTCAGT LESSION #: 1	equence n #: NM_005 70 21   AAGGGTCCCC GCACCATCCG CTACAGCCCT CAAAGCTCTC CCCAGCCAAA CTACAACCGC GAGAATGGTG CAAAAGATCCC CAGCTCCAGC CAGCTCCAGC CAGCTCCAGC CACATTCCCAC CAATTCCCAC CAATTCCCAC CAATTCCCAC CAATTCCCAC CACTCTATTAG In sequence IP_005212.1	31   AGCATCCGAT TCTCAGGAAT ACGGGGGGAG AACCCTACC GCTTATGCCG GTCCCAAGCG AATGGCAAAC GCATTACAGA GCCGCCTCGC AAGATCAAGA GCCCCAATGG GACCCAATGG CGCCTCGC AGCTACCTGG CTGCCGCCCGC	CCGGCGACTT CCCCGCACGG GGTATTAGCTA ACTATAGCTA CCACCAACCA CAAAGAAAGT TGGATTCATCA TGGATTCAC TGGATTCAC GCACCACCC AGAACTCTGC GCACCACCC AGAACTCTGC CGGGCTCCTT	CCAAGCTCCG GCCGAGTCT CTACTGCTCT TCACGGCGTG GCCAGAGAAA TCGTAAACCC GAAGACTCAG AAACGGGGAG ACAACACAG AAACGGGATCT TCATGCCAC ATCCTGGTAC ACAGCACCCG	120 180 240 360 420 480 540 660 720 780 840.
40 45 50 55 60	Seq ID NO: Nucleic Aci Coding sequ  1   ATGACAGGAG TTCAGACTACCG CTTACCTCGG AACGGCTCCG TACCACAGT GAAGTGACCG TGCAAAATCT TTACCTCGCCT GTGAAAATCT CCTCCGACCT ACTGCGCTGG CCTGCGCCTGG Seq ID NO: Protein Acc	688 DNA seid Accession sence: 18'  11   TGTTTGACAG CCGCAGCTAT ATTCTGACTA ACTCCTATGG AGCAGCTA ATTCAGACTA TTCCAGATT TGCCGGAACG GGTTTCAGAA AGCACAGTCC CCAGCTCAAT CCTCCGGGACCCAACCAGTC CCAGCTCAAT CCTCCGGGACG GGTGTAT CGGGAGCCCAACCAGTC CCAGCTCAAT CCTCCGGGACC GS Proteigession #: N	equence a #: NM_005 70 21   AAGGGTCCCC GCACCATCCG CTACAGCCCT CCCAGCCAAC CTACAACCGC GAGAATGTG CAAAAGATCC CAGCTGCC CAGCTGCC CAGCTCAGC CAGCTCAGC CAATTCCAC ACTCTATTAG IN population In popu	31   AGCATCCGAT TCTCAGGAAT ACGGGGGGAG AACCCTAAC GCTTATGCCG GTCCCAAGCG AATGGCAAAC GCATTACAGA GCCGCCTCGC AAGATCAAGA GACCAATGG CGCTCGCTCA AGCTACCTGG CTGCCGCCGC  31   SQESPTLPES	CCGGCGACTT CCCCGCACGA GTATCAGTA ACTATAGCTA ACTATAGCTA CCACCAACA CAAAGAAAGT GAAGGTTCA AGATCATGAA CGTGTAACTC GCCACCACCC AGAACTCTGC CGGGCTCCTT  41   SATDSDYYSP	CCAAGCTCCG GCCGAGTCT CTACTGCTCT TCACGGCGTG GCCAGAGAAA TCGTAAACCC GAAGACACAG AAACGGGGAG ACAACACAG AAACGCGAGTT TCATGCCCAC ATCCTGGTAC ACAGCACCCG	120 180 240 300 360 420 480 540 660 720 780 840.
40 45 50 55	Seq ID NO: Nucleic Ac: Coding sequ  1   ATGACAGGAG TTCCAGACGT TCAGCTACCTCGG AACGGCTCCG TACCACCAGT GAAGTGACCG GAGGACTATTT TACCTCGCCT ATGCCACCGG CCAGCGGTGT CCTCCGACCT ACAAGTGACA Seq ID NO: Protein Acc  1   MTGVFDRRVP PTSASYGKAL	688 DNA seid Accession lence: 18'  11   TGTTTGACAG CCGCAGCTAT ATTCTGACTA CTTCCTATGG CCGGAGCTA ACGCGGGGCGA AGCCCGAGGTT TGCGGGAACG GGTTTCAGAA AGCACAGTC CCAGCTCAT CCCAGCTCAT CCCAGCTCAT CCTAGCGACCAGT CCAGCTCAT CCTAGGACAGTC CCAGCTCAT CCTAGGACAGTC CCAGCTCAAT CTTCCGGGAC 689 Proteinession #: N	equence a #: NM_005 70 21   AAGGGTCCCC GCACCATCCG CTACAGCCT CAAAGCTCTC CCCAGCCAA CTACAACGC GAGAATGGTG TAGCTGGC CAAAAGATCC CAGCTCCAGC CAAATGCTG CAAAAGATCC CACTCCAGC CAATCCCAG ACTCTATTAG in sequence iP_005212.1 21   FOTSAAMHHP NGSAGSYPAK	31	CCGGCGACTT CCCGCACGG GCCAACTTT CCCCGCACGG AGTATCAGTA ACTATAGCTA CCACCAACCA CAAAGAAAGT TGGGATTTCA TGGGATTTCA CGCCACCCA AGAACTCTGC AGAACTCGCACACC AGAACTCACACACC AGAACTCACACACACACACACACACACACACACACACACA	CCAAGCTCCG GCCGAGTCT CTACTGCTCT TCACGCGTG GCCAGAGAAA TCGTAACACC GAAGACTCAG ACAACCACG AAACGGGGAG TCATGCCCAC ATCCTGGTAC ACAGCACCCG  51   TGGAPHGYCS VPSATNOPEK	120 180 240 300 360 420 480 540 660 720 780 840.
40 45 50 55 60	Seq ID NO: Nucleic Ac: Coding sequ  1   ATGACAGGAG TTCAGACGT TCAGCTACCTCGG AACGGCTCCG TACCACCAGT GAAGTGACCG CTACCTCGCCT GTCAAAATCT ATGCCCCCGG CCAGCGGTGT CCTCCGACCT ACAGTGCAG CTGCCCTG Seq ID NO: Protein Acc  1   MTGVFDRRVP PTSASYGKAL EVTEPEVRNV	688 DNA seid Accession lence: 18'  11   TGTTTGACAG CCGCAGCTAT ATTCTGACTA ATTCTGACTA ACGCCGGAGCTA ACGCCGAGCTA ACGCCGAGCTA ACGCCGAGCTA ACGCCAGCTA CCACCTAC GCGAGCCCA CCAACCATC CCAGCTCAA CCTCCGGAC  689 Protei lession #: N  11   SIRSGDPQAP NPYQYQYHGV NGKPKKVRKP	equence  a #: NM_005  21  AAGGGTCCCC GCACCATCCG CTACAGCCCT CAAAGCTCTC CCCAGCCAAA CTACAACCGC GAGAATGGTG CAAAAGATCC CAAAACGC GGCGAGCTG CAAAAGATCC CAACTCCAGC CCCAGCTCCA CACTCTATTAG  In sequence IP_005212.1  21  FQTSAAMHHP FGTSAAMHHP FGSAAGSYPAK RTIYSSFPLA	31	CCGGCGACTT CCCCGCACGG GGCATTT CCCCGCACGG AGTATCAGTA ACTATAGCTA CCACCAACCA CAAAGAAAGT TGGATTCATGAA CGGATCATGAA CGGTCAACTC GCCACCACCC AGAACTCTGC CGGGCTCCTT  41   SATDSDYYSP YHQYGGAYNR YLALPERAEL	CCAAGCTCCG GCCGAGTCT CTACTGCTCT CTACTGCTCT CTACGGCGTG GCCAGAGAAA TCGTAAACCC GAAGACTCAG AAACGGGGAG ACACGGCAGCATCT TCATGCCAC ATCCTGGTAC ACAGCACCCG  51 IGGAPHGYCS VPSATNOPEK AASLGLTQTQ	120 180 240 300 360 420 540 600 660 720 780 840.
40 45 50 55 60	Seq ID NO: Nucleic Aci Coding sequ  1   ATGACAGGAG TTCAGACTACCG CCTACCTCGG AACGGCTCCG AGGACTACTT ATGCCCCCGG CCAGCGGTTG ATGCCCCGG CCAGCGGTTG CCTCCGACCT ATGCCCCCGG CCAGCGGTGT CCTCCGACCT ACAAGTGCAG Seq ID NO: Protein Acc  1   MTGVFDRRVP PTSASYGRAL EVTEPEVRMV VKIWFQNKRS	688 DNA seid Accession pence: 18'  11   TGTTTGACAG CCGCAGCTAT ATTCTGACTA ATTCTGATA ACGCCGGAGCTA ACGCCGGAGCTA ACGCCGGAGCTA ACGCCGGAGCTA ACGCCGGAACG GGTTCAGATA CCACCAGTC CCACCTCAGT CCACCTCAGT CCACCTCAGT  11   SIRSGDPQAP NPYQYQHGV NGKPKKVPKPP KIKKIMKNGE	equence a #: NM_005 70 21   AAGGGTCCCC GCACCATCCG CTACAGCCT CAAAGCTCTC CCCAGCCAA CTACAACGC GAGAATGGTG TAGCTGGC CAAAAGATCC CAGCTCCAGC CAAATGCTG CAAAAGATCC CACTCCAGC CAATCCCAG ACTCTATTAG in sequence iP_005212.1 21   FOTSAAMHHP NGSAGSYPAK	31   AGCATCCGAT TCTCAGGAAT ACGGGGGGAG AACCCTTACC GTCCCAAGCG AATGCAAAC GCCGCTCGC AAGATCAAGA GCCCAATGG GACCAATGG CGCTCGCTCA AGCTACCTCG AGCTACCTCCTCG AGCTACCTCG AGCTACCTCG AGCTACCTCCTCG AGCTACCTCCTCG AGCTACCTCCTCG AGCTACCTCCTCCTCTCCT	CCGGCGACTT CCCCGCACGA GTATCAGTA ACTATAGCTA ACTATAGCTA CCACCAACCA CAAAGAAAGT GAAGGTTCA AGATCATGAA AGATCATGAA CGGGCACCACCA AGAACTCTGC CCGGCTCCTT  41   SATDSDYYSP YHCYGGAYNR YHCYGGAYNR PAVWEPGGSS	CCAAGCTCCG GCCGAGTCT CTACTGCTCT CTACTGCTCT CTACGGCGTG GCCAGAGAAA TCGTAAACCC GAAGACTCAG AAACGGGGAG ACACGGCAGCATCT TCATGCCAC ATCCTGGTAC ACAGCACCCG  51 IGGAPHGYCS VPSATNOPEK AASLGLTQTQ	120 180 240 300 360 420 480 540 660 720 780 840.

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein neorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

#### WHAT IS CLAIMED IS:

	WIMI IS CL	MINIUL	7 IO.	
1		1.	A method of detecting a lung cancer-associated transcript in a cell	
2	from a patient, the method comprising contacting a biological sample from the patient with a			
3	polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence			
4	as shown in T	ables 12	A-16.	
1		2.	The method of claim 1, wherein the polynucleotide selectively	
2	hybridizes to		nce at least 95% identical to a sequence as shown in Tables 1A-16.	
	,	•		
1		3.	The method of claim 1, wherein the biological sample is a tissue	
2	sample.			
1		4.	The method of claim 1, wherein the biological sample comprises	
2	isolated nucle	ic acids	•	
	•	_	The state of the s	
1		5.	The method of claim 4, wherein the nucleic acids are mRNA.	
1		6.	The method of claim 4, further comprising the step of amplifying	
2	nucleic acids	before t	he step of contacting the biological sample with the polynucleotide.	
1	•	7.	The method of claim 1, wherein the polynucleotide comprises a	
2	sequence as sl		Tables 1A-16.	
_	1			
1		8.	The method of claim 1, wherein the polynucleotide is labeled.	
1		9.	The method of claim 8, wherein the label is a fluorescent label.	
1		10.	The method of claim 1, wherein the polynucleotide is immobilized on	
2	a solid surface	е.		
1		11.	The method of claim 1, wherein the patient is undergoing a therapeutic	
2	regimen to tre	at lung	cancer.	
1		12.	The method of claim 1, wherein the patient is suspected of having lung	
1 2	cancer	14.	The memor of claim 1, wherein the patient is suspected of having thing	
۷	cancer.			
1		13, .	A method of monitoring the efficacy of a therapeutic treatment of lung	

cancer, the method comprising the steps of:

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3	(i) providing a biological sample from a patient undergoing the therapeutic
4	treatment; and
5	(ii) determining the level of a lung cancer-associated transcript in the
6	biological sample by contacting the biological sample with a polynucleotide that selectively
7	hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16,
8	thereby monitoring the efficacy of the therapy.
1	14. The method of claim 13, further comprising the step of: (iii) comparing
2	the level of the lung cancer-associated transcript to a level of the lung cancer-associated
3	transcript in a biological sample from the patient prior to, or earlier in, the therapeutic
4	treatment.
1	15. The method of claim 13, wherein the patient is a human.
1	16. A method of monitoring the efficacy of a therapeutic treatment of lung
2	cancer, the method comprising the steps of:
3	(i) providing a biological sample from a patient undergoing the therapeutic
4	treatment; and
5	(ii) determining the level of a lung cancer-associated antibody in the biological
6	sample by contacting the biological sample with a polypeptide encoded by a polynucleotide
7	that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in
8	Tables 1A-16, wherein the polypeptide specifically binds to the lung cancer-associated
9	antibody, thereby monitoring the efficacy of the therapy.
1	17. The method of claim 16, further comprising the step of: (iii) comparing
2	the level of the lung cancer-associated antibody to a level of the lung cancer-associated
3	antibody in a biological sample from the patient prior to, or earlier in, the therapeutic
4	treatment.
1	18. The method of claim 16, wherein the patient is a human.
1	19. A method of monitoring the efficacy of a therapeutic treatment of lung
2	cancer, the method comprising the steps of:
3	(i) providing a biological sample from a patient undergoing the therapeutic

treatment; and

5	(ii) determining the level of a lung cancer-associated polypeptide in the				
6	biological sample by contacting the biological sample with an antibody, wherein the antibody				
7	specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to				
8	a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby				
9	monitoring the effica	cy of the therapy.			
1	20.	The method of claim 19, further comprising the step of: (iii) comparing			
2		cancer-associated polypeptide to a level of the lung cancer-associated			
3	polypeptide in a biol	ogical sample from the patient prior to, or earlier in, the therapeutic			
4	treatment.				
1	21.	The method of claim 19, wherein the patient is a human.			
1	22.	An isolated nucleic acid molecule consisting of a polynucleotide			
2	sequence as shown in	n Tables 1A-16.			
1	23.	The nucleic acid molecule of claim 22, which is labeled.			
1	24.	The nucleic acid of claim 23, wherein the label is a fluorescent label			
1	25.	An expression vector comprising the nucleic acid of claim 22.			
1	26.	A host cell comprising the expression vector of claim 25.			
1	27.	An isolated polypeptide which is encoded by a nucleic acid molecule			
2	having polynucleotic	le sequence as shown in Tables 1A-16.			
1	28.	An antibody that specifically binds a polypeptide of claim 27.			
1	29.	The antibody of claim 28, further conjugated to an effector component.			
1	30.	The antibody of claim 29, wherein the effector component is a			
2	fluorescent label.				
1	31.	The antibody of claim 29, wherein the effector component is a			
2	radioisotope or a cytotoxic chemical.				
1	32.	The antibody of claim 29, which is an antibody fragment.			

l	33.	The antibody of claim 29, which is a humanized antibody
ı	34.	A method of detecting a lung cancer cell in a biological sample from a
2	patient, the method c	omprising contacting the biological sample with an antibody of claim
3	28.	
l	35.	The method of claim 34, wherein the antibody is further conjugated to
2	an effector componer	nt.
	26	The method of claim 35, wherein the effector component is a
	36.	The method of claim 33, wherein the effector component is a
2	fluorescent label.	
1	37.	A method of detecting antibodies specific to lung cancer in a patient,
2	the method comprisis	ng contacting a biological sample from the patient with a polypeptide
3	encoded by a nucleic	acid comprises a sequence from Tables 1A-16.
	•	
1	38.	A method for identifying a compound that modulates a lung cancer-
2	associated polypeptic	le, the method comprising the steps of:
3	(i) con	ntacting the compound with a lung cancer-associated polypeptide, the
4	polypeptide encoded	by a polynucleotide that selectively hybridizes to a sequence at least
5	80% identical to a se	quence as shown in Tables 1A-16; and
5	(ii) de	termining the functional effect of the compound upon the polypeptide.
1	39.	The method of claim 38, wherein the functional effect is a physical
,	effect.	1.0
-	Official.	
i	40.	The method of claim 38, wherein the functional effect is a chemical
2	effect.	•
ł	41.	The method of claim 38, wherein the polypeptide is expressed in a
2	eukaryotic host cell c	or cell membrane.
l	42.	The method of claim 38, wherein the functional effect is determined by
2	measuring ligand bin	ding to the polypeptide.
	3 -	
i	43.	The method of claim 38, wherein the polypeptide is recombinant.

1	44. A method of inhibiting proliferation of a lung cancer-associated cell to				
2	treat lung cancer in a patient, the method comprising the step of administering to the subject				
3	therapeutically effective amount of a compound identified using the method of claim 38.				
1	45. The method of claim 44, wherein the compound is an antibody.				
1	46. The method of claim 45, wherein the patient is a human.				
1	47. A drug screening assay comprising the steps of				
2	(i) administering a test compound to a mammal having lung cancer or a cell				
3	isolated therefrom;				
4	(ii) comparing the level of gene expression of a polynucleotide that selectively				
5	hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16 in a				
6	treated cell or mammal with the level of gene expression of the polynucleotide in a control				
7	cell or mammal, wherein a test compound that modulates the level of expression of the				
8	polynucleotide is a candidate for the treatment of lung cancer.				
1	48. The assay of claim 47, wherein the control is a mammal with lung				
2	cancer or a cell therefrom that has not been treated with the test compound.				
1	49. The assay of claim 47, wherein the control is a normal cell or mammal				
1	50. A method for treating a mammal having lung cancer comprising				
2	administering a compound identified by the assay of claim 47.				
1	51. A pharmaceutiPcal composition for treating a mammal having lung				
2	cancer, the composition comprising a compound identified by the assay of claim 47 and a				
3	physiologically acceptable excipient.				

#### REVISED VERSION

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#### PATENT COOPERATION TREATY

# **PCT**

### DECLARATION OF NON-ESTABLISHMENT OF INTERNATIONAL SEARCH REPORT

(PCT Article 17(2)(a), Rule 13ter.1(c) and 39)

Applicant's or agent's file reference		I	Date of mailing (day/month/year)	
18501-15-3PC	IMPORTANT DECLARATION		15 AUG 2003	
International application No.	International filing date (day/	nonth/year) (	Earliest) Priority date (day/month/year)	
PCT/US02/12476	18 April 2002 (18.04.2002)	1	0 May 2001 (10.05.2001)	
International Patent Classification (IPC)	or both national classification a	nd IPC		
IPC(7): C07H 21/02, 21/04; C12Q 1/68	and US Ci.: 435/6, 536/23.1, 2	23.5		
Applicant				
EOS BIOTECHNOLOGY, INC	<del></del>		•	
a. scientific theories. b. mathematical theorie c. plant varieties. d. animal varieties. e. essential biological pand the products of schemes, rules or m schemes, rules or m schemes, rules or m i. methods for treatment i. methods for treatment.	upplication for the reasons indicernational application relates to:  es  processes for the production of such processes.  ethods of doing business.  ethods of performing purely methods of playing games.  not of the human body by surger not of the animal body by surger practised on the human or animal por animal processed on the human or animal processes.	plants and animals, or ental acts. y or therapy. y or therapy.	international search report  ther than microbiological processes	
m. Computer programs	for which this International Sea	rching Authority is no	ot equipped to search prior art.	
2. The failure of the following pa meaningful search from being	arts of the international applicat carried out:	ion to comply with pr	rescribed requirements prevents a	
the description	the claims	th	e drawings	
The failure of the nucleotide and/or amino acid sequence listing to comply with the standard provided for in Annex C of the Administrative Instructions prevents a meaningful search from being carried out:  the written form has not been furnished or does not comply with the standard.  the computer readable form has not been furnished or does not comply with the standard.				
4. Further comments:				
Nome and mailing all the control of		···		
Name and mailing address of the ISA/US Mail Stop PCT, Atm: ISA/US Commissioner for Patents P.O. Box 1450		Authorized officer  Carla Myers	Ca Can AND CARLA J. MYERS	
Alexandria, Virginia 22313-1450		Tolonhams No. 200	PRIMARY EXAMINER	
Facsimile No. (703)305-3230 orm PCT/ISA/203 (July 1998)	<del>,</del>	Telephone No. 703-	-308-0190	
(Suly 1990)				

#### PATENT COOPERATION TREATY

From the INTERNATIONAL SEARCHING AUTHORITY

To: TOWNSEND AND TOWNSEND AND CREW LLP TWO EMBARCADERO CENTER EIGHTH FLOOR SAN FRANCISCO, CA 94111-3834	PCT  NOTIFICATION OF TRANSMITTAL OF THE INTERNATIONAL SEARCH REPORT		
	OR THE DECLARATION (PCT Rule 44.1)		
	Date of Mailing (day/month/year) 15 AUG 2003		
Applicant's or agent's file reference			
18501-15-3PC	FOR FURTHER ACTION See paragraphs 1 and 4 below		
International application No. PCT/US02/12476	International filing date (day/month/year) 18 April 2002 (18.04.2002)		
Applicant EOS BIOTECHNOLOGY, INC	•		
The applicant is hereby notified that the international sear  Filing of amendments and statement under Article 19:	rch report has been established and is transmitted horewith.		
The applicant is entitled, if he so wishes, to amend the cl			
When? The time limit for filing such amendments i international search report,	s normally two months from the date of transmittal of the		
Where? Directly to the International Bureau of WIP 1211 Geneva 20, Switzerland, Facsimile No	0, 34, chemin des Colombettes b.: (41-22) 740.14.35		
For more detailed instructions, see the notes on the a	accompanying sheet.		
The applicant is hereby notified that no international search report will be established and that the declaration under Article 17(2)(a) to that effect is transmitted herewith.			
3. With regard to the protest against payment of (an) addi-	tional fee(s) under Rule 40.2, the applicant is notified that:		
	en transmitted to the International Buresu together with the protest and the decision thereon to the designated Offices.		
no decision has been made yet on the protest; the ap	plicant will be notified as soon as a decision is made.		
4. Reminders			
Shortly after 18 months from the priority date, the international application will be published by the International Bureau. If the applicant wishes to avoid or postpone publication, a notice of withdrawal of the international application, or of the priority claim, must reach the International Bureau as provided in Rules 90 bis.1 and 90 bis.3, respectively, before the completion of the technical preparations for international publication.			
examination must be filed if the applicant wishes to postpone the	t of some designated Offices, a demand for international preliminary to entry into the national phase until 30 months from the priority date thin 20 months from the priority date, perform the prescribed acts for		
In respect of other designated Offices, the time limit of 30 month	hs (or later) will apply even if no demand is filed within 19 months.		
See the Annex to Form PCT/IB/301 and, for details about the ap Volume II, National Chapters and the WIPO Internet site.	pplicable time limits, Office by Office, see the PCT Applicant's Guide,		
Name and mailing address of the ISA/US	Authorized officer		
Mail Stop PCT, Attn: ISA/US Commissioner for Patents	Dalerie Bell-Harrisfor		
P.O. Box 1450 Alexandria, Virginia 22313-1450	Telephone No. 703-308-0196		

F.O. Hox 1430
Alexandria, Virginia 22313-1450
Facsimile No. (703)305-3230
Form PCT/ISA/220 (April 2002)

(See notes on accompanying sheet)

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